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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*

For: "*Corynebacterium Glutamicum Genes Encoding Regulatory Proteins*"

Enclosed are:

- ☒ 60 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 5 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 11 pages of Table 4;
- ☒ 66 pages of Appendix A;
- ☒ 21 pages of Appendix B;
- ☒ 433 pages of Sequence Listing;
- ☒ Diskette Containing Sequence Listing;
- ☒ Transmittal Letter for Diskette Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney; and
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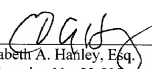
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***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING REGULATORY
PROTEINS**

Related Applications

- 5 This application claims priority to U.S. Provisional Patent Application No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application No. 60/142690, filed July 1, 1999, and also to U.S. Provisional Patent Application No. 60/151251, filed August 27, 1999. This application also claims priority to German Patent Application No. 19930476.9, filed July 1, 1999, German Patent Application No. 19931419.5, filed 10 July 8, 1999, German Patent Application No. 19931420.9, filed July 8, 1999, German Patent Application No. 19932122.1, filed July 9, 1999, German Patent Application No. 19932128.0, filed July 9, 1999, German Patent Application No. 19932134.5, filed July 9, 1999, German Patent Application No. 19932206.6, filed July 9, 1999, German Patent Application No. 19932207.4, filed July 9, 1999, German Patent Application No. 15 19933003.4, filed July 14, 1999, German Patent Application No. 19941390.8, filed August 31, 1999, German Patent Application No. 19942088.2, filed September 3, 1999, and German Patent Application No. 19942124.2, filed September 3, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein by this reference.

20

Background of the Invention

- Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', 25 include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful 30 organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

35

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C.*

- 5 *glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as metabolic regulatory (MR) proteins.

- C. glutamicum* is a gram positive, aerobic bacterium which is commonly used in
10 industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The MR nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, e.g., by fermentation processes. Modulation of the expression of the MR nucleic acids of the
15 invention, or modification of the sequence of the MR nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (e.g., to improve the yield or production of one or more fine chemicals from a *Corynebacterium* or *Brevibacterium* species).

- The MR nucleic acids of the invention may also be used to identify an organism
20 as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a
25 region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

- 30 The MR nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered *Corynebacterium* or *Brevibacterium* species.
e.g., . The MR proteins encoded by the novel nucleic acid molecules of the invention
35 are capable of, for example, performing a function involved in the transcriptional, translational, or posttranslational regulation of proteins important for the normal metabolic functioning of cells. Given the availability of cloning vectors for use in

- Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (e.g., *lactofermentum*) (Yoshihama *et al.*, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals.

This improved yield, production and/or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation. Specifically, alterations in *C. glutamicum* MR proteins which normally regulate the yield, production and/or efficiency of production of a fine chemical metabolic pathways may have a direct impact on the overall production or rate of production of one or more of these desired compounds from this organism. Alterations in the proteins involved in these metabolic pathways may also have an indirect impact on the yield, production and/or efficiency of production of a desired fine chemical. Regulation of metabolism is necessarily complex, and the regulatory mechanisms governing different pathways may intersect at multiple points such that more than one pathway can be rapidly adjusted in accordance with a particular cellular event. This enables the modification of a regulatory protein for one pathway to have an impact on the regulation of many other pathways as well, some of which may be involved in the biosynthesis or degradation of a desired fine chemical. In this indirect fashion, the modulation of action of an MR protein may have an impact on the production of a fine chemical produced by a pathway different from one which that MR protein directly regulates.

- The nucleic acid and protein molecules of the invention may be utilized to directly improve the yield, production, and/or efficiency of production of one or more desired fine chemicals from *Corynebacterium glutamicum*. Using recombinant genetic techniques well known in the art, one or more of the regulatory proteins of the invention may be manipulated such that its function is modulated. For example, the mutation of an MR protein involved in the repression of transcription of a gene encoding an enzyme which is required for the biosynthesis of an amino acid such that it no longer is able to repress transcription may result in an increase in production of that amino acid. Similarly, the alteration of activity of an MR protein resulting in increased translation or activating posttranslational modification of a *C. glutamicum* protein involved in the biosynthesis of a desired fine chemical may in turn increase the production of that chemical. The opposite situation may also be of benefit: by increasing the repression of transcription or translation, or by posttranslational negative modification of a *C.*

glutamicum protein involved in the regulation of a degradative pathway for a compound, one may increase the production of this chemical. In each case, the overall yield or rate of production of the desired fine chemical may be increased.

- It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the yield, production, and/or efficiency of production of fine chemicals through indirect mechanisms. The metabolism of any one compound is necessarily intertwined with other biosynthetic and degradative pathways within the cell, and necessary cofactors, intermediates, or substrates in one pathway are likely supplied or limited by another such pathway. Therefore, by modulating the activity of one or more of the regulatory proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. Further, the manipulation of one or more regulatory proteins may increase the overall ability of the cell to grow and multiply in culture, particularly in large-scale fermentative culture, where growth conditions may be suboptimal. For example, by mutating an MR protein of the invention which would normally cause a repression in the biosynthesis of nucleotides in response to suboptimal extracellular supplies of nutrients (thereby preventing cell division) such that it is decreased in repressor ability, one may increase the biosynthesis of nucleotides and perhaps increase cell division. Changes in MR proteins which result in increased cell growth and division in culture may result in an increase in yield, production, and/or efficiency of production of one or more desired fine chemicals from the culture, due at least to the increased number of cells producing the chemical in the culture.

- The invention provides novel nucleic acid molecules which encode proteins, referred to herein as metabolic pathway proteins (MR), which are capable of, for example, performing an enzymatic step involved in the transcriptional, translational, or posttranslational regulation of metabolic pathways in *C. glutamicum*. Nucleic acid molecules encoding an MR protein are referred to herein as MR nucleic acid molecules. In a preferred embodiment, the MR protein participates in the transcriptional, translational, or posttranslational regulation of one or more metabolic pathways. Examples of such proteins include those encoded by the genes set forth in Table 1.

- Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (e.g., cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an MR protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of MR-encoding nucleic acid (e.g., DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide

sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred MR proteins of the present invention also preferably possess at least one of the MR activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, *e.g.*, sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an MR activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (*e.g.*, an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an MR fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* MR protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an MR protein by culturing the host cell in a suitable medium. The MR protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an MR gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated MR sequence as a transgene. In another embodiment, an endogenous MR gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered MR gene. In another embodiment, an endogenous or introduced MR gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MR protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an MR gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the MR gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated MR protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated MR protein or portion thereof transcriptionally, translationally, or posttranslationally regulates one or more metabolic pathways in *C. glutamicum*. In another preferred embodiment, the isolated MR protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to transcriptionally, translationally, or posttranslationally regulate one or more metabolic pathways in *C. glutamicum*.

The invention also provides an isolated preparation of an MR protein. In preferred embodiments, the MR protein comprises an amino acid sequence of Appendix

B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated MR protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to transcriptionally, translationally, or posttranslationally regulate one or more metabolic pathways in *C. glutamicum*, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated MR protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of MR proteins also have one or more of the MR bioactivities described herein.

The MR polypeptide, or a biologically active portion thereof, can be operatively linked to a non-MR polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the MR protein alone. In other preferred embodiments, this fusion protein transcriptionally, translationally, or posttranslationally regulates one or more metabolic pathways in *C. glutamicum*. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an MR protein, either by interacting with the protein itself or a substrate or binding partner of the MR protein, or by modulating the transcription or translation of an MR nucleic acid molecule of the invention. Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an MR nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an MR nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment,

the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates MR protein activity or MR nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* metabolic pathway regulatory systems, such that the yields or rate of production of a desired fine chemical by this microorganism is improved. The agent which modulates MR protein activity can be an agent which stimulates MR protein activity or MR nucleic acid expression. Examples of agents which stimulate MR protein activity or MR nucleic acid expression include small molecules, active MR proteins, and nucleic acids encoding MR proteins that have been introduced into the cell. Examples of agents which inhibit MR activity or expression include small molecules and antisense MR nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant MR gene into a cell, either maintained on a separate plasmid or integrated into the genome of the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides MR nucleic acid and protein molecules which are involved in the regulation of metabolism in *Corynebacterium glutamicum*, including regulation of fine chemical metabolism. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (e.g., where modulation of the activity of a lysine biosynthesis regulatory protein has a direct impact on the yield, production, and/or efficiency of production of lysine from that organism), or may have an indirect impact which nonetheless results in an increase in yield, production, and/or efficiency of production of the desired compound (e.g., where modulation of the regulation of a nucleotide biosynthesis protein has an impact on the production of an organic acid or a

fatty acid from the bacterium, perhaps due to concomitant regulatory alterations in the biosynthetic or degradation pathways for these chemicals in response to the altered regulation of nucleotide biosynthesis). Aspects of the invention are further explicated below.

5

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in *Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCs Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) *Chemicals by Fermentation*, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. Amino Acid Metabolism and Uses

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ullmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids

have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. *Biochemistry*, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine, valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/L-methionine are common feed additives. (Leuchtenberger, W. (1996) *Amino acids - technical production and use*, p. 466-502 in Rehm *et al.* (eds.) *Biotechnology* vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's *Encyclopedia of Industrial Chemistry*, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E. (1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α -ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β -carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase.

Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. *Biochemistry* 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them. Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. *Biochemistry*, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's *Encyclopedia of Industrial Chemistry*, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins

- may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements
- 5 having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (e.g., polyunsaturated fatty acids).

- The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial
- 10 Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research - Asia, held Sept.
- 15 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

- Thiamin (vitamin B₁) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B₂) is synthesized from guanosine-5'-triphosphate (GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of
- 20 compounds collectively termed 'vitamin B₆' (e.g., pyridoxine, pyridoxamine, pyridoxal-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate
- 25 biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to pantothenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the
- 30 precursors of Coenzyme A. These enzymes not only catalyze the formation of pantothenate, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B₅), pantetheine (and its derivatives) and coenzyme A.

- Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been
- 35 identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it

becomes part of the pyruvate dehydrogenase complex and the α -ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which in turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B₁₂) and porphyrins belong to a group of chemicals characterized by a tetrapyrrole ring system. The biosynthesis of vitamin B₁₂ is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B₆, pantothenate, and biotin. Only Vitamin B₁₂ is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (e.g. Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (e.g., thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (e.g., ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (e.g., IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) *Nucleotides and Related Compounds in Biotechnology* vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: *Progress in Nucleic Acid Research and Molecular Biology*, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

- Trehalose consists of two glucose molecules, bound in α, α -1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) *J. Japan* 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Mechanisms of Metabolic Regulation

- All living cells have complex catabolic and anabolic metabolic capabilities with many interconnected pathways. In order to maintain a balance between the various parts of this extremely complex metabolic network, the cell employs a finely-tuned regulatory network. By regulating enzyme synthesis and enzyme activity, either independently or simultaneously, the cell is able to control the activity of disparate metabolic pathways to reflect the changing needs of the cell.

- The induction or repression of enzyme synthesis may occur at either the level of transcription or translation, or both. Gene expression in prokaryotes is regulated by several mechanisms at the level of transcription (for review see *e.g.*, Lewin, B (1990) *Genes IV*, Part 3: "Controlling prokaryotic genes by transcription", Oxford University Press: Oxford, p. 213-301, and references therein, and Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley & Sons). All such known regulatory processes are mediated by additional genes, which themselves respond to external influences of various kinds (*e.g.*, temperature, nutrient availability, or light). Exemplary protein factors which have been implicated in this type of regulation include the transcription factors. These are proteins which bind to DNA, thereby either increasing the expression of a gene (positive regulation, as in the case of *e.g.* the *ara* operon from *E. coli*) or decreasing gene expression (negative regulation, as in the case of the *lac* operon from *E. coli*). These expression-modulating transcription factors can themselves be the subject of regulation. Their activity can, for example, be regulated by the binding of low molecular weight compounds to the DNA-binding protein, thereby stimulating (as in the case of arabinose for the *ara* operon) or inhibiting (as in the case of the lactose for the *lac* operon) the binding of these proteins to the appropriate binding site on the DNA (see, for example, Helmann, J.D. and Chamberlin, M.J. (1988) "Structure and function of bacterial sigma factors." *Ann. Rev. Biochem.* 57:

- 839-872; Adhya, S. (1995) "The lac and gal operons today" and Boos, W. *et al.*, "The maltose system.", both in: Regulation of Gene Expression in *Escherichia coli* (Lin, E.C.C. and Lynch, A.S., eds.) Chapman & Hall: New York, p. 181-200 and 201-229; and Moran, C.P. (1993) "RNA polymerase and transcription factors." in: *Bacillus subtilis* and other gram-positive bacteria, Sonenshein, A.L. *et al.*, eds. ASM: Washington, D.C., p. 653-667.)

- Aside from the transcriptional level, protein synthesis is also often regulated at the level of translation. There are multiple mechanisms by which such regulation may occur, including alteration of the ability of the ribosome to bind to one or more mRNAs, binding of the ribosome to the mRNA, the maintenance or removal of mRNA secondary structure, the utilization of common or less common codons for a particular gene, the degree of abundance of one or more tRNAs, and special regulation mechanisms, such as attenuation (see Vellanoweth, R.I. (1993) Translation and its regulation in *Bacillus subtilis* and other gram-positive bacteria, Sonenshein, A.L. *et al.*, eds. ASM: Washington, D.C., p. 699-711 and references cited therein).

- Transcriptional and translational regulation may be targeted to a single protein (sequential regulation) or simultaneously to several proteins in different metabolic pathways (coordinate regulation). Often, genes whose expression is coordinately regulated are physically located near one another in the genome, in an operon or regulon. Such up- or down-regulation of gene transcription and translation is governed by the cellular and extracellular levels of various factors, such as substrates (precursor and intermediate molecules used in one or more metabolic pathways), catabolites (molecules produced by biochemical pathways concerned with the production of energy from the breakdown of complex organic molecules such as sugars), and end products (the molecules resulting at the end of a metabolic pathway). Typically, the expression of genes encoding enzymes necessary for the activity of a particular pathway is induced by high levels of substrate molecules for that pathway. Similarly, such gene expression tends to be repressed when there exist high intracellular levels of the end product of the pathway (Snyder, L. and Champness, W. (1997) *The Molecular Biology of Bacteria* ASM: Washington). Gene expression may also be regulated by other external and internal factors, such as environmental conditions (e.g., heat, oxidative stress, or starvation). These global environmental changes cause alterations in the expression of specialized modulating genes, which directly or indirectly (via additional genes or proteins) trigger the expression of genes by means of binding to DNA and thereby inducing or repressing transcription (see, for example, Lin, E.C.C. and Lynch, A.S., eds. (1995) *Regulation of Gene Expression in Escherichia coli*. Chapman & Hall: New York).

Yet another mechanism by which cellular metabolism may be regulated is at the level of the protein. Such regulation is accomplished either by the activities of other proteins, or by binding of low-molecular-weight components which either impede or enable the normal functioning of the protein. Examples of protein regulation by the binding of low-molecular-weight compounds include the binding of GTP or NAD. The binding of a low-molecular-weight chemical is typically reversible, as is the case with the GTP-binding proteins. These proteins exist in two stages (with bound GTP or GDP), one stage being the activated form of the protein, and one stage being inactive.

Regulation of protein activity by the action of other enzymes typically takes the form of covalent modification of the protein (*i.e.*, phosphorylation of amino acid residues such as histidine or aspartate, or methylation). Such covalent modification is typically reversible, as mediated by an enzyme of the opposite activity. An example of this is the opposite activities of kinases and phosphorylases in protein phosphorylation; protein kinases phosphorylate specific residues on a target protein (*e.g.*, serine or threonine), while protein phosphorylases remove phosphate groups from such proteins. Typically, enzymes which modulate the activity of other proteins are themselves modulated by external stimuli. These stimuli are mediated through proteins which function as sensors. A well known mechanism by which such sensor proteins may mediate these external signals is by dimerization, but others are also known (see, for example, Msadek, T. *et al.* (1993) "Two-Component Regulatory Systems", in: *Bacillus subtilis* and Other Gram-Positive Bacteria, Sonenshein, A.L. *et al.*, eds., ASM: Washington p. 729-745 and references cited therein).

A thorough understanding of the regulatory networks governing cellular metabolism in microorganisms is critical for the high-yield production of chemicals by fermentation. Control systems for the down-regulation of metabolic pathways could be removed or lessened to improve the synthesis of desired chemicals, and similarly, those for the up-regulation of metabolic pathways for a desired product could be constitutively activated or optimized in activity (As shown in Hirose, Y. and Okada, H. (1979) "Microbial Production of Amino Acids", in: Peppler, H.J. and Perlman, D. (eds.) *Microbial Technology* 2nd ed. Vol. 1, ch. 7 Academic Press: New York.)

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as MR nucleic acid and protein molecules, which regulate, by transcriptional, translational, or post-translational means, one or more metabolic pathways in *C. glutamicum*. In one embodiment, the MR molecules transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. In

- a preferred embodiment, the activity of the MR molecules of the present invention to regulate one or more *C. glutamicum* metabolic pathways has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the MR molecules of the invention are modulated in activity, such that the
- 5 *C. glutamicum* metabolic pathways which the MR proteins of the invention regulate are modulated in efficiency or output, which either directly or indirectly modulates the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

- The language, "MR protein" or "MR polypeptide" includes proteins which
- 10 transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. Examples of MR proteins include those encoded by the MR genes set forth in Table 1 and Appendix A. The terms "MR gene" or "MR nucleic acid sequence" include nucleic acid sequences encoding an MR protein, which consist of a coding region and also corresponding untranslated 5' and 3' sequence regions. Examples of MR
- 15 genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (e.g., kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long
- 20 it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (i.e., fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered
- 25 molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the
- 30 breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (e.g., the metabolism of an amino acid
- 35 such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The term, "regulation" is art-recognized and includes the activity of a protein to govern the activity of another protein. The term,

“transcriptional regulation” is art-recognized and includes the activity of a protein to impede or activate the conversion of a DNA encoding a target protein to mRNA. The term, “translational regulation” is art-recognized and includes the activity of a protein to impede or activate the conversion of an mRNA encoding a target protein to a protein molecule. The term, “posttranslational regulation” is art-recognized and includes the activity of a protein to impede or improve the activity of a target protein by covalently modifying the target protein (e.g., by methylation, glucosylation, or phosphorylation).

In another embodiment, the MR molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a microorganism such as *C. glutamicum*. Using recombinant genetic techniques, one or more of the regulatory proteins of the invention for metabolic pathways may be manipulated such that its function is modulated. For example, a biosynthetic enzyme may be improved in efficiency, or its allosteric control region destroyed such that feedback inhibition of production of the compound is prevented. Similarly, a degradative enzyme may be deleted or modified by substitution, deletion, or addition such that its degradative activity is lessened for the desired compound without impairing the viability of the cell. In each case, the overall yield or rate of production of one of these desired fine chemicals may be increased.

It is also possible that such alterations in the protein and nucleotide molecules of the invention may improve the production of fine chemicals in an indirect fashion. The regulatory mechanisms of metabolic pathways in the cell are necessarily intertwined, and the activation of one pathway may lead to the repression or activation of another in a concomitant fashion. Therefore, by modulating the activity of one or more of the proteins of the invention, the production or efficiency of activity of another fine chemical biosynthetic or degradative pathway may be impacted. For example, by decreasing the ability of an MR protein to repress the transcription of a gene encoding a particular amino acid biosynthetic protein, one may concomitantly derepress other amino acid biosynthetic pathways, since these pathways are interrelated. Further, by modifying the MR proteins of the invention, one may uncouple the growth and division of cells from their extracellular surroundings to a certain degree; by impairing an MR protein which normally represses biosynthesis of a nucleotide when the extracellular conditions are suboptimal for growth and cell division such that it now lacks this function, one may permit growth to occur even when the extracellular conditions are poor. This is of particular relevance in large-scale fermentative growth, where conditions within the culture are often suboptimal in terms of temperature, nutrient supply or aeration, but would still support growth and cell division if the cellular regulatory systems for these factors were eliminated.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* MR DNAs and the predicted amino acid sequences of the *C.*

- 5 *glutamicum* MR proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode metabolic pathway regulatory proteins.

- The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B.
- 10 As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, e.g., the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%,
- 15 and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

- The MR protein or a biologically active portion or fragment thereof of the invention can transcriptionally, translationally, or posttranslationally regulate a
- 20 metabolic pathway in *C. glutamicum*, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections:

25 *A. Isolated Nucleic Acid Molecules*

- One aspect of the invention pertains to isolated nucleic acid molecules that encode MR polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of MR-encoding nucleic acid (e.g., MR DNA). As used herein, the term
- 30 "nucleic acid molecule" is intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20
- 35 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated

from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated MR nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (*e.g.*, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* MR DNA can be isolated from a *C. glutamicum* library using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an MR nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* MR DNAs of the invention. This DNA comprises sequences encoding MR proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA, RXN, or RXS number having the designation "RXA", "RXN", or "RXS" followed by 5 digits (*i.e.*, RXA00603, RXN03181, or RXS00686). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, or RXS designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA, RXN, or RXS designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA, RXN, or RXS designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequences in Appendix B designated RXA00603, RXN03181, and RXS00686 are translations of the coding regions of the nucleotide sequence of nucleic acid molecules RXA00603, RXN03181, and RXS00686, respectively, in Appendix A. Each of the RXA, RXN, and RXS nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1. For example, as shown in Table 1, the nucleotide sequence of RXA00603 is SEQ ID NO:5 and the amino acid sequence of RXA00603 is SEQ ID NO: 6.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, or RXS designation. For example, SEQ ID NO:3, designated, as indicated on Table 1, as "F RXA02880", is an F-designated gene, as are SEQ ID NOs: 21, 27, and 33 (designated on Table 1 as "F RXA02493", "F RXA00291", and "F RXA00651", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is

significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

- In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

- In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

- Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an MR protein. The nucleotide sequences determined from the cloning of the MR genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning MR homologues in other cell types and organisms, as well as MR homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in

Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone MR homologues. Probes based on the MR nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred
5 embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an MR protein, such as by measuring a level of an MR-encoding nucleic acid in a sample of cells, *e.g.*, detecting MR mRNA levels or determining
10 whether a genomic MR gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to transcriptionally, translationally, or posttranslationally
15 regulate a metabolic pathway in *C. glutamicum*. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix
20 B such that the protein or portion thereof is able to transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. Protein members of such metabolic pathways, as described herein, may function to regulate the biosynthesis or degradation of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an MR protein" contributes to the overall
25 regulation of one or more fine chemical metabolic pathway, or contributes, either directly or indirectly, to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of MR protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most
30 preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

Portions of proteins encoded by the MR nucleic acid molecules of the invention are preferably biologically active portions of one of the MR proteins. As used herein, the term "biologically active portion of an MR protein" is intended to include a portion,
35 *e.g.*, a domain/motif, of an MR protein that transcriptionally, translationally, or posttranslationally regulates a metabolic pathway in *C. glutamicum*, or has an activity as set forth in Table 1. To determine whether an MR protein or a biologically active

portion thereof can transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*, an assay of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

- 5 Additional nucleic acid fragments encoding biologically active portions of an MR protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the MR protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the MR protein or peptide.

- 10 The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same MR protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

- 20 It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00603 (SEQ ID NO:5), a nucleotide sequence which is greater than and/or at least 55% identical to the nucleotide sequence designated RXA00129 (SEQ ID NO:29), and a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00006 (SEQ ID NO:35). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%,
- 35

- 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

- In addition to the *C. glutamicum* MR nucleotide sequences shown in Appendix A, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of MR proteins may exist within a population (e.g., the *C. glutamicum* population). Such genetic polymorphism in the MR gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an MR protein, preferably a *C. glutamicum* MR protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the MR gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in MR that are the result of natural variation and that do not alter the functional activity of MR proteins are intended to be within the scope of the invention.

- Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* MR DNA of the invention can be isolated based on their homology to the *C. glutamicum* MR nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under

stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein). In one embodiment, the nucleic acid encodes a natural

5 C. *glutamicum* MR protein.

In addition to naturally-occurring variants of the MR sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded MR protein, without altering the functional ability of the MR protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the MR proteins (Appendix B) without altering the activity of said MR protein, whereas an "essential" amino acid residue is required for MR protein activity. Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having MR activity) may not be essential for activity and thus are likely to be amenable to alteration without altering MR activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding MR proteins that contain changes in amino acid residues that are not essential for MR activity. Such MR proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the MR activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is capable of transcriptionally, translationally, or posttranslationally regulating a metabolic pathway in *C. glutamicum*, or has one or more activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (e.g., one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein

or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence (e.g., one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (e.g., a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (i.e., as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % homology = # of identical positions/total # of positions x 100).

10 An isolated nucleic acid molecule encoding an MR protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an MR protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an MR coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an MR activity described herein to identify mutants that retain MR activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

35 In addition to the nucleic acid molecules encoding MR proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is

complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire MR coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an MR protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO:1(RXN03181) comprises nucleotides 1 to 414). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding MR. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding MR disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of MR mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of MR mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of MR mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-

isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the
5 antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered
10 to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an MR protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through
15 specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve
20 sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms
25 specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a
30 ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to
35 catalytically cleave MR mRNA transcripts to thereby inhibit translation of MR mRNA. A ribozyme having specificity for an MR-encoding nucleic acid can be designed based upon the nucleotide sequence of an MR DNA disclosed herein (*i.e.*, SEQ ID NO:1

(RXN03181 in Appendix A)). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an MR-encoding mRNA. See, e.g., Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No.

- 5 5,116,742. Alternatively, MR mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

- Alternatively, MR gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an MR nucleotide sequence (e.g.,
10 an MR promoter and/or enhancers) to form triple helical structures that prevent transcription of an MR gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

15 *B. Recombinant Expression Vectors and Host Cells*

- Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an MR protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid",
20 which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other
25 vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are
30 often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

- 35 The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory

sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as *cos*-, *tac*-, *trp*-, *tet*-, *trp-tet*-, *lpp*-, *lac*-, *lpp-lac*-, *lacI^q*-, *T7*-, *T5*-, *T3*-, *gal*-, *trc*-, *ara*-, *SP6*-, *amy*-, *SPO2*-, λ -*P_R*- or λ *P_L*-, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as *ADC1*, *MFa*, *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH*, promoters from plants such as *CaMV/35S*, *SSU*, *OCS*, *lib4*, *usp*, *STLS1*, *B33*, *nos* or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by one of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (e.g., MR proteins, mutant forms of MR proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of MR proteins in prokaryotic or eukaryotic cells. For example, MR genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* -mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells.

Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

- 5 Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein;
- 10 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes,
- 15 and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

- Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant
- 20 protein. In one embodiment, the coding sequence of the MR protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant MR protein unfused to GST can be recovered by cleavage of the fusion
- 25 protein with thrombin.

- Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λ gt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; and
- 30 Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by
- 35 a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation

- of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming *Streptomyces*, while plasmids pUB110, pC194, or pBD214 are suited for transformation of *Bacillus* species. Several plasmids of use in the transfer of genetic information into
- 5 *Corynebacterium* include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York ISBN 0 444 904018). One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San
- 10 Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be
- 15 carried out by standard DNA synthesis techniques.

- In another embodiment, the MR protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ , pAG-1, Yep6, Yep13, pEMBLYe23, pMfa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge
- 20 University Press: Cambridge, and Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York (ISBN 0 444 904018).

- Alternatively, the MR proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf9 cells) include the pAc series (Smith *et al.*
- 30 (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

- In another embodiment, the MR proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include
- 35 those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for

plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) *Cloning Vectors*. Elsevier: New York IBSN 0 444 904018).

- In yet another embodiment, a nucleic acid of the invention is expressed in
- 5 mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2,
- 10 cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual*. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.
- 15 In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.*
- 20 (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477),
- 25 pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).
- 30

- The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an
- 35 RNA molecule which is antisense to MR mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for

instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an MR protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to one of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., linear DNA or RNA (e.g., a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (e.g., a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (e.g., resistance to antibiotics) is

generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an MR protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (e.g., cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an MR gene into which a deletion, addition or substitution has been introduced to thereby alter, e.g., functionally disrupt, the MR gene. Preferably, this MR gene is a *Corynebacterium glutamicum* MR gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous MR gene is functionally disrupted (i.e., no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous MR gene is mutated or otherwise altered but still encodes functional protein (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous MR protein). In the homologous recombination vector, the altered portion of the MR gene is flanked at its 5' and 3' ends by additional nucleic acid of the MR gene to allow for homologous recombination to occur between the exogenous MR gene carried by the vector and an endogenous MR gene in a microorganism. The additional flanking MR nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see e.g., Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (e.g., by electroporation) and cells in which the introduced MR gene has homologously recombined with the endogenous MR gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an MR gene on a vector placing it under control of the lac operon permits expression of the MR gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous MR gene in a host cell is disrupted (e.g., by homologous recombination or other genetic means known in the art) such that expression of its protein product does not occur. In another embodiment, an endogenous

or introduced MR gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional MR protein. In still another embodiment, one or more of the regulatory regions (e.g., a promoter, repressor, or inducer) of an MR gene in a microorganism has been altered (e.g., by deletion, truncation, inversion, or point mutation) such that the expression of the MR gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described MR gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

10 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) an MR protein. Accordingly, the invention further provides methods for producing MR proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an MR protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or
15 altered MR protein) in a suitable medium until MR protein is produced. In another embodiment, the method further comprises isolating MR proteins from the medium or the host cell.

20 C. Isolated MR Proteins

Another aspect of the invention pertains to isolated MR proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when
25 chemically synthesized. The language "substantially free of cellular material" includes preparations of MR protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of MR protein having less than about 30% (by dry weight) of non-MR protein (also referred to herein
30 as a "contaminating protein"), more preferably less than about 20% of non-MR protein, still more preferably less than about 10% of non-MR protein, and most preferably less than about 5% non-MR protein. When the MR protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than
35 about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of MR protein in which the protein is separated from

chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of MR protein having less than about 30% (by dry weight) of chemical precursors or non-MR chemicals, more preferably less than
5 about 20% chemical precursors or non-MR chemicals, still more preferably less than about 10% chemical precursors or non-MR chemicals, and most preferably less than about 5% chemical precursors or non-MR chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the MR protein is derived. Typically, such proteins are
10 produced by recombinant expression of, for example, a *C. glutamicum* MR protein in a microorganism such as *C. glutamicum*.

An isolated MR protein or a portion thereof of the invention can transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*, or has one or more of the activities set forth in Table 1. In preferred
15 embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*. The portion of the protein is preferably a biologically active portion as described herein. In another
20 preferred embodiment, an MR protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the MR protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, e.g., hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still
25 another preferred embodiment, the MR protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about
30 95%, 96%, 97%, 98%, 99% or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (e.g., 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended
35 to be included. The preferred MR proteins of the present invention also preferably possess at least one of the MR activities described herein. For example, a preferred MR protein of the present invention includes an amino acid sequence encoded by a

nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which can transcriptionally, translationally, or posttranslationally regulate a metabolic pathway in *C. glutamicum*, or which has one or more of the activities set forth in Table 1.

5 In other embodiments, the MR protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the MR protein is a protein which comprises an amino acid sequence
10 which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more
15 homologous to an entire amino acid sequence of Appendix B and which has at least one of the MR activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are
20 intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

Biologically active portions of an MR protein include peptides comprising amino acid sequences derived from the amino acid sequence of an MR protein, *e.g.*, the amino acid sequence shown in Appendix B or the amino acid sequence of a protein
25 homologous to an MR protein, which include fewer amino acids than a full length MR protein or the full length protein which is homologous to an MR protein, and exhibit at least one activity of an MR protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or
30 more amino acids in length) comprise a domain or motif with at least one activity of an MR protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an MR protein include one or more selected domains/motifs or portions thereof having
35 biological activity.

MR proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression

vector (as described above), the expression vector is introduced into a host cell (as described above) and the MR protein is expressed in the host cell. The MR protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an MR protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native MR protein can be isolated from cells (e.g., endothelial cells), for example using an anti-MR antibody, which can be produced by standard techniques utilizing an MR protein or fragment thereof of this invention.

The invention also provides MR chimeric or fusion proteins. As used herein, an MR "chimeric protein" or "fusion protein" comprises an MR polypeptide operatively linked to a non-MR polypeptide. An "MR polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an MR protein, whereas a "non-MR polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the MR protein, e.g., a protein which is different from the MR protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the MR polypeptide and the non-MR polypeptide are fused in-frame to each other. The non-MR polypeptide can be fused to the N-terminus or C-terminus of the MR polypeptide. For example, in one embodiment the fusion protein is a GST-MR fusion protein in which the MR sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant MR proteins. In another embodiment, the fusion protein is an MR protein containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression and/or secretion of an MR protein can be increased through use of a heterologous signal sequence.

Preferably, an MR chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel

et al. John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An MR-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the MR protein.

- 5 Homologues of the MR protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the MR protein. As used herein, the term "homologue" refers to a variant form of the MR protein which acts as an agonist or antagonist of the activity of the MR protein. An agonist of the MR protein can retain substantially the same, or a subset, of the biological activities of the MR protein. An antagonist of the
- 10 MR protein can inhibit one or more of the activities of the naturally occurring form of the MR protein, by, for example, competitively binding to a downstream or upstream member of the MR regulatory cascade which includes the MR protein. Thus, the *C. glutamicum* MR protein and homologues thereof of the present invention may modulate the activity of one or more metabolic pathways which MR proteins regulate in this
- 15 microorganism.

- In an alternative embodiment, homologues of the MR protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the MR protein for MR protein agonist or antagonist activity. In one embodiment, a variegated library of MR variants is generated by combinatorial mutagenesis at the nucleic acid
- 20 level and is encoded by a variegated gene library. A variegated library of MR variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential MR sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of MR sequences therein.
- 25 There are a variety of methods which can be used to produce libraries of potential MR homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding
- 30 the desired set of potential MR sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477).

- In addition, libraries of fragments of the MR protein coding can be used to
- 35 generate a variegated population of MR fragments for screening and subsequent selection of homologues of an MR protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an

MR coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by
5 treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the MR protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA
10 libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of MR homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of
15 vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify MR homologues (Arkin and Yourvan (1992) *PNAS*
20 89:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated MR library, using methods well known in the art.

D. Uses and Methods of the Invention

25 The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of MR protein
30 regions required for function; modulation of an MR protein activity; modulation of the activity of one or more metabolic pathways; and modulation of cellular production of a desired compound, such as a fine chemical.

The MR nucleic acid molecules of the invention have a variety of uses. First, they may be used to identify an organism as being *Corynebacterium glutamicum* or a
35 close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the

extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present.

Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Corynebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (e.g., the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in *C. glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The MR nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The metabolic processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the MR nucleic acid molecules of the invention may result in the production of MR proteins having functional differences from the wild-type MR proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an MR protein, either by interacting with the protein itself or a substrate or binding partner of the MR protein, or by modulating the transcription or translation of an MR nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more MR proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the MR protein is assessed.

Such changes in activity may directly modulate the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, by optimizing the activity of an MR protein which activates the transcription or translation of a gene encoding a biosynthetic protein for a desired fine chemical, or by impairing or abrogating the activity of an MR protein which represses the transcription or translation of such a gene, one may also increase the activity or rate of activity of that biosynthetic pathway due to the presence of increased levels of what may have been a limiting enzyme. Similarly, by altering the activity of an MR protein such that it constitutively posttranslationally inactivates a protein involved in a degradation pathway for a desired fine chemical, or by altering the activity of an MR protein such that it constitutively represses the transcription or translation of such a gene, one may increase the yield and/or rate of production of the fine chemical from the cell, due to decreased degradation of the compound.

Further, by modulating the activity of one or more MR proteins, one may indirectly stimulate the production or improve the rate of production of one or more fine

chemicals from the cell due to the interrelatedness of disparate metabolic pathways. For example, by increasing the yield, production, and/or efficiency of production by activating the expression of one or more lysine biosynthetic enzymes, one may concomitantly increase the expression of other compounds, such as other amino acids, which the cell would naturally require in greater quantities when lysine is required in greater quantities. Also, regulation of metabolism throughout the cell may be altered such that the cell is better able to grow or replicate under the environmental conditions of fermentative culture (where nutrient and oxygen supplies may be poor and possibly toxic waste products in the environment may be at high levels). For example, by mutagenizing an MR protein which represses the synthesis of molecules necessary for cell membrane production in response to high levels of waste products in the extracellular medium (in order to block cell growth and division in suboptimal growth conditions) such that it no longer is able to repress such synthesis, one may increase the growth and multiplication of the cell in cultures even when the growth conditions are suboptimal. Such enhanced growth or viability should also increase the yields and/or rate of production of a desired fine chemical from fermentative culture, due to the relatively greater number of cells producing this compound in the culture.

The aforementioned mutagenesis strategies for MR proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated MR nucleic acid and protein molecules such that the yield and/or efficiency of production of a desired compound is improved. This desired compound may be any natural product of *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

- 5 A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose,
- 10 2.46 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l NaCl, 2 g/l $\text{MgSO}_4 \times 7\text{H}_2\text{O}$, 0.2 g/l CaCl_2 , 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $\text{FeSO}_4 \times \text{H}_2\text{O}$, 10 mg/l $\text{ZnSO}_4 \times 7\text{H}_2\text{O}$, 3 mg/l $\text{MnCl}_2 \times 4\text{H}_2\text{O}$, 30 mg/l H_3BO_3 , 20 mg/l $\text{CoCl}_2 \times 6\text{H}_2\text{O}$, 1 mg/l $\text{NiCl}_2 \times 6\text{H}_2\text{O}$, 3 mg/l $\text{Na}_2\text{MoO}_4 \times 2\text{H}_2\text{O}$, 500 mg/l complexing agent
- 15 (EDTA or citric acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting
- 20 protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca. 18 h at 37°C. The DNA was purified by
- 25 extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20
- 30 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA
- 35 prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (see e.g., Sambrook, J. et al. (1989) "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. et al. (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see e.g., Fleischman, R.D. et al. (1995) "Whole-genome Random Sequencing and Assembly of *Haemophilus Influenzae* Rd.", *Science*, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to one of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as e.g., pHM1519 or pBL1) which replicate autonomously (for review see, e.g.,

- Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli* and *C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159:306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an *Mcr*-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other *Corynebacterium* or *Brevibacterium* species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction

endonuclease mediated integration (REMI) (see, e.g., DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (e.g., a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) From Genes to Clones - Introduction to Gene Technology. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for *Corynebacteria* are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebi (1992) "The Genus *Corynebacterium*, in: The Prokaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(\text{NH}_4)_2\text{SO}_4$, NH_4OH , nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (eds. P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if

necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH₄OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the microorganisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD₆₀₀ of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2.5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – In vitro Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well

- within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979)
- 5 Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN
- 10 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

- The activity of proteins which bind to DNA can be measured by several well-
- 15 established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as
- 20 beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

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Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

- The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified
- 30 microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical
- 35 chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in:

- Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)
- 10 In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall yield, production, and/or efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium
- 15 (e.g., sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-
- 20 163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

- Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art.
- 25 If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum*
- 30 cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

- The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the
- 35 impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate

chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

- There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. *Biochemical Engineering Fundamentals*, McGraw-Hill: New York (1986).

- The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotehnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) *Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology*, John Wiley and Sons; Fallon, A. *et al.* (1987) *Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology*, vol. 17.

20 **Example 11: Analysis of the Gene Sequences of the Invention**

- The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to MR nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to MR protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN
5 program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM, described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

- 10 The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blosom 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the
15 GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

- A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, e.g., Bexevanis and Ouellette, eds. (1998) *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins*. John Wiley and Sons: New York). The gene sequences of the invention
20 were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (e.g., a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (e.g., a
25 combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the
30 length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP
35 (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment

homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

5 **Example 12: Construction and Operation of DNA Microarrays**

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; 10 DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label 15 may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, e.g., 20 Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice 25 and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide 30 synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the 35 synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (e.g., mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or
5 fluorescently labeled nucleotides, e.g., during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (e.g., in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as
10 described in Schena, M. *et al.* (1995) *supra* and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations
15 based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

20

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein
25 populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (e.g., in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (e.g., during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

30 Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing
35 polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the

consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (e.g., ³⁵S-methionine, ³⁵S-cysteine, ¹⁴C-labelled amino acids, ¹⁵N-amino acids, ¹⁵NO₃ or ¹⁵NH₄⁺ or ¹³C-labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, e.g., Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (e.g., different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (e.g., metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the

5 following claims.

What is claimed:

- 5 1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding a metabolic pathway regulatory protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1..
- 10 2. The isolated nucleic acid molecule of claim 1, wherein said metabolic pathway regulatory protein is selected from the group consisting of proteins involved in the regulation of metabolism of organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, and enzymes.
- 15 3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
- 20 4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
- 25 5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
- 30 6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.
- 35 7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group

consisting of those sequences set forth in Appendix A, provides that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.
9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.
10. A vector comprising the nucleic acid molecule of claim 1.
11. The vector of claim 10, which is an expression vector.
12. A host cell transfected with the expression vector of claim 11.
13. The host cell of claim 12, wherein said cell is a microorganism.
14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.
16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.
18. An isolated metabolic pathway regulatory polypeptide from *Corynebacterium glutamicum*, or a portion thereof.
19. The protein of claim 18, wherein said polypeptide is selected from the group of metabolic pathway proteins which participate in the regulation of metabolism of

organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, and enzymes.

- 5 20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 10 21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 15 22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.
- 20 23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.
- 25 24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.
- 30 25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.
26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.
- 35 27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium*.
- 5 29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum*, *Corynebacterium herculis*, *Corynebacterium lilium*, *Corynebacterium acetoacidophilum*, *Corynebacterium acetoglutamicum*, *Corynebacterium acetophilum*, *Corynebacterium ammoniagenes*, *Corynebacterium fujikense*, *Corynebacterium nitrilophilus*, *Brevibacterium ammoniagenes*,
10 *Brevibacterium butanicum*, *Brevibacterium divaricatum*, *Brevibacterium flavum*, *Brevibacterium healii*, *Brevibacterium ketoglutamicum*, *Brevibacterium ketosoreductum*, *Brevibacterium lactofermentum*, *Brevibacterium linens*, *Brevibacterium paraffinolyticum*, and those strains set forth in Table 3.
- 15 30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.
31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine
20 and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.
32. The method of claim 25, wherein said fine chemical is an amino acid.
- 25 33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.
- 30 34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.
- 35 35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not

encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group
5 consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

37. A host cell comprising a nucleic acid molecule selected from the group
consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic
10 acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

38. A host cell comprising a nucleic acid molecule selected from the group
consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory
15 region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

***CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING REGULATORY
PROTEINS**

Abstract of the Disclosure

5

Isolated nucleic acid molecules, designated MR nucleic acid molecules, which encode novel MR proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing MR nucleic acid molecules, and host cells into which the expression
10 vectors have been introduced. The invention still further provides isolated MR proteins, mutated MR proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of MR genes in this organism.

Customer Number: 000959

Attorney's
Docket No. BGI-123CP

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

Corynebacterium Glutamicum Genes Encoding Regulatory Proteins
the specification of which

(check one)

X is attached hereto.

was filed on _____ as

Application Serial No. _____

and was amended on _____
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

☐ no such applications have been filed.

☒ such applications have been filed as follows

**EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION**

Country	Application Number	Date of Filing (month.day.year)	Priority Claimed Under 35 USC 119
DE	19930476.9	07/01/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931419.5	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19931420.9	07/08/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932122.1	07/09/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932128.0	07/09/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932134.5	07/09/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932206.6	07/09/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19932207.4	07/09/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19933003.4	07/14/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19941390.8	08/31/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19942088.2	09/03/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>
DE	19942124.2	09/03/99	<input checked="" type="checkbox"/> Yes No <input type="checkbox"/>

**ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS
(6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION**

CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/141,031

(Application Serial No.)

June 25, 1999

(Filing Date)

60/142,690

(Application Serial No.)

July 1, 1999

(Filing Date)

60/151,251

(Application Serial No.)

August 27, 1999

(Filing Date)

CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

(Application Serial No.)

(Filing Date)

(Status)
(patented,pending,aband.)

(Application Serial No.)

(Filing Date)

(Status)
(patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Giulio A. DeConti, Jr., Esq., (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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TABLE 1: GENES INCLUDED IN THE APPLICATION

Nucleic Acid SEQ ID NO	Amino Acid ID NO	Amino Acid SEQ	Identification	Contig.	NT Start	NT Stop	Function
1	2	FXA00181	Code	V00338	196	609	GLUCOSE-RESISTANCE AMYLASE REGULATOR
2	4	FXA002680	FXA00181	GR10018	417	4	TRANSCRIPTIONAL REPRESSOR CYTR
3	6	FXA000603	GR10018	GR00159	4982	5434	LEUCINE-RESPONSIVE REGULATORY PROTEIN
4	8	FXA002946	V00127	V00127	7000	7458	FATTY ACYL RESPONSIVE REGULATORY
5	10	RXN01845	V00234	V00234	1093	686	FUMARATE AND NITRATE REDUCTION REGULATORY PROTEIN
6	12	RXN02910	V00135	V00135	30560	29856	TRANSCRIPTIONAL ACTIVATOR PROTEIN LYSR
7	14	RXN02553	V00101	V00101	3454	4017	CRYPTIC BETA-GLUCOSIDE BGL OPERON ANTI-TERMINATOR
8	16	RXN00686	RXN00686	V00005	30857	30054	ACETATE OPERON REPRESSOR
9	18	RXN00774	RXN00774	V00103	22390	22397	TRANSCRIPTIONAL REPRESSOR
10	20	RXN02483	RXN02483	V00007	8481	9719	PHOSPHATE REGULON SENSOR PROTEIN PHOR
11	22	FXA002493	FXA002493	GR00720	2351	1184	PHOSPHATE REGULON SENSOR PROTEIN PHOR
12	24	RXN00631	RXN00631	V00135	18302	16846	PHOSPHATE REGULON SENSOR PROTEIN PHOR

Genes for signal transduction pathways, regulation of proteins and transcription

Nucleic Acid SEQ ID NO	Amino Acid ID NO	Amino Acid SEQ	Identification	Contig.	NT Start	NT Stop	Function
25	26	RXN00291	Code	V00041	6431	4860	SENSOR KINASE CITA (EC 2.7.3.-)
26	28	FXA000291	FXA000291	GR00047	2	1075	SENSOR KINASE CITA (EC 2.7.3.-)
27	30	RXN00129	RXN00129	GR00020	6205	9709	SENSOR PROTEIN CPXA (EC 2.7.3.-)
28	32	RXN00651	V00109	V00109	5452	4119	Hypothetical Sensor Histidine Kinase (EC 2.7.3.-)
29	34	FXA000651	GR00169	GR00169	5905	6471	SENSOR PROTEIN DEGS (EC 2.7.3.-)
30	36	RXN00006	GR00006	GR00006	6905	1484	SENSOR PROTEIN FIXL (EC 2.7.3.-)
31	38	RXN01860	GR00529	GR00529	2368	2368	SENSOR PROTEIN FIXL (EC 2.7.3.-)
32	40	RXN01861	GR00529	GR00529	4332	2368	SENSOR PROTEIN RESE (EC 2.7.3.-)
33	42	FXA002669	GR00753	GR00753	8893	10008	SENSOR PROTEIN UHPB (EC 2.7.3.-)
34	44	RXN01211	V00169	V00169	5106	6362	SENSOR PROTEIN UHPB (EC 2.7.3.-)
35	46	FXA01211	GR00349	GR00349	741	1535	SENSORY TRANSDUCTION PROTEIN REGX3
36	48	RXN01248	GR00362	GR00362	165	593	SENSORY TRANSDUCTION PROTEIN REGX3
37	50	RXN02568	GR00753	GR00753	8171	8893	putative two-component response regulator [Mycobacterium tuberculosis]
38	52	RXN02532	GR00748	GR00748	4863	4168	putative two-component sensor [Mycobacterium tuberculosis]
39	54	RXN02631	GR00748	GR00748	4096	2732	TWO COMPONENT RESPONSE REGULATOR
40	56	RXN00609	RXN00609	GR00161	226	891	ANKYRIN HOMOLOG PRECURSOR
41	58	RXN00284	GR00045	GR00045	1318	2332	PROTEIN KINASE PKNA
42	60	RXN01827	GR00016	GR00016	6308	4902	SECRETORY PROTEIN KINASE
43	62	RXN00813	GR00016	GR00016	1345	2475	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKNB (EC 2.7.1.-)
44	64	RXN01626	GR00016	GR00016	1492	2985	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKNB (EC 2.7.1.-)
45	66	RXN02699	GR00057	GR00057	357	3504	LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE (EC 3.1.3.48)
46	68	RXN00319	GR00056	GR00056	305	80	PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE PHOSPHATASE
47	70	RXN01272	GR00367	GR00367	23049	2547	PUTATIVE PHOSPHOPROTEIN PHOSPHATASE
48	72	RXN01630	GR00016	GR00016	10410	9058	

Nucleic Acid SEQ ID NO	Amino Acid ID NO	Identification Code	Contig	NT Start	NT Stop	Function
73	74	RXA02747	GR00764	277	2352	[PROTEIN-PII] URIDYLYL TRANSFERASE (EC 2.7.7.59)
75	76	GR00048	GR00048	1922	2485	Hypothetical Transcriptional Regulator
77	78	RXA00221	GR00032	20855	21703	Hypothetical Transcriptional Regulator
79	80	VV0079	GR00144	352	30471	Hypothetical Transcriptional Regulator
81	82	RXA00551	GR00144	352	5	Hypothetical Transcriptional Regulator
83	84	RXA01763	GR00500	1967	1523	Hypothetical Transcriptional Regulator
85	86	RXA02867	GR00753	7863	1270	Hypothetical Transcriptional Regulator
87	88	RXA00348	GR00085	1507	1052	Hypothetical Transcriptional Regulator
89	90	RXA01500	GR00424	1351	786	Hypothetical Transcriptional Regulator
91	92	RXA01125	VV00512	1130	1598	Hypothetical Transcriptional Regulator
93	94	RXA00822	VV00512	21521	20841	Hypothetical Transcriptional Regulator
95	96	RXA00822	GR00221	3073	2353	putative transcriptional regulator
97	98	RXA00846	VV0067	4701	4381	Hypothetical Transcriptional Regulator
99	100	F RXA00848	GR00231	378	698	possible transcriptional regulator
101	102	RXA00350	GR00757	1143	775	PUTATIVE TRANSCRIPTIONAL REGULATOR
103	104	RXA02830	GR00666	1144	1470	Hypothetical Transcription Initiation Factor
105	106	RXA00947	GR00259	4164	3329	Helix-turn-helix domain-containing transcriptional regulators
107	108	RXA01635	GR00517	4370	3666	(ALD1287) probable transcriptional regulator [Mycobacterium tuberculosis]
109	110	RXA00292	GR00047	1078	1731	transcriptional regulator Ctr
111	112	RXA00182	GR00028	4247	7348	POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L
113	114	RXA02760	GR00767	1154	201	TRANSCRIPTIONAL REGULATOR PROTEIN CTR
115	116	RXA02306	GR00663	3214	2924	TRANSCRIPTIONAL REGULATOR PROTEIN CTR
117	118	RXA00130	GR00020	6985	6308	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
119	120	RXA00885	GR00242	11301	12326	TRANSCRIPTIONAL REGULATOR PROTEIN GLTC
121	122	RXA01418	GR00415	776	531	Hypothetical Transcriptional Regulator
123	124	RXA01759	GR00498	4075	34955	NIA OPERON TRANSCRIPTIONAL REGULATOR
125	126	RXA00363	VV0176	35684	1929	KDP OPERON TRANSCRIPTIONAL REGULATOR
127	128	F RXA00563	GR00073	592	479	KDP OPERON TRANSCRIPTIONAL REGULATOR
129	130	RXA00516	GR00131	592	1311	PUTATIVE AGA OPERON TRANSCRIPTIONAL REPRESSOR
131	132	RXA01537	GR00720	4829	4179	putative regulatory protein
133	134	RXA02494	GR00003	8910	8374	Hypothetical Transcriptional Regulator
135	136	RXA00029	GR00169	5443	278	PUTATIVE REGULATORY PROTEIN
137	138	RXA00655	GR00169	5443	278	REGULATORY PROTEIN
139	140	RXA00655	GR00169	5443	278	Hypothetical Regulatory Protein
141	142	RXA00645	GR00168	5831	8161	Hypothetical Regulatory Protein
143	144	RXA00645	GR00168	5831	8161	REGULATORY PROTEIN SIR2 HOMOLOG
145	146	RXA00645	GR00168	5831	8161	PROBABLE RHIZOPHANE CATABOLISM REGULATORY PROTEIN MOCR
147	148	RXA00645	GR00168	5831	8161	PROBABLE RHIZOPHANE CATABOLISM REGULATORY PROTEIN MOCR
149	150	RXA00645	GR00168	5831	8161	PROBABLE RHIZOPHANE CATABOLISM REGULATORY PROTEIN MOCR
151	152	RXA00645	GR00168	5831	8161	PROBABLE RHIZOPHANE CATABOLISM REGULATORY PROTEIN MOCR
153	154	RXA00645	GR00168	5831	8161	PROBABLE RHIZOPHANE CATABOLISM REGULATORY PROTEIN MOCR
155	156	RXA00645	GR00168	5831	8161	PROBABLE RHIZOPHANE CATABOLISM REGULATORY PROTEIN MOCR
157	158	RXA00645	GR00168	5831	8161	PROBABLE RHIZOPHANE CATABOLISM REGULATORY PROTEIN MOCR
159	160	RXA00645	GR00168	5831	8161	PROBABLE RHIZOPHANE CATABOLISM REGULATORY PROTEIN MOCR
161	162	RXA00126	GR00020	2269	1607	Hypothetical Transcriptional Regulator
163	164	RXA00126	VV0107	10940	10386	Hypothetical Transcriptional Regulator

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Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig	NT Start	NT Stop	Function
165	166	F RXA02450	GR00710	2533	3087	POTENTIAL ACRA8 OPERON REPRESSOR
167	168	RXA01898	GR00544	1178	1870	OPERON REGULATOR
169	170	RXA00004	GR00001	4293	3823	NITRILASE REGULATOR
171	172	RXA01001	GR00284	516	833	hex regulation repressor' hexR
173	174	RXA01375	GR00400	2560	1106	FRNA
175	176	RXA02831	GR00818	411	4	EXTRAGENIC SUPPRESSOR PROTEIN SJNH
177	178	RXA01110	GR00306	16399	16971	TETRACYCLINE REPRESSOR PROTEIN CLASS C
179	180	RXA00253	GR00308	1064	1801	TETRACYCLINE REPRESSOR PROTEIN CLASS E
181	182	RXA01118	GR00309	1787	2551	regulator of the <i>trp</i> operon
183	184	RXA01840	GR00521	2	955	ALPHA-AMIDASE EXPRESSION-REGULATING PROTEIN
185	186	RXA00400	GR00057	1163	2141	ALS OPERON REGULATORY PROTEIN
187	188	RXA02787	GR00777	885	2141	ACTIVATOR 1.41 KD SUBUNIT
189	190	RXA00346	GR00346	116	1145	ADAPTIVE RESPONSE REGULATORY PROTEIN
191	192	RXA01887	GR00689	328	2219	N-ACETYLGLUCOSAMINE REPRESSOR
193	194	RXA01955	GR00655	8902	7739	N-ACETYLGLUCOSAMINE REPRESSOR
195	196	F RXA02270	V0020	13880	13260	Hypothetical Transcriptional Regulator member of the regulatory protein family SIR2
197	198	RXA00638	GR00655	5005	4385	LEXA REPRESSOR (EC 3.4.21.88)
199	200	RXA01241	GR00339	739	1218	6 ACTVA REGION GENES OF THE ACTINORHODIN BIOSYNTHETIC GENE CLUSTER
201	202	RXA02127	GR00637	2715	2082	Uncharacterized ACR (translation initiation regulator?)
203	204	RXA00583	GR00156	10203	9466	Uncharacterized ACR (translation initiation regulator?)
205	206	RXA00592	GR00158	2121	1663	(U67196) DNA-binding response regulator [Thermotoga maritima]
207	208	RXA00630	GR00166	2	160	DNA-binding response regulator
209	210	F RXA00638	GR00167	2862	3245	GTPASE-ACTIVATING PROTEIN 1
211	212	RXA00894	GR00244	1926	799	GTP-BINDING PROTEIN
213	214	RXA01450	GR00419	1237	1800	GTP-BINDING PROTEIN
215	216	RXA01451	GR00419	1760	2326	GTP-BINDING PROTEIN ERA
217	218	RXA02376	GR00689	3064	1562	GTP-BINDING PROTEIN HELIX
219	220	RXA01065	GR00288	2	583	GTP-BINDING PROTEIN HELIX
221	222	RXA02232	GR00653	5286	6812	GTP-BINDING PROTEIN LEPA
223	224	RXA00848	GR00230	2125	1995	GTP-BINDING PROTEIN LEPA
225	226	F RXA00839	GR00228	372	4	GTP-BINDING PROTEIN LEPA
227	228	F RXA00845	GR00229	907	5	GTP-BINDING PROTEIN LEPA
229	230	RXA02365	GR00666	1568	1029	GTP-BINDING PROTEIN LEPA
231	232	F RXA02392	GR00666	1264	3663	2',3'-cyclic-nucleotide 2'-phosphodiesterase
233	234	RXA01573	GR00436	5144	1694	Hypothetical Sensor Histidine Kinase (EC 2.7.3.-)
235	236	RXA01445	V00138	1652	2822	Hypothetical Sensor Histidine Kinase (EC 2.7.3.-)
237	238	RXA003143	V00138	1652	2822	Hypothetical Sensor Protein
239	240	RXA00772	V00040	6	344	Hypothetical Sensor Protein
241	242	RXA01773	V00040	396	830	PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48)
243	244	RXA003090	V00054	1128	1604	SENSORY COMPONENT OF SENSORY TRANSDUCTION HISTIDINE KINASE (EC 2.7.3.-)
245	246	RXA000617	V00054	5296	4076	SENSORY COMPONENT OF SENSORY TRANSDUCTION HISTIDINE KINASE (EC 2.7.3.-)
247	248	RXA00617	V00054	4053	3826	SENSORY COMPONENT OF SENSORY TRANSDUCTION HISTIDINE KINASE (EC 2.7.3.-)
249	250	RXA00980	V00073	1352	1948	REGULATORY PROTEIN RECX
251	252	RXA003100	V00064	11866	11549	ALPHA-AMIDASE EXPRESSION-REGULATING PROTEIN
253	254	RXA00031	V00127	54780	55181	PHOSPHOHISTIDINE PHOSPHATASE SIXA (EC 3.1.3.-)
255	256	RXA02758	V00084	29359	28061	PHOSPHOSERINE PHOSPHATASE (EC 3.1.3.3)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification	Contig	NT Start	NT Stop	Function
257	258	RXN00978	V0149	1360	1974	NNRR
258	259	RXN01349	V0123	1531	755	REGULATORY PROTEIN BET1
259	260	RXN0467	V0086	60275	60943	IRON REPRESSOR
261	262	RXN02954	V00015	2893	3430	Hypothetical Transcriptional Regulator
263	264	RXN03023	V00003	6100	5744	Hypothetical Transcriptional Regulator
265	266	RXN03127	V0119	8276	7957	Hypothetical Transcriptional Regulator
267	268	RXN03155	V0186	2	1899	Hypothetical Transcriptional Regulator
269	270	RXN01315	V0082	13796	3146	Hypothetical Transcriptional Regulator
271	272	RXN00035	V0020	24855	24499	Hypothetical Transcriptional Regulator
273	274	RXN00049	V0174	21833	2374	Hypothetical Transcriptional Regulator
275	276	RXN0496	V0086	33895	34744	Hypothetical Transcriptional Regulator
277	278	RXN01081	V0064	4187	3213	Hypothetical Transcriptional Regulator
279	280	RXN01160	V0298	194	3555	Hypothetical Transcriptional Regulator
281	282	RXN02097	V0020	9528	10040	Hypothetical Transcriptional Regulator
283	284	RXN02265	V0007	11237	7539	FERRIC UPTAKE REGULATION PROTEIN
285	286	RXN02392	V0051	11237	7539	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
287	288	RXN03062	V0007	25030	24149	PYRIMIDINE OPERON REGULATORY PROTEIN PTRR
289	290	RXN03506	V0129	34206	33541	CCPA PROTEIN
291	292	RXN0826	V0180	2560	3110	NITRATE/NITRITE SENSOR PROTEIN NARX (EC 2.7.3.-)
293	294	RXN00070	V0019	32468	32899	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARL
295	296	RXN00133	V0046	201	1013	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
297	298	RXN00144	V0134	20478	21053	Hypothetical Cytosolic Protein
299	300	RXN00205	V0096	4885	3779	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
301	302	RXN00470	V0096	27401	28669	Hypothetical Cytosolic Protein
303	304	RXN00471	V0096	28715	29404	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
305	306	RXN00481	V0096	43354	43938	Hypothetical Cytosolic Protein
307	308	RXN00649	V0109	10679	10224	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
309	310	RXN00650	V0109	9485	10120	Hypothetical Cytosolic Protein
311	312	RXN00657	V0109	2820	3522	ACR Protein
313	314	RXN00719	V0232	7281	9853	Hypothetical GTP-Binding Protein
315	316	RXN00738	V0254	3	385	Hypothetical Cytosolic Protein
317	318	RXN01082	V0084	35406	34747	IRON REPRESSOR
319	320	RXN01123	V0143	24824	25270	Hypothetical Protein
321	322	RXN01189	V0169	5386	5370	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
323	324	RXN01242	V0068	17647	17971	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
325	326	RXN01607	V0139	2822	3451	NITRATE/NITRITE RESPONSE REGULATOR PROTEIN NARP
327	328	RXN01674	V0248	2141	2988	PROBABLE HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR
329	330	RXN01872	V0102	8076	8549	TRANSCRIPTIONAL REGULATORY PROTEIN
331	332	RXN02117	V0127	51473	50828	Hypothetical Cytosolic Protein
333	334	RXN02266	V0127	2475	50828	GLYCEROL-3-PHOSPHATE REGULON REPRESSOR
335	336	RXN02627	V0098	2981	2918	ACR Protein
337	338	RXN02627	V0314	2981	2139	DTXR/IRON-REGULATED LIPOPROTEIN PRECURSOR
339	340	RXN02891	V0098	55962	56768	FATTY ACYL RESPONSIVE REGULATOR
341	342	RXN02891	V0145	7640	8677	RIBOSE OPERON REPRESSOR
343	344	RXN02730	V0145	7640	8677	Hypothetical Protein
345	346	RXN02818	V0347	611	6	Hypothetical Cytosolic Protein
347	348	RXN02911	V0135	24643	25101	Hypothetical Cytosolic Protein

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Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
349	350	RXSC0066	VV0038	7298	6636	Hypothetical Protein
351	352	RXSC0068				DIPHTheria Toxin Repressor
353	354	RXSC0069	GR00052	467	6	DIPHTheria Toxin Repressor
355	356	RXSC0219				LACH-FAMILY TRANSCRIPTION REGULATOR
357	358	FRX02763	GR00768	1603	2586	MALTOSE OPERON TRANSCRIPTIONAL REPRESSOR
359	360	RXSC0200				PROBABLE HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-amino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moedel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from corynebacterium bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Corynebacterium bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	disR		Kimura, E. et al. "Molecular cloning of a novel gene, disR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	disR1; disR2		
AB020624	murI	D-glutamate racemase	
AB020377	tkt	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenylyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	Wehmeier, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppGpp metabolism." <i>Microbiology</i> , 144:1853-1862 (1998)
AF038651	dc1AE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	
AF053071	aroB	Dehydroquininate synthetase	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinate; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY; glnB; glnD; sfp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> : Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEBS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichter, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum A112036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hlk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987233392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987233392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diamino pelargonic acid aminotransferase and deshiobiotin synthetase and its utilization," Patent: JP 199230284-A 1 11/18/92
E04041		Deshiobiotin synthetase	Kohama, K. et al. "Gene coding diamino pelargonic acid aminotransferase and deshiobiotin synthetase and its utilization," Patent: JP 199230284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sorouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/50/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipicolinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kojima, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and deethiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in corynebacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
F12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758 E12764		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
L01508	ilvA	Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L07603		Threonine dehydratase	Moeschel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L09232	ilvB; ilvN; ilvC	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEBS Microbiol. Lett.</i> , 107:223-230 (1993)
		Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isolation and synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	P ₅ M	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A. et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in <i>Escherichia coli</i> and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H.-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in <i>Corynebacterium glutamicum</i> ," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jeffer, M. S. et al. "Structural and functional analysis of pyruvate kinase from <i>Corynebacterium glutamicum</i> ," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	Oguzia, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the <i>Corynebacterium diphtheriae</i> dixR from <i>Brevibacterium lactofermentum</i> ," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
L35906	dixR	Diphtheria toxin repressor	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the <i>Corynebacterium glutamicum</i> pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M13774		Prephenate dehydratase	Park, Y.-H. et al. "Phylogenetic analysis of the corynebacterium bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16175	5S rRNA		
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of <i>Brevibacterium lactofermentum</i> , a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of <i>Corynebacterium glutamicum</i> ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; brnQ; ybbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein ybbw	Rosso, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminothylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isolation and uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthrax toxin phosphotransferase	O'Garra, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cgII; cgIIR; elgIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cgII gene encoding a 5-cytosine in an MsrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965 U31224	recA ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

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U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thrB; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al., "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxy-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al., "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'-5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al., "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al., "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Ekman, B.J. et al., "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepinec, L. et al., "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al., "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of C. glutamicum fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bommasie, S. et al., "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

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X54223		AtB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambdacorynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap-pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bornmann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

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X66078	cop1	Ps1 protein	Jolliff, G. et al. "Cloning and nucleotide sequence of the <i>cop1</i> gene encoding PS1, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PS1 is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> <i>gltA</i> gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	Peyret, J.L. et al. "Characterization of the <i>espB</i> gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69103	esp2	Surface layer protein PS2	Bonamy, C. et al. "Identification of ISI206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X69104		IS3 related insertion element	
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Luciferase synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of <i>leuA</i> , and effect of <i>leuA</i> inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> <i>icd</i> gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDH/A	Glutamate dehydrogenase (NADP+)	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75083, X70584	mirA	5-methyltryptophan resistance	Fitzpatrick, R. et al. "Construction and characterization of <i>recA</i> mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75085	recA		Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GeneBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argI	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta, ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Atribacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

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X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrjlic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

GeneBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Salm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthetase for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	
Y00140	thrB	Homoserine kinase	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00476	thrA	Homoserine dehydrogenase	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y09163	putP	High affinity proline transport system	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Genet. Genet.</i> , 259(1):97-104 (1998)
Y09548	pyc	Pyruvate carboxylase	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicum and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09578	leuB	3-isopropylmalate dehydrogenase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y12472		Attachment site bacteriophage Phi-16	Paek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
			Moreau, S. et al. "Site-specific integration of corynebacteriophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP." <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I." <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	Moreau, S. et al. "Analysis of the integration functions of ϕ phi304L: An integrase module among corynephages." <i>Virology</i> , 255(1):150-159 (1999)
Y18059		Attachment site Corynephage 304L	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine." <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function." <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase." <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z29563	thrC	Threonine synthase	
Z46753	16S rDNA	Gene for 16S ribosomal RNA	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB." <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "The galP gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene." <i>Gene</i> , 177:103-107 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB." <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869." <i>Gene</i> , 170(1):91-94 (1996)
Z66534		Transposase	

¹ A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: *Corynebacterium* and *Brevibacterium* Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCIC	DSMZ
Brevibacterium	ammoniaenes	21054							
Brevibacterium	ammoniaenes	19350							
Brevibacterium	ammoniaenes	19351							
Brevibacterium	ammoniaenes	19352							
Brevibacterium	ammoniaenes	19353							
Brevibacterium	ammoniaenes	19354							
Brevibacterium	ammoniaenes	19355							
Brevibacterium	ammoniaenes	19356							
Brevibacterium	ammoniaenes	21055							
Brevibacterium	ammoniaenes	21077							
Brevibacterium	ammoniaenes	21553							
Brevibacterium	ammoniaenes	21580							
Brevibacterium	ammoniaenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetosaccharophilum	21476							
Corynebacterium	acetosaccharophilum	13870							
Corynebacterium	acetoglutamicum				B11473				
Corynebacterium	acetoglutamicum				B11475				
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophillum				B3671				
Corynebacterium	ammoniaenes	6872						2399	
Corynebacterium	ammoniaenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum		B8183						
Corynebacterium	glutamicum		B8182						
Corynebacterium	glutamicum		B12416						
Corynebacterium	glutamicum		B12417						
Corynebacterium	glutamicum		B12418						
Corynebacterium	glutamicum		B11476						
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus								
Corynebacterium	spec.	21419					11594		
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

TABLE 4: ALIGNMENT RESULTS

ID #	length (NT)	Genbank Hit	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
ra00004	594	GB_JN1.CELT277	34660	Caenorhabditis elegans cosmid T277.	Caenorhabditis elegans	36.42	24-MAY-1996
		GB_PR4.AC005531	161910	Human sapiens PAC clone D0701016 from 7q33-q36, complete sequence.	Homo sapiens	38.672	13-Jan-99
		GB_EST36.AV186136	360	AV186136 Yui Kohara unpublished cDNA.Siran N2 hermaphrodite embryo.	Caenorhabditis elegans	44.380	22-Jul-99
ra00006	568	GB_BA1.AB024708	8734	Caenorhabditis elegans cDNA clone y449512 5' mRNA sequence.	Corynebacterium glutamicum	39.525	13-MAR-1999
		GB_EST5.N23892	434	Caenorhabditis elegans cDNA clone y449512 5' mRNA sequence.	Corynebacterium glutamicum	39.525	13-MAR-1999
		GB_BA1.AB024708	8734	Caenorhabditis elegans cDNA clone y449512 5' mRNA sequence.	Homo sapiens	38.462	28-DEC-1995
ra00029		GB_BA1.AB024708	8734	Caenorhabditis elegans cDNA clone y449512 5' mRNA sequence.	Corynebacterium glutamicum	38.981	13-MAR-1999
ra00126				Caenorhabditis elegans cDNA clone y449512 5' mRNA sequence.			
ra00129	1620	GB_BA1.MT20811	36330	Myobacterium tuberculosis H37Rv complete genome; segment 139/162.	Myobacterium tuberculosis	40.788	17-Jun-98
		GB_BA1.MT14909	1799	Myobacterium tuberculosis Mtb (ntrB) gene, complete cds.	Myobacterium tuberculosis	54.422	11-Sep-96
		GB_HTG2.AC006888	140702	Caenorhabditis elegans clone Y61A9L. *** SEQUENCING IN PROGRESS ***.	Caenorhabditis elegans	35.863	26-Feb-99
ra00130	801	GB_BA1.MT20811	36330	Myobacterium tuberculosis H37Rv complete genome; segment 139/162.	Myobacterium tuberculosis	41.069	17-Jun-98
		GB_BA1.MT101971	689	Myobacterium tuberculosis H37Rv MtrA (mtrA) gene, complete cds.	Myobacterium tuberculosis	66.183	11-Sep-96
		GB_BA1.NM001PR	618	N meningitidis ompF gene.	Nisseria meningitidis	50.249	31-OCT-1995
ra00182	3225	GB_BA1.CGPUTP	3791	Corynebacterium glutamicum pulP gene.	Corynebacterium glutamicum	41.126	8-Sep-97
		GB_BA1.MT020	5143	Myobacterium tuberculosis H37Rv complete genome; segment 94/162.	Myobacterium tuberculosis	48.140	17-Jun-98
		GB_BA1.BSUB0019	212610	Bacillus subtilis complete genome (section 19 of 21); from 35970910 to 3809700.	Bacillus subtilis	44.221	24-Jun-99
ra00221	342	GB_PL2.AF020584	1415	Wetwischia mirabilis cytochrome c oxidase (cox) gene, mitochondrial gene encoding mitochondrial protein, partial cds.	Mitochondrion Wetwischia mirabilis	36.656	5-Jan-99
		GB_PR4.AC007421	95240	Human sapiens chromosome 17, clone HRPIC.1030.O_14, complete sequence.	Homo sapiens	35.061	27-Aug-99
ra00253	861	GB_BA2.AE01272	60232	Lactococcus lactis DPC3147 plasmid pMR001, complete plasmid sequence.	Lactococcus lactis	37.764	11-Sep-98
		GB_BA2.AF126953	1838	Corynebacterium glutamicum cystathionine gamma-synthase (ntrB) gene, complete cds.	Corynebacterium glutamicum	41.107	10-Sep-99
		GB_PR3.HS.659F15	148440	Human DNA sequence from clone 659F15 on chromosome Xp11.21-11.4, complete sequence.	Homo sapiens	36.190	23-Nov-99
		GB_HTG1.HS510D11	129149	Human sapiens chromosome 1 clone RP3-510D11, *** SEQUENCING IN PROGRESS ***.	Homo sapiens	36.450	23-Nov-99
ra00284	1188	GB_PR2.HS179P9	108260	Human DNA sequence from PAC 179p9 on chromosome 6q22. Contains transmembrane tyrosine-specific protein kinase (ROS1), EST's and STS.	Homo sapiens	36.370	23-Nov-99
		GB_PR4.AF.08076	113345	Human sapiens chromosome 7 map 7q36 BAC H6, complete sequence.	Homo sapiens	35.340	19-DEC-1998

TABLE 4: ALIGNMENT RESULTS

na00287	587	GB_PQ2HS179P9	108260	Z98880	Human DNA sequence from PAC 179P9 on chromosome 6q22. Contains transmembrane tyrosine-specific protein kinase (ROST), ESTs and STS. Aedes albopictus ribosomal protein L34 (rpL34) gene, complete cds. vt14409.11 Soares mouse mammary gland NMMMG Mus musculus cDNA clone IMAGE:875464.5 similar to gp-X37671 M musculus mRNA for 3BP-1, an SH3 domain binding (MOUSE), mRNA sequence. Mus musculus mRNA for 3BP-1, an SH3 domain binding protein. Homo sapiens clone DJ1111F22 complete sequence. CE213144 Chris Martin sorted cDNA library Caenorhabditis elegans cDNA clone Caenorhabditis elegans chr2144.5 similar to pepsinogen A homologous peptide, mRNA sequence.	35,344	23-Nov-99
na00291	1606	GB_PQ4AC004067	138107	AC004067	Mus musculus	39,828	3-Jun-99
		GB_EST1:M89319	418	M89319	Mus musculus	37,063	18-Jun-97
		GB_PQ4MM3BP1	2359	X87671	Mus musculus	34,635	20-OCT-1995
		GB_PQ4AC004067	138107	AC004067	Homo sapiens	36,785	5-Jun-99
		GB_EST1:M89319	418	M89319	Caenorhabditis elegans	38,418	02-DEC-1992
na00292	777	GB_GSS15:AQ041399	569	AQ041399	Typanosoma brucei	39,106	8-Jul-99
		GB_PL1YSCKG02	2112	M34531	Saccharomyces cerevisiae	37,330	27-Apr-93
		GB_PL1SCN0M1	9851	X61236	Saccharomyces cerevisiae	35,070	06-DEC-1991
		GB_PL1SC8358	43468	Z50046	Saccharomyces cerevisiae	35,070	11-Aug-97
na00319	549	GB_BA1BACJH642	282700	D84432	Bacillus subtilis	43,256	6-Feb-99
		GB_BA1BSUB0014	213420	Z99117	Bacillus subtilis	34,264	26-Nov-97
		GB_BA1BSUB0014	213420	Z99117	Bacillus subtilis	35,622	26-Nov-97
na00348	519	GB_PL2ATAAC007045	68554	AC007045	Arabidopsis thaliana chromosome II BAC F23M2 genomic sequence, complete sequence.	43,513	31-MAR-1999
		GB_PL2ATH133743	5777	AJ133743	Arabidopsis thaliana tlg1 gene.	38,247	18-Jun-99
		GB_PL1AB010068	74589	AB010068	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence.	34,387	20-Nov-99
na00350	450	GB_PL1SCXV5K6B	54719	Z70678	Saccharomyces cerevisiae XV DNA, 54.7 kb region.	35,347	16-MAY-1997
		GB_PL1SCYOR02C	1732	Z74960	Saccharomyces cerevisiae XV reading frame ORF YOR052c.	35,347	11-Aug-97
		GB_BA1PSE6703	2600	AJ006703	Pseudomonas sp. gene encoding for glutamine synthetase.	37,978	19-Jan-99
na00363	843	GB_V1SNMMDGB1	9215	M27470	Simian immunodeficiency virus, complete genome.	35,379	13-MAR-1997
		GB_ON4BTU05642	1198	U35642	Bos taurus alpha1-microglobulin/mRNA, complete cds.	40,131	5-Sep-96
		GB_PL1MD0011518	1633	AJ011518	Mus musculus acs synthase gene, exon 1, 4 partial.	40,343	23-OCT-1998
na00400	1002	GB_HTG2AC006174	203407	AC006174	Homo sapiens chromosome 10 clone CT1987SK-1057L21 map 10q25, ***SEQUENCING IN PROGRESS ***; 8 unordered pieces.	38,320	09-DEC-1998
		GB_HTG2AC006174	203407	AC006174	Homo sapiens chromosome 10 clone CT1987SK-1057L21 map 10q25, ***SEQUENCING IN PROGRESS ***; 8 unordered pieces.	38,320	09-DEC-1998
		GB_HTG2AC006174	203407	AC006174	Homo sapiens chromosome 10 clone CT1987SK-1057L21 map 10q25, ***SEQUENCING IN PROGRESS ***; 6 unordered pieces.	37,693	09-DEC-1998
na00464							

TABLE 4: ALIGNMENT RESULTS

GB_B42AF040435	4097	AF040435	Brevibacillus brevis	18-Nov-97
GB_B42AF040435	4097	AF040435	Brevibacillus brevis tyrocidine biosynthesis operon, tyrocidine synthetase 1 (tycA), tyrocidine synthetase 2 (tycB), tyrocidine synthetase 3 (tycC), putative ABC-transporter Tyce (tycE) and putative thioesterase Gist1 homolog (tycF) genes, complete cds.	
GB_PR3HS84F12	78011	AL008712	Human DNA sequence from PAC B4F12 on chromosome Aq25-Aq28.3. Contains Glypican-3 precursor (intrinsic protein OC1-5) (GTR2.4), ESTs and CA repeat.	23-Nov-99
GB_PR3AC005239	37005	AC005239	Homo sapiens chromosome 19, cosmid F23149, complete sequence.	3-Jul-98
GB_PR3AF020503	208880	AF020503	Homo sapiens FRAB3B common fragile region, diadenosine triphosphate hydrolase (FHT1) gene, exon 5.	23-Jun-98
GB_HTG2AC007100	210344	AC007100	Homo sapiens clone NH0462D13. *** SEQUENCING IN PROGRESS ***. 5 unordered pieces.	7-Apr-99
GB_HTG2AC007100	210344	AC007100	Homo sapiens clone NH0462D13. *** SEQUENCING IN PROGRESS ***. 5 unordered pieces.	7-Apr-99
GB_EST77AA05761	607	AA05761	GH-Z5883.3 spmne GH Drosophila melanogaster head p072 Drosophila melanogaster cDNA clone GH-Z5883.3 spmne mRNA sequence.	8-Feb-99
GB_EST77AA05774	607	AA05774	GH-Z5902.3 spmne GH Drosophila melanogaster head p072 Drosophila melanogaster cDNA clone GH-Z5902.3 spmne mRNA sequence.	8-Feb-99
GB_EST722AA063444	674	AA063444	GH-Z0363.3 spmne GH Drosophila melanogaster head p072 Drosophila melanogaster cDNA clone GH-Z0363.3 spmne mRNA sequence.	24-Nov-98
GB_BA1CORAHP5	2570	LR07603	Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene, complete cds.	26-Apr-93
GB_BA1MTV0025	67200	AF021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162. A californica KRP-A gene.	24-Jun-99
GB_IN1AKT0A17	849	GBX8555	Californica KRP-A gene.	30-Jun-98
GB_IN2AC005467	62091	AC005467	Drosophila melanogaster, chromosome 2R, region 46C1-48C2. P1 clone DS00568, complete sequence.	12-DEC-1998
GB_IN2AC005467	62091	AC005467	Drosophila melanogaster, chromosome 2R, region 46C1-48C2. P1 clone DS00568, complete sequence.	12-DEC-1998
GB_BA1MTV0025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	24-Jun-99
GB_BA1MSB577CO	37770	LR1263	M. leprae genomic dna sequence, cosmid b577.	14-Jun-96
GB_BA2AF114720	2366	AF114720	Xanthomonas campestris pv. vesicatoria avirulence protein AvrBs2 (avrBs2) gene, complete cds.	1-Feb-99
GB_BA1R0PU1TRA	4357	X78346	R. capsulatus (B105) puflr and pufla genes	08-DEC-1995
GB_GSS10AQ227452	474	AQ227452	HS-105, B2, B07, MR, CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=14 Row=d, genomic survey sequence.	26-Sep-98
GB_GSS3B80643	251	B60643	CIT-HSP-2015D14 TRB CIT-HSP Homo sapiens genomic clone 2015D14, genomic survey sequence.	21-Jun-98
GB_HTG3AC009346	105005	AC009346	Drosophila melanogaster chromosome 3 clone BACR03P13 (D872) RPCL-98 03 P 13 map 83A-83B strain y; on bw sp. *** SEQUENCING IN PROGRESS***. 83 unordered pieces.	27-Aug-99

TABLE 4: ALIGNMENT RESULTS

GB_HTG3/AC0089346	105005	AC009346	Drosophila melanogaster chromosome 3 done BACR03P13 (0872) RPCI 98 03.P.13 map 83A-83B strain y, on bw sp. *** SEQUENCING IN PROGRESS***, 83 unordered pieces.	Drosophila melanogaster	31,261	27-Aug-99
GB_HTG3/AC0089346	105005	AC009346	Drosophila melanogaster chromosome 3 done BACR03P13 (0872) RPCI 98 03.P.13 map 83A-83B strain y, on bw sp. *** SEQUENCING IN PROGRESS***, 83 unordered pieces.	Drosophila melanogaster	30,072	27-Aug-99
GB_BA1.MTC9389	36850	780226	Mycobacterium tuberculosis H37Rv complete genome, segment 36162.	Mycobacterium tuberculosis	60,870	17-Jun-98
GB_BA1.SCH48	15580	AL020958	Streptomyces coelicolor cosmid 4H8	Streptomyces coelicolor	46,537	10-DEC-1997
GB_BA1.MTC9389	37218	771162	Mycobacterium tuberculosis H37Rv complete genome, segment 25152	Mycobacterium tuberculosis	48,474	17-Jun-98
GB_PR2.AP000165	100000	AF000165	Homo sapiens genomic DNA, chromosome 21q22.1, 121S225-AML region, done B234AF14-150EB, segment 119, complete sequence.	Homo sapiens	35,685	20-Nov-99
GB_RO.AC005835	132297	AC005835	Mus musculus clone UGVC-mbad2z from 14D1D2 (T-Cell Receptor Alpha Loc), complete sequence.	Mus musculus	37,851	21-OCT-1998
GB_PR2.AP000165	100000	AF000165	Homo sapiens genomic DNA, chromosome 21q22.1, 121S225-AML region, done B234AF14-150EB, segment 119, complete sequence.	Homo sapiens	35,610	20-Nov-99
GB_PR3.AC004460	113803	AC004460	Homo sapiens PAC clone DJ1086D14, complete sequence.	Homo sapiens	38,606	24-MAR-1998
GB_PL1.CRERSP44	7707	M87526	Chlamydomonas reinhardtii flagellar radial spoke protein (RSP4) and RSP6 genes, complete cds.	Chlamydomonas reinhardtii	39,067	27-Apr-93
GB_EST38.AV041495	517	AV041495	EST1284359 tomato mixed elicitor, B71 Lycopersicon esculentum cDNA clone cLET14F2, mRNA sequence.	Lycopersicon esculentum	38,760	18-OCT-1999
GB_BA1.MSGBP70B	1009	D38230	Mycobacterium bovis DNA for MPB70, complete cds, strain: BCG Tokyo.	Mycobacterium bovis	40,956	8-Feb-99
GB_BA1.MTC974	39591	Z74024	Mycobacterium tuberculosis H37Rv complete genome, segment 128162.	Mycobacterium tuberculosis	41,447	19-Jun-98
GB_BA1.MSGBP70A	1009	D38229	Mycobacterium bovis DNA for MPB70, complete cds, strain: BCG Pasteur.	Mycobacterium bovis	40,956	8-Feb-99
GB_BA1.MTC975	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome, segment 155162.	Mycobacterium tuberculosis	64,925	24-Jun-99
GB_EST35.A1857185	646	A1857185	603007G10 x1 603 - stressed root cDNA library from Wang/Bohnet lab Zea mays cDNA, mRNA sequence.	Zea mays	40,206	16-Jul-99
GB_PR3.HS95C20	138849	297181	Homo sapiens DNA sequence from PAC 95C20 on chromosome X011.3-11.4, contains STSs and the DXS7' locus with GT and GTG repeat polymorphisms, complete sequence.	Homo sapiens	37,633	23-Nov-99
GB_BA1.MTC165	34331	Z95584	Mycobacterium tuberculosis H37Rv complete genome, segment 50162.	Mycobacterium tuberculosis	63,215	17-Jun-98
GB_BA1.MSCT346	40058	AD000020	Mycobacterium tuberculosis sequence from clone y348.	Mycobacterium tuberculosis	47,938	10-DEC-1996
GB_HTG3.AC008608	207341	AC008608	Homo sapiens chromosome 5 done CIT978SKB, 11920, *** SEQUENCING IN PROGRESS **, 10 unordered pieces.	Homo sapiens	43,001	3-Aug-99
GB_HTGA.AC007305	216524	AC007305	Mus musculus *** SEQUENCING IN PROGRESS **, 10 unordered pieces.	Mus musculus	38,379	23-OCT-1999
GB_HTGA.AC007305	216524	AC007305	Mus musculus *** SEQUENCING IN PROGRESS **, 10 unordered pieces.	Mus musculus	38,379	23-OCT-1999
GB_HTGA.AC007305	216524	AC007305	Mus musculus *** SEQUENCING IN PROGRESS **, 10 unordered pieces.	Mus musculus	38,379	23-OCT-1999
GB_EST36.AV178106	300	AV178106	AV178106 Yui Kohara unpublished cDNA,Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA,Strain N2 hermaphrodite embryo	Caenorhabditis elegans	39,057	21-Jul-99
GB_EST16.C30090	300	C30090	C30090 Yui Kohara unpublished cDNA,Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA,Strain N2 hermaphrodite embryo	Caenorhabditis elegans	38,000	18-OCT-1999
GB_INT.CET2003	32679	Z68220	Caenorhabditis elegans cDNA clone yK2662.3, mRNA sequence.	Caenorhabditis elegans	36,067	2-Sep-99
GB_EST120.AA890639	281	AA890639	TEN50989 T. cruzi eplasmid normalized cDNA Library Trypanosoma cruzi cDNA clone 689.5, mRNA sequence.	Trypanosoma cruzi	39,779	29-OCT-1998

TABLE 4: ALIGNMENT RESULTS

[illegible]

TABLE 4: ALIGNMENT RESULTS

na01248	529	GB_BA1.ECOUW93	338534	173897	AC007521	Drosophila melanogaster chromosome X clone BACR49A04 (D698) RPCI-98 49 A.A map 10x2-10B2 strain Y, on bw sp. *** SEQUENCING IN PROGRESS***, 56 unordered pieces.	Drosophila melanogaster	40,137	17-Nov-99
		GB_BA1.DRO600	137740	D90900	U14003	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	40,546	17-Apr-96
		GB_BA1.ECOUW93	338534	U14003	U14003	Synechocystis sp. PCC6803 complete genome, 2/27, 133680-271599.	Synechocystis sp.	32,177	7-Feb-99
na01272	726	GB_EST10.AA181367	520	AA181367	520	Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.	Escherichia coli	37,044	17-Apr-96
		GB_VI.FBU42580	330742	U42580	330742	IMAGE612116.3 mRNA sequence.	Homo sapiens	41,408	09-MAR-1998
		GB_VI.AF053866	236120	AF053866	236120	Paramecium bursaria Chlorella virus 1, complete genome.	Paramecium bursaria	38,265	4-Nov-99
na01388	435	GB_BA2.AF164439	783	AF164439	783	Myeloplasma sanguinipes entomopoxvirus, complete genome.	Chlorella virus 1	38,579	22-DEC-1998
		GB_BA1.MTV015	1688	AL021840	1688	Myobacterium smegmatis WhmD (whmD) gene, complete cds; and unknown gene.	Myobacterium smegmatis	57,477	4-Aug-99
		GB_BA1.SGWHIB	593	X69708	593	Myobacterium tuberculosis H37Rv complete genome, segment 140/162.	Myobacterium tuberculosis	37,617	17-Jun-98
na01375	1578	GB_BA1.MTCY71	42729	Z92771	42729	S. gregocarnum whB-SN gene.	Streptomyces gregocarnus	53,586	17-Jan-94
		GB_IN2.AC005935	29330	AC005935	29330	Myobacterium tuberculosis H37Rv complete genome, segment 141/162.	Myobacterium tuberculosis	52,638	10-Feb-99
		GB_IN2.AF005195	1952	AF005195	1952	Leishmania major chromosome 3 clone LZ34 strain Friedlin, complete sequence.	Leishmania major	39,177	15-Nov-99
na01418	369	GB_IN2.CELC53B7	29535	U42830	29535	Trypanosoma cruzi parafagellar rod component Par3 (par3b) mRNA, complete cds.	Trypanosoma cruzi	40,304	17-Aug-98
		GB_IN1.CEU49449	1118	U49449	1118	Caenorhabditis elegans cosmid C53B7.	Caenorhabditis elegans	34,375	03-MAR-1998
		GB_EST35.A1871077	295	A1871077	295	Caenorhabditis elegans olfactory receptor Od1-10 (odr-10) mRNA, complete cds.	Caenorhabditis elegans	47,111	17-MAY-1996
na01450	687	GB_BA1.MTV017	67200	AL021897	67200	wf70c12.x1 NCL CGAP. Brn25 Homo sapiens cDNA clone IMAGE 2430282 3' similar to gb:X70683, cds1 SOX-4 PROTEIN (HUMAN), mRNA sequence.	Homo sapiens	37,722	30-Aug-99
		GB_BA1.MAMAMIRM	4072	X79027	4072	Myobacterium tuberculosis H37Rv complete genome, segment 48/162.	Myobacterium tuberculosis	60,659	24-Jun-99
		GB_HTG3.AC009121	46469	AC009121	46469	M. ammoniaphilum genes mamIR and mamIM.	Microbacterium ammoniaphilum	39,912	20-Nov-96
na01451	690	GB_BA1.MTV017	67200	AL021897	67200	Homo sapiens chromosome 16 clone RPCI-11_48557, *** SEQUENCING IN PROGRESS ***. 32 unordered pieces.	Homo sapiens	55,507	3-Aug-99
		GB_BA1.MAMAMIRM	4972	X79027	4972	Myobacterium tuberculosis H37Rv complete genome, segment 48/162.	Myobacterium tuberculosis	63,516	24-Jun-99
na01500	567	GB_BA1.MLCB1222	34714	AL049491	34714	M. ammoniaphilum genes mamIR and mamIM.	Microbacterium ammoniaphilum	37,113	20-Nov-96
		GB_IN1.CEC0365	28688	Z46791	28688	Myobacterium leprae cosmid B1222.	Myobacterium leprae	36,324	24-Jun-99
		GB_GSS9.AC096256	390	AC096256	390	Caenorhabditis elegans cosmid C9G55, complete sequence.	Caenorhabditis elegans	36,398	2-Sep-99
		GB_HTG1.HS1099D15	1301	AL035456	1301	HS_3037.A1.F11.MF.CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3037, Col=E21 Row=K, genomic survey sequence.	Homo sapiens	46,316	27-Aug-98
na01537	774	GB_RO.RNCSYCLMB	2354	X64589	2354	Homo sapiens chromosome 20 clone RPS-1099D15, *** SEQUENCING IN PROGRESS ***. In unordered pieces.	Homo sapiens	39,388	23-Nov-99
		GB_RO.RATCYCLMB	1465	L11995	1465	R. norvegicus mRNA for cyclin B.	Rattus norvegicus	40,584	29-MAR-1994
		GB_RO.RNCSYCLMB	1902	X60768	1902	Rattus norvegicus cyclin B mRNA, complete cds.	Rattus norvegicus	40,584	3-Feb-98
						Rat mRNA for cyclin B.	Rattus norvegicus	40,530	15-Aug-96

TABLE 4: ALIGNMENT RESULTS

rsx01573	2205	GB_HTG4.ACO11317	40524	AC011317	Homo sapiens chromosome 3 seeders done RPO111-103G8, ***SEQUENCING IN PROGRESS ***. 31 unordered pieces.	34,814	21-OCT-1999
		GB_HTG4.ACO11317	40524	AC011317	Homo sapiens chromosome 3 seeders done RPO111-103G8, ***SEQUENCING IN PROGRESS ***. 31 unordered pieces.	34,814	21-OCT-1999
		GB_INT1.CEI.K06A5	24323	AF039038	Caenorhabditis elegans cosmid K06A5.	38,899	1-Jan-98
rsx01655	1482	GB_GSS15.AO624398	460	AQ624398	Hs_2106, B2, C03, TTC.CTC Approved Human Genomic Sperm Library D	36,449	16-Jun-99
		GB_BA1.SC6G10	36734	AL049467	Homo sapiens genomic clone Plate=2106 Col=6 Row=F, genomic survey sequence.	39,098	24-MAR-1999
		GB_BA1.MLCB288	38859	AL026802	Streptomyces coelicolor cosmid 6G10.	39,891	27-Aug-99
		GB_OVPMU11880	16201	U11880	Petromyzon marinus mitochondrion, complete genome.	36,977	24-Sep-96
		GB_STS.G39160	605	G39160	Z13915 Zebrafish AB Danio rerio STS genomic, sequence tagged site.	36,093	30-Jul-98
		GB_STS.G39160	605	G39160	Z13915 Zebrafish AB Danio rerio STS genomic, sequence tagged site.	36,093	30-Jul-98
rsx01763	586	GB_GSS4.AQ701186	454	AQ701186	HS_2129, A2, D04, TTC.CTC Approved Human Genomic Sperm Library D	40,000	7-Jul-99
		GB_BA1.ENNEPD1	5363	D28859	Homo sapiens genomic clone Plate=2129 Col=8 Row=G, genomic survey sequence.	37,117	7-Feb-99
		GB_BA1.ENNEPD1A	8526	D78016	Enterococcus faecalis Plasmid pPD1 DNA for IPD1, TrAB, TrAC, ORF1 and TrAC, complete cds.	35,788	5-Feb-99
		GB_BA1.MLCB11770	37821	Z70722	Enterococcus faecalis Plasmid pPD1 genes for REPB, REPA, TRAC, TRAB, TRAA, IPD1, TRAE, TRAF, complete cds and partial cds.	37,524	29-Aug-97
		GB_BA1.SC6H9	35824	AL079308	Myobacterium leprae cosmid B1770.	51,185	15-Jun-99
		GB_BA1.SC6D3	33779	AL066822	Streptomyces coelicolor cosmid H69.	38,775	8-Jul-99
		GB_BA1.MTCY10H4	39160	Z80233	Streptomyces coelicolor cosmid GD3.	37,815	17-Jun-98
rsx01827	4530	GB_BA1.A016932	2711	AF016932	Myobacterium tuberculosis H37Rv complete genome, segment Z162.	42,543	11-Nov-98
		GB_RO.AF145705	2201	AF145705	Streptomyces coelicolor protein gene for protein seneithreonine kinase, complete cds.	40,438	2-Jun-99
rsx01830	1476	GB_PR2.HSU02672	156854	U82672	Mus musculus T2K protein kinase homolog mRNA, complete cds.	36,389	12-MAY-1997
		GB_BA2.AF087482	26245	AF087482	Human chromosome X clone Cc15B1, complete sequence.	40,805	31-OCT-1998
		GB_PR2.HSU02672	156854	U82672	Pseudomonas aeruginosa cdc and ohbH genes, Lys-R type regulatory protein (cdtR), chlorocatechol-1,2-dioxygenase (cdA), chlorocatechol cycloisomerase (cdB), dienealdolase (cdC), methylglutamate reductase (cdE), transposase (tnpA), ATP-binding protein (tnpB), putative regulatory protein (ohbR), o-halobenzoyl dioxygenase reductase (ohbA), o-halobenzoyl dioxygenase alpha subunit (ohbS), o-halobenzoyl dioxygenase beta subunit (ohbC), o-halobenzoyl dioxygenase ferredoxin (ohbD), putative membrane spanning protein (ohbE), ATP-binding protein (ohbF), putative substrate binding protein (ohbG), and putative dioxygenase genes, complete cds; and unknown gene.	36,301	12-MAY-1997
		GB_PR2.HSU02672	156854	U82672	Human chromosome X clone Cc15B1, complete sequence.	33,481	10-MAR-1998

TABLE F. 4: ALIGNMENT RESULTS

GB_EST18-AA692868	461	AA62868	vr5812 st1 Knowles Soller mouse 2 cell Mus musculus cDNA clone IMAGE:1124903 5' mRNA sequence.	Mus musculus	16-DEC-1997
GB_PR3-HSDJ660P4	156791	AL049594	Human DNA sequence from clone 880P4 on chromosome 20 Contains ESTs, STSs, GSSs and a CpG island, complete sequence.	Homo sapiens	23-Nov-99
GB_BA1-D09814	145709	D09814	Synchoyistis sp. PC6803 complete genome, 16/27 1590-2137258.	Synchoyistis sp.	7-Feb-99
GB_EST25-AU041657	306	AU041657	AU041657 Mouse four-cell embryo cDNA Mus musculus cDNA clone J1007D01 3' mRNA sequence.	Mus musculus	04-DEC-1998
GB_PL2-AU829633	474	U82933	Alternaria alternata Alt a 1 subunit mRNA, complete cds.	Alternaria alternata	13-Jan-97
GB_PL2-AU829635	97789	AC004235	Arabisopsis italiana BAC T11F9 complete cDNA, complete sequence.	Arabisopsis italiana	18-Apr-98
GB_BA1-BSU00005	213190	Z99107	Bacillus subtilis complete genome (section 4 of 21): from 600701 to 613990.	Bacillus subtilis	26-Nov-97
GB_BA1-BSU00016	20341	D86418	Bacillus subtilis genomic DNA 69-70 degree region, partial sequence.	Bacillus subtilis	7-Feb-99
GB_HTG4-AC009949	173517	AC009949	Homo sapiens chromosome unknown clone NH068907, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	29-OCT-1999
GB_HTG4-AC009949	173517	AC009949	Homo sapiens chromosome unknown clone NH068907, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	29-OCT-1999
GB_HTG4-AC009949	173517	AC009949	Homo sapiens chromosome unknown clone NH068907, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	29-OCT-1999
GB_HTG1-CEV48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	1-Apr-99
GB_HTG1-CEV48B6	293827	AL021151	Caenorhabditis elegans chromosome II clone Y48B6, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	1-Apr-99
GB_HTG1-CEV53FA_2	2110000	Z92860	Caenorhabditis elegans chromosome II clone Y53FA, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	Z92860
GB_PR3-HSB4259P1	48094	AL080273	Human DNA sequence from clone 259P1 on chromosome 22. Contains STSs, GSSs, genomic markers D22S1154, D22S310 and D22S890, and a g repeat polymorphism, complete sequence.	Homo sapiens	23-Nov-99
GB_BA1-RHMIN0	2882	M19019	R.fedi1 host-inducible protein genes A and B, complete cds.	Shinorhizobium fredii	26-Apr-93
GB_BA2-AE000108	10894	AE000108	Rhizobium sp. NGR234 plasmid pNGR234a, section 45 of 46 of the complete plasmid sequence.	Rhizobium sp. NGR234	12-DEC-1997
GB_BA1-D09811	143051	D09811	Synchoyistis sp. FC6803 complete genome, 13/27 1576593-1719643	Synchoyistis sp.	7-Feb-99
GB_PR2-AC002477	124095	AC002477	Human PAC clone DJ327A19 from Xq25-q26, complete sequence.	Homo sapiens	22-Aug-97
GB_PR2-AC002477	124095	AC002477	Human PAC clone DJ327A19 from Xq25-q26, complete sequence.	Homo sapiens	22-Aug-97
GB_BA1-AB025424	2995	AB025424	Corynebacterium glutamicum gene for acetylase, partial cds.	Corynebacterium glutamicum	3-Apr-99
GB_EST15-AA534896	4890	AA534896	nrF602 s1 NC1, CGAP. C03 Homo sapiens cDNA clone IMAGE:526042 3', mRNA sequence.	Homo sapiens	21-Aug-97
GB_BA1-AB025424	2995	AB025424	Corynebacterium glutamicum gene for acetylase, partial cds.	Corynebacterium glutamicum	3-Apr-99
GB_BA1-MTCVY154	13935	Z98209	Mycobacterium tuberculosis H37Rv complete genome, segment 121/162.	Mycobacterium tuberculosis	17-Jun-98
GB_BA1-MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone Y154.	Mycobacterium tuberculosis	03-DEC-1996
GB_BA1-SC4H2	38400	AL022268	Streptomyces coelicolor complete cds.	Streptomyces coelicolor	6-Apr-98
GB_BA1-AP000004	217000	AP000004	Pycococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (47).	Pycococcus horikoshii	8-Feb-99
GB_BA1-AP000004	217000	AP000004	Pycococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (47).	Pycococcus horikoshii	8-Feb-99
GB_HTG3-AC008403	199233	AC008403	Homo sapiens chromosome 19 clone CIT-HSPC, Z73B12, *** SEQUENCING IN PROGRESS ***, 82 unordered pieces.	Homo sapiens	3-Aug-99

TABLE 4: ALIGNMENT RESULTS

na02306	414	GB_EST8:AA011641	313	AA011641	20z011.s1 Soares, fetal, liver, spleen, INFILS, S1 Homo sapiens cDNA clone IMAGE:423644.3 mRNA sequence.	Homo sapiens	35,235	09-MAY-1997
		GB_GSS1:CN500NAO	527	AL081678	Arabidopsis thaliana genome survey sequence SP8 end of BAC F3H19 of IGF library from strain Columbia of Arabidopsis thaliana, genomic survey sequence.	Arabidopsis thaliana	40,615	28-Jun-99
na02376	1626	GB_EST4:C97772	494	C97772	C97772 Rice callus Oyza saliva cDNA clone C92702_6Z, mRNA sequence.	Oyza saliva	36,667	19-OCT-1998
		GB_BA1:U00016	42301	U00016	Mycobacterium leprae cosmid B1937.	Mycobacterium leprae	67,483	01-MAR-1994
		GB_BA1:MTCY253	41230	21358	Mycobacterium tuberculosis H37Rv complete genome, segment 106/162.	Mycobacterium tuberculosis	37,888	17-Jun-98
		GB_BA1:BACJH642	282700	D94432	Bacillus subtilis DNA, 283 kb region containing sig element.	Bacillus subtilis	58,496	6-Feb-99
		GB_BA2:CGU31230	3005	U31230	Corynebacterium glutamicum Olg protein homolog gene, partial cds, gamma glutamyl kinase (proB) gene, complete cds, and (unintd) gene, complete cds.	Corynebacterium glutamicum	97,504	2-Aug-96
		GB_BA1:D87915	1647	D87915	Streptomyces coelicolor DNA for Olg, complete cds.	Streptomyces coelicolor	58,013	7-Feb-99
		GB_BA1:MTV016	53662	AL021841	Mycobacterium tuberculosis H37Rv complete genome, segment 143/162.	Mycobacterium tuberculosis	38,051	23-Jun-99
na02450	678	GB_BAZ:AE000654	12391	AE000654	Helicobacter pylori 26695 section 132 of 134 of the complete genome.	Helicobacter pylori	36,269	6-Apr-99
		GB_HTG3:AC009298	155826	AC009298	Homo sapiens clone NH001706, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.	Homo sapiens	35,886	13-Aug-99
		GB_HTG4:AC010187_2	110000	AC010187	Homo sapiens chromosome 3 seeders clone RPC111-38909, ***SEQUENCING IN PROGRESS ***, 164 unordered pieces.	Homo sapiens	38,939	AC010187
na02463	1362	GB_BA1:GGBETPQEN	2339	X93514	C. glutamicum bsp. gene.	Corynebacterium glutamicum	38,346	8-Sep-97
		GB_BA1:SHGCP1R	107379	X86780	S. hygroscopicus gene cluster for polyketide immunosuppressant rapamycin.	Streptomyces hygroscopicus	42,566	16-Aug-96
		GB_HTG2:AC007084	138793	AC007084	26 A.16 map 43F-44A strain y, on bw sp. *** SEQUENCING IN PROGRESS***, 19 unordered pieces.	Drosophila melanogaster	35,985	2-Aug-99
na02494	819	GB_BA1:U00018	42991	U00018	Mycobacterium leprae cosmid B2168.	Mycobacterium leprae	42,105	01-MAR-1994
		GB_BA1:MTCY2059	37218	277182	Mycobacterium tuberculosis H37Rv complete genome, segment 251/62.	Mycobacterium tuberculosis	64,552	17-Jun-98
		GB_BA1:MBY11827	2208	Y13627	Mycobacterium bovis BCG senX3, repX3 genes.	Mycobacterium bovis BCG	64,428	6-Jan-98
na02631	1488	GB_EST17:AA655226	468	AA655226	v08a410.s1 Knowles Soller mouse 2 cell Mus musculus cDNA clone IMACE-1108966.5 similar to gb-J03827 Y BOX BINDING PROTEIN-1 (HUMAN), gb-M62867 Mouse Y box transcription factor (MOUSE), mRNA sequence.	Mus musculus	36,052	4-Nov-97
		GB_GSS1:CN5012G3	898	AL101527	Drosophila melanogaster genome survey sequence T7 end of BAC BACN07105 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	Drosophila melanogaster	34,149	26-Jul-99
		GB_GSS3:B10133	1137	B10133	F2H22-17 IGF Arabidopsis thaliana genomic clone F2H22, genomic survey sequence.	Arabidopsis thaliana	38,011	14-MAY-1997
na02632	819	GB_BA1:MTCY369	36850	260226	Mycobacterium tuberculosis H37Rv complete genome, segment 361/62.	Mycobacterium tuberculosis	50,124	17-Jun-98
		GB_BA1:579966	480	S79966	[BCG2 insert site] Mycobacterium tuberculosis, BCG Japan, IS6110IS986, insertion, 480 nt].	Mycobacterium tuberculosis	39,437	27-Jul-95
		GB_PR3:AC005019	186362	AC005019	Homo sapiens BAC clone GS204A16 from 7p21-p22, complete sequence.	Homo sapiens	36,763	27-Aug-98
		GB_BA1:MSGY23	40506	AD000016	Mycobacterium tuberculosis sequence from clone y23.	Mycobacterium tuberculosis	55,142	10-DEC-1996
na02667	717	GB_BA1:MTV024	8169	AL020275	Mycobacterium tuberculosis H37Rv complete genome, segment 151/162.	Mycobacterium tuberculosis	39,474	17-Jun-96
		GB_BA1:MLCB1450	38065	AL035159	Mycobacterium leprae cosmid B1450.	Mycobacterium leprae	39,896	27-Aug-99

TABLE 4: ALIGNMENT RESULTS

na02668 846	GB_HTG32:AC007739	158262	AC007739	Homo sapiens clone NH0091L03 *** SEQUENCING IN PROGRESS ***	4	Homo sapiens	38,659	5-Jun-99
	GB_HTG32:AC007739	158262	AC007739	unordered pieces.				
	GB_HTG32:AC007739	158262	AC007739	Homo sapiens clone NH0091L03 *** SEQUENCING IN PROGRESS ***	4	Homo sapiens	38,659	5-Jun-99
	GB_EST14:A1190741	443	A1190741	q651a09 x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:173944		Homo sapiens	39,661	28-OCT-1998
	GB_HTG32:AC007739	158262	AC007739	3' mRNA sequence.		Homo sapiens	36,230	5-Jun-99
na02669 1239	GB_HTG32:AC007739	158262	AC007739	Homo sapiens clone NH0091L03 *** SEQUENCING IN PROGRESS ***	4	Homo sapiens	36,230	5-Jun-99
	GB_HTG32:AC007739	158262	AC007739	unordered pieces.				
	GB_GSS9:AO128685	425	AO128685	Homo sapiens clone NH0091L03 *** SEQUENCING IN PROGRESS ***	4	Homo sapiens	36,235	23-Sep-98
	GB_EST18:AA704727	398	AA704727	Homo sapiens genomic clone Plasmid-3026: Cui=20 Row=H1 genomic survey		Homo sapiens	40,470	24-DEC-1997
	GB_PR2:AP000228	76698	AP000228	IMAG4:450945 3' mRNA sequence.		Homo sapiens	42,616	20-Nov-99
	GB_PR2:AP000140	100000	AP000140	Homo sapiens genomic DNA, chromosome 21q21.2, LL56-APP region, clone R49K20, complete sequence.		Homo sapiens	42,616	20-Nov-99
na02699 2271	GB_GSS12:AQ364540	497	AQ364540	Homo sapiens genomic DNA, chromosome 21q21.2, LL56-APP region, clone B2291C14-R44F-3, segment 5' to 10, complete sequence.		Oryza sativa	37,903	3-Feb-99
	GB_PR4:AC006044	141509	AC006044	nbx0001009r CUGI Rice BAC Library Oryza sativa genomic clone		Homo sapiens	36,360	18-MAR-1999
	GB_PR2:HSFA001552	91528	AF001552	nbx0001009r genomic survey sequence.		Homo sapiens	35,352	21-Aug-97
	GB_HTG32:HSU13908	167079	AL096814	Homo sapiens BAC clone NH0539624 from 7p15.1-p14, complete sequence.		Homo sapiens	38,820	03-DEC-1999
na02724 967	GB_HTG32:HSU13908	167079	AL096814	Homo sapiens chromosome 6 clone RP1-139D8 map p12.1, 2.1.1, ***SEQUENCING IN PROGRESS ***		Homo sapiens	38,820	03-DEC-1999
	GB_BA1:AB015853	5461	AB015853	Homo sapiens chromosome 6 clone RP1-139D8 map p12.1, 2.1.1, ***SEQUENCING IN PROGRESS ***		Homo sapiens	39,121	13-Nov-98
na02747 2199	GB_BA1:CAJ10319	5368	AJ010319	Pseudomonas aeruginosa gene for MexX and MexY, complete cds.		Pseudomonas aeruginosa	100,000	14-MAY-1999
	GB_GSS13:AO463737	463	AO463737	Corynebacterium glutamicum amrP, glnB, glnD genes and partial tsyA and srp genes.		Corynebacterium glutamicum	37,549	23-Apr-99
	GB_BA1:CAJ10319	5368	AJ010319	HS_5951, B2, D05, SPRE RPOC-11 Human Male BAC Library Homo sapiens genomic clone Plasmid-827 Cui=10 Row=H1 genomic survey sequence.		Corynebacterium glutamicum	100,000	14-MAY-1999
na02760 1077	GB_IN2:AC004295	84551	AC004295	Corynebacterium glutamicum amrP, glnB, glnD genes and partial tsyA and srp genes.		Corynebacterium glutamicum	40,303	29-Jul-98
	GB_HTG6:AC011647	141830	AC011647	Drosophila melanogaster DNA sequence (P1 DS08374 (D180)), complete sequence.		Drosophila melanogaster	38,158	04-DEC-1999
	GB_HTG6:AC011647	141830	AC011647	Homo sapiens clone RP11-15D18, *** SEQUENCING IN PROGRESS ***	29	Homo sapiens	36,321	04-DEC-1999
	GB_HTG6:AC011647	141830	AC011647	unordered pieces.				
	GB_BA1:MSGB937CS	38614	L78820	Homo sapiens clone RP11-15D18, *** SEQUENCING IN PROGRESS ***	29	Homo sapiens	57,533	27-Aug-99
na02787 1500	GB_BA1:MSGB937CS	38614	L78820	unordered pieces.			57,533	27-Aug-99
	GB_PR4:AC006474	69718	AC006474	Mycobacterium leprae cosmid B1259		Mycobacterium leprae	57,600	15-Jun-96
	GB_PR4:AC006474	69718	AC006474	Mycobacterium leprae cosmid B937 DNA sequence.		Mycobacterium leprae	37,246	1-Jul-99
	GB_PR4:AC006474	69718	AC006474	Homo sapiens clone DJ069117, complete sequence.		Homo sapiens		

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 Ser Asn Pro Phe Phe Leu Glu Ile Phe Arg Gly Ala Gln His Ala Ala 35
 25 30

agc act cag ggc tat acg gtt gcg ctt gtc gac gcc cgg gag tcg gcg 259
 Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp Ala Arg Glu Ser Ala 50
 40 45

att aag tcc agg gag gtg ctg gac aag atc gtc ccc cac gcc gat ggc 307
 Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val Pro His Ala Asp Gly 65
 55 60

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 Leu Leu Leu Ala Ala Ser Arg Met Asp Ser Gly Glu Ile His Lys Val 85
 70 75 80

gcg cgg gaa att ccc act gta tta atg agc cgt gaa gtg caa ggt att 403
 Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg Glu Val Gln Gly Ile 100
 90 95

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 Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala Pro Lys Ala Val Val 115
 105 110

cat ttg gtg gat cag ggg tgc cgc tcc att acc tat atc gcc ggt cct 499
 His Leu Val Asp Gln Gly Cys Arg Ser Ile Thr Tyr Ile Ala Gly Pro 130
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Ala Gln His Ala Ala Ser Thr Gln Gly Tyr Thr Val Ala Leu Val Asp 45
 35 40

Ala Arg Glu Ser Ala Ile Lys Ser Arg Glu Val Leu Asp Lys Ile Val 60
 50 55

Pro His Ala Asp Gly Leu Leu Ala Ala Ser Arg Met Asp Ser Gly 80
 65 70 75

Glu Ile His Lys Val Ala Arg Glu Ile Pro Thr Val Leu Met Ser Arg 95
 85 90

Glu Val Gln Gly Ile Pro Ser Val Met Val Asp Asn Tyr Asp Gly Ala 110
 100 105

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120 125 130

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 Ala Gly Leu
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 <213> Corynebacterium glutamicum

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 35 40 45
 Arg Glu Thr Ala Gln Thr Thr Ser Thr Val Glu Gln Arg Val Ala Ala
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 Ala Leu Gln His Leu Asp Ala Lys Leu Gly Gln Ile Arg Gln Asp Gly
 65 70 75 80
 Ser Ser Leu Leu Gln Val Arg Leu Arg Arg Asp Asp Val Ala Gly Thr
 85 90 95
 Thr Val Glu Ser Ala Ser Arg Ala Met Ala Arg Met Lys Lys Thr Gly
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 <223> RXN02910

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 Val Glu Ile Arg Trp
 1 5
 ttg gaa ggc ttt atc gcg gtc gcg gaa gaa ttg cac ttt agt aat gct 163
 Leu Glu Gly Phe Ile Ala Val Ala Glu Glu Leu His Phe Ser Asn Ala
 10 15 20

gcg att cgt ttg ggg atg ccg caa tgc ccg ttg agt cag ttg atc cgg 211
 Ala Ile Arg Leu Gly Met Pro Gln Ser Pro Leu Ser Gln Leu Ile Arg
 25 30 35

cgg ttg gag tgc gag ttg ggg cag aag ctt ttt gat cgc agt acc cgg 259
 Arg Leu Glu Ser Glu Leu Gly Gln Lys Leu Phe Asp Arg Ser Thr Arg
 40 45 50

tgc gtg gag tta act gcc gcg ggt cgg gcg ttt ttg cca cat gcc agg 307
 Ser Val Glu Leu Thr Ala Ala Gly Arg Ala Phe Leu Pro His Ala Arg
 55 60 65

ggg att gtg gcg agc gct gcg gtg gcg agg gaa gct gtg aat gct gcc 355
 Gly Ile Val Ala Ser Ala Ala Val Ala Arg Glu Ala Val Asn Ala Ala
 70 75 80 85

gag ggg gag atc gtt ggt gtt gtt cgc att ggt ttt tct ggt gtg ctg 403
 Glu Gly Glu Ile Val Gly Val Val Arg Ile Gly Phe Ser Gly Val Leu
 90 95 100

aac tat tcc acg ctg ccg ctt ttg acc agt gag gtg cat aaa cgg ctt 451
 Asn Tyr Ser Thr Leu Pro Leu Leu Thr Ser Glu Val His Lys Arg Leu
 105 110 115

cct aat gtg gag ttg gag ctg gtt ggt cag aag ttg acg agg gaa gcg 499
 Pro Asn Val Glu Leu Glu Leu Val Gly Gln Lys Leu Thr Arg Glu Ala
 120 125 130

gta agt ttg ctg cgc ttg ggg gcg ttg gat att acg ttg atg ggt ttg 547
 Val Ser Leu Leu Arg Leu Gly Ala Leu Asp Ile Thr Leu Met Gly Leu
 135 140 145

ccc att gag gat cca gag att gag act cgg ctg att agt ttg gaa gag 595
 Pro Ile Glu Asp Pro Glu Ile Glu Thr Arg Leu Ile Ser Leu Glu Glu
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 Phe Cys Val Val Leu Pro Lys Asp His Arg Leu Ala Gly Glu Gly Val
 170 175 180

gtg gat ttg gtg gat ctg gct aaa gat ggg ttt gtg acg acg ccg gag 691
 Val Asp Leu Val Asp Leu Ala Lys Asp Gly Phe Val Thr Thr Pro Glu
 185 190 195

ttt gcg ggg tct gtg ttt agg aat tcc acc ttt cag ttg tgt gct gag 739
 Phe Ala Gly Ser Val Phe Arg Asn Ser Thr Phe Gln Leu Cys Ala Glu
 200 205 210

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 Ala Gly Phe Val Pro Arg Ile Ser Gln Gln Val Asn Asp Pro Tyr Met
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Gly Ile Pro Pro Leu Pro Pro Ala Glu Val Val Ala Ile Ser Leu His	50	55	60
Leu Val Asn Ala Gly Phe Arg Thr Glu Asp Leu Ala Glu Thr Tyr Val	65	70	75
Met Thr Gly Val Phe Glu Gln Leu Phe Glu Val Ile Asp Ser Ser Phe	85	90	95
Gly Ile Thr Leu Asp Arg Gln Ser Val Asn Ala Ala Arg Phe Ile Thr	100	105	110
His Met Arg Tyr Phe Phe Val Arg Val His His Asp Gly Gln Leu Asn	115	120	125
Asp Gly Met Ser Val Leu Arg Asn Ser Leu Glu Ile Ser His Pro Asp	130	135	140
Ser Val Ala Cys Ala Glu Arg Leu Ser Gln Ile Leu Ser Leu Arg Leu	145	150	155
Gly Ala Glu Leu Ser Ser Asp Glu Gln Thr Tyr Leu Ala Leu His Val	165	170	175
Ala Arg Leu Ala Glu Asp Arg Gly Thr Thr Ala Asp	180	185	

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 5

 cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga 163
 Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly 20
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 Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu 35
 25
 30

ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta 259
 Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu
 40 45 50

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg 307
 Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
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 Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
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gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403
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 90 95 100

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 Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp
 105 110 115

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 Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly
 120 125 130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt 547
 Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe
 135 140 145

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 Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala
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tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg 643
 Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu
 170 175 180

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 Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg
 185 190 195

atc gcc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg 739
 Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu
 200 205 210

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 215 220 225

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 Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys
 230 235 240 245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat 883
 Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn
 250 255 260

gca gaa cga aaa ggc gat acc taaacccgcc ctccatctgc ata 927
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00502674-152300

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 65 70 75 80
 Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
 85 90 95
 Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
 100 105 110
 Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
 115 120 125
 Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
 130 135 140
 Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
 145 150 155 160
 Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
 165 170 175
 Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
 180 185 190
 His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
 195 200 205
 His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
 210 215 220
 Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
 225 230 235 240
 Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
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<213> *Corynebacterium glutamicum*

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<223> RXS00774

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Asp Ala Leu Leu Arg Thr Ser Leu Ala Ser Ala Glu Ser Ala Leu Gly
10 15 20

aat gca gaa aag ctt gaa gag ctt cgt act gga tgc gag tct caa gcc 211
Asn Ala Glu Lys Leu Glu Glu Leu Arg Thr Gly Cys Glu Ser Gln Ala
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gtc gaa ctt ttg gcg ctt gaa act cct gta gcc cgt gat ctt cgc cag 259
Val Glu Leu Leu Ala Leu Glu Thr Pro Val Ala Arg Asp Leu Arg Gln
40 45 50

gtt gtc tcc tcc atc tac atc gtc gag gaa att acc cgt atg ggt gct 307
Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile Thr Arg Met Gly Ala
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 Leu Ala Met His Val Ala Asn Ser Val Arg Arg Arg Tyr Pro Asp Pro
 70 75 80 85

gtg atc ccg gag gac atg cgt ggc tat ttc aag gag atg gcc cgc ctc 403
Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys Glu Met Ala Arg Leu
90 95 100

gca gct gac atg aca gat cat att cgt cag atc ctc att gat cct gaa 451
Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile Leu Ile Asp Pro Glu
105 110 115

cca gat ctt gcc cta gag atg gct aaa agc gat gac gcg gtg gat gat 499
Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp Asp Ala Val Asp Asp
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Leu His Gln His Ile Met Arg Ile Leu Thr Leu Arg Pro Trp Pro His
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Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala Arg Ile Ile Tyr Leu
170 175 180

tcc acc ggg ctg cac ccg gag gag tac atg gaa aag cgc gag caa caa 691
Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu Lys Arg Glu Gln Gln
185 190 195

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Arg Asp Leu Arg Gln Val Val Ser Ser Ile Tyr Ile Val Glu Glu Ile
50 55 60

Thr Arg Met Gly Ala Leu Ala Met His Val Ala Asn Ser Val Arg Arg
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Arg Tyr Pro Asp Pro Val Ile Pro Glu Asp Met Arg Gly Tyr Phe Lys
85 90 95

Glu Met Ala Arg Leu Ala Ala Asp Met Thr Asp His Ile Arg Gln Ile
100 105 110

Leu Ile Asp Pro Glu Pro Asp Leu Ala Leu Glu Met Ala Lys Ser Asp
115 120 125

Asp Ala Val Asp Asp Leu His Gln His Ile Met Arg Ile Leu Thr Leu
130 135 140

Arg Pro Trp Pro His Asp Thr Lys Ser Ala Val Asp Leu Thr Leu Leu
145 150 155 160

Ser Arg Phe Tyr Glu Arg Tyr Ala Asp His Thr Val Asn Val Ala Ala
165 170 175

Arg Ile Ile Tyr Leu Ser Thr Gly Leu His Pro Glu Glu Tyr Met Glu
180 185 190

Lys Arg Glu Gln Gln Arg Ala Asp Ala Asp Met Glu Lys Arg Trp Ala
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Glu Leu Glu Arg Gln Phe Arg Thr Ser Glu
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<213> *Corynebacterium glutamicum*

<223> RXN02493

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Val Ser Thr Leu Leu
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Ala Phe Val Leu Gly Val Val Leu Met Gly Leu Ala Leu Pro Ala Tyr
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acg aaa att aaa gat cgg atg cgt cgc cac aag tcc gcg gtc acc ctg 211
Thr Lys Ile Lys Asp Arg Met Arg Arg His Lys Ser Ala Val Thr Leu
25 30 35

tcc gaa aac cag gtc acc acg gtg ggg cag gtc ctc cac ctg gcg att 259
Ser Glu Asn Gln Val Thr Thr Val Gly Gln Val Leu His Leu Ala Ile
40 45 50

caa ggc tcc cca acg gga atc acg gtt gtc gat cgc acc ggc gac gtc 307
Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp Arg Thr Gly Asp Val
55 60 65

atc tta tcc aac ggc cgc gcc cac gaa ttg ggc atc gtc cac gaa aga 355
Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly Ile Val His Glu Arg
70 75 80 85

tcc gtc gac ggc aac gtt tgg cgc gtc gcc cag gaa gcc ttc caa gac 403
Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln Glu Ala Phe Gln Asp
90 95 100

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Gln Glu Thr His Ser Leu Asp Val His Pro Asp Arg Asn Pro Arg Arg
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Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val Val Lys Pro Leu Thr
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Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala Ser Asp Glu Ser Glu
135 140 145

aac gtg cgc atg gaa tcg gca cgc cga gac ttc gtc gca aac gtc tcc 595
Asn Val Arg Met Glu Ser Ala Arg Arg Asp Phe Val Ala Asn Val Ser
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cac gaa ctg aaa acc ccc gtc ggc ggc atg gca ctc ctc gcg gaa gcc 643
His Glu Leu Lys Thr Pro Val Gly Gly Met Ala Leu Leu Ala Glu Ala
170 175 180

ctc atg gaa tcc tcc gac gac cca gaa caa gtc gaa tac ttc gga tcc 691
Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val Glu Tyr Phe Gly Ser

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<213> Corynebacterium glutamicum

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35 40 45

Leu His Leu Ala Ile Gln Gly Ser Pro Thr Gly Ile Thr Val Val Asp
50 55 60

Arg Thr Gly Asp Val Ile Leu Ser Asn Gly Arg Ala His Glu Leu Gly
65 70 75 80

Ile Val His Glu Arg Ser Val Asp Gly Asn Val Trp Arg Val Ala Gln
85 90 95

Glu Ala Phe Gln Asp Gln Glu Thr His Ser Leu Asp Val His Pro Asp
100 105 110

Arg Asn Pro Arg Arg Pro Gly Ser Arg Ile Thr Ala Val Gln Ala Val
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Val Lys Pro Leu Thr Leu Ile Asp Asp Arg Phe Val Ile Ile Tyr Ala
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Val Ala Asn Val Ser His Glu Leu Lys Thr Pro Val Gly Gly Met Ala
165 175

Leu Leu Ala Glu Ala Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val
180 185 190

Glu Tyr Phe Gly Ser Arg Leu His Arg Glu Ala His Arg Met Ala Asp
195 200 205

Met Ile Asn Glu Leu Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg
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Leu Pro Asp Met Glu Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala
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260 265 270

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275 280 285

Lys Ser Val Pro Val Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val
290 295 300

1995

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ccg	ggt	agt	cgc	atc	acc	gca	gtg	cag	gca	gtg	gtc	aag	cct	tta	acg		120				499
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Leu	Ile	Asp	Asp	Arg	Phe	Val	Ile	Ile	Tyr	Ala	Ser	Asp	Glu	Ser	Glu						
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Asn	Val	Arg	Met	Glu	Ser	Ala	Arg	Arg	Asp	Phe	Val	Ala	Asn	Val	Ser						
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cac	gaa	ctg	aaa	acc	ccc	gtc	ggc	ggc	atg	gca	ctc	ctc	cgc	gaa	gcc		165				643
His	Glu	Leu	Lys	Thr	Pro	Val	Gly	Gly	Met	Ala	Leu	Leu	Ala	Glu	Ala						
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Gly	Val	Trp	Val	Glu	Ala	Asp	Arg	Ser	Leu	Leu	Val	Thr	Ala	Leu	Ala						
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Val Ala Asn Val Ser His Glu Leu Lys Thr Pro Val Gly Gly Met Ala
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Leu Leu Ala Glu Ala Leu Met Glu Ser Ser Asp Asp Pro Glu Gln Val
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Glu Tyr Phe Gly Ser Arg Leu His Arg Glu Ala His Arg Met Ala Asp
195 200 205

Met Ile Asn Glu Leu Ile Ser Leu Ser Lys Leu Gln Gly Ala Glu Arg
210 215 220

Leu Pro Asp Met Glu Pro Val Gln Ala Asp Asp Ile Ile Ser Glu Ala
225 230 235 240

Ile Glu Arg Thr Gln Leu Ala Ala Asp Asn Ala Asn Ile Glu Ile Ile
245 250 255

Arg Gly Asp Arg Thr Gly Val Trp Val Glu Ala Asp Arg Ser Leu Leu
260 265 270

Val Thr Ala Leu Ala Asn Leu Ile Ser Asn Ala Ile Asn Tyr Ser Pro
275 280 285

Lys Ser Val Pro Val Ser Val Ser Gln Ser Ile Arg Asn Asp Val Val
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Met Ile Arg Val Thr Asp Arg Gly Ile Gly Ile Ala Pro Glu Asp Gln
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Gly Arg Val Phe Glu Arg Phe Phe Arg Val Asp Lys Ala Arg Ser Arg
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Gln Thr Gly Gly Thr Gly Leu Gly Leu Ala Ile Val Lys His Val Met
340 345 350

Ala Asn His Gly Gly Ser Ile Ser Leu Trp Ser Arg Pro Gly Thr Gly
355 360 365

Ser Thr Phe Thr Leu Glu Leu Pro Val Tyr His Pro Glu Ser Lys Glu
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<223> RXN00631

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Met Glu Asn Pro Tyr

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135 140 145																
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gtt gaa gag acc gcc acc agg att gcg ggc ggt gat ttg gat cga cgt	787															
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caa aaa gaa gct cag atg cgc cga ttc gtt ggc gat gcc tcc cac gag 931
 Gln Lys Glu Ala Gln Met Arg Arg Phe Val Gly Asp Ala Ser His Glu
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ctc cgc aca cca ctg acc tct gtg aag ggc ttc acc gag ctg tat tca 979
 Leu Arg Thr Pro Leu Thr Ser Val Lys Gly Phe Thr Glu Leu Tyr Ser
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 Ser Gly Ala Thr Asp Asp Ala Asn Trp Val Met Ser Lys Ile Gly Gly
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cgt gcc gaa ggc cag caa atg gag aag cac cgc gtt gac gtg ctg gaa 1123
 Arg Ala Glu Gly Gln Gln Met Glu Lys His Arg Val Asp Val Leu Glu
 330 335 340

ctc gcc ttg gca gta cgc gga tcc atg cga gca gcc tgg cca gat cgc 1171
 Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala Ala Trp Pro Asp Arg
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 Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile Pro Val Val Lys Gly
 360 365 370

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 Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn Leu Val Ala Asn Gly
 375 380 385

cta aac cac ggc gga cag gac gcg gaa gtc agc att gag atc aac acc 1315
 Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser Ile Glu Ile Asn Thr
 390 395 400 405

gat gga caa aac gtg agg att ctc gtg gca gac aac ggt gtc gga atg 1363
 Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp Asn Gly Val Gly Met
 410 415 420

tct gaa gaa gat gct cag cat atc ttc gag cgt ttc tac cgc gcc gat 1411
 Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg Phe Tyr Arg Ala Asp
 425 430 435

tcc tcc cgc tca cgc gca tcc ggc gga tgc ggc ctc ggc ctt gcg atc 1459
 Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly Leu Gly Leu Ala Ile
 440 445 450

acg aaa tcc ctg gtc gaa ggc cac ggc ggc aca gtc acc gtc gac agc 1507
 Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr Val Thr Val Asp Ser
 455 460 465

gtg caa ggc gaa ggc acg gtg ttc acg atc acc ttg cag gcg gtt tct 1555
 Val Gln Gly Glu Gly Thr Val Phe Thr Ile Thr Leu Pro Ala Val Ser
 470 475 480 485

1123
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275 280 285
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 Ser Lys Ile Gly Gly Glu Ala Gln Arg Met Ser Val Leu Val Glu Asp
 305 310 315 320
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 325 330 335
 Val Asp Val Leu Glu Leu Ala Leu Ala Val Arg Gly Ser Met Arg Ala
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 Ala Trp Pro Asp Arg Thr Val Asn Val Ser Asn Lys Ala Glu Ser Ile
 355 360 365
 Pro Val Val Lys Gly Asp Pro Thr Arg Leu His Gln Val Leu Thr Asn
 370 375 380
 Leu Val Ala Asn Gly Leu Asn His Gly Gly Pro Asp Ala Glu Val Ser
 385 390 395 400
 Ile Glu Ile Asn Thr Asp Gly Gln Asn Val Arg Ile Leu Val Ala Asp
 405 410 415
 Asn Gly Val Gly Met Ser Glu Glu Asp Ala Gln His Ile Phe Glu Arg
 420 425 430
 Phe Tyr Arg Ala Asp Ser Ser Arg Ser Arg Ala Ser Gly Gly Ser Gly
 435 440 445
 Leu Gly Leu Ala Ile Thr Lys Ser Leu Val Glu Gly His Gly Gly Thr
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 Leu Pro Ala Val Ser
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 <223> RXN00291

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 Ile Phe Ala Val Leu Met Met Asp Gln Met Lys Thr Glu Ala Glu His
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gaa Glu	tta Leu	gcc Ala	gat Asp 65	gga Gly	gat Asp	atc Ile	caa Gln	gcg Ala 70	ggt Val	gca Ala	cag Gln	gcg Ala	gcc Ala 75	aat Asn	gaa Glu	242
cgc Arg	act Thr	gga Gly 80	gct Ala	ttg Leu	ttt Phe	gtc Val	ggt Val 85	atc Ile	act Thr	gac Asp	ggt Gly	tta Leu 90	ggt Leu	atc Ile	cgc Arg	290
ctg Leu	tcc Ser 95	cac His	cca Pro	gat Asp	gag Glu 100	gaa Glu	cgt Arg	ctg Leu	ggg Gly	gag Glu 105	cag Gln	gtg Val	agc Ser	act Thr	agc Ser	338
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acc Thr	ctc Leu	ggt Gly	gcg Ala	tcc Ser 130	gcg Ala	cga Arg	gca Ala	aaa Lys	gtg Val 135	cct Pro	atc Ile	ttt Phe	gcg Ala	ccg Pro 140	gat Asp 140	434
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ctg Leu	gcg Ala	ctg Ser	agc Arg 225	cca Pro	aac Asn	gga Gly	aca Thr	att Ile 230	ggg Gly	gtg Val	gat His	aat Asn	cag Glu 235	cag Gln	gcg Ala	722
caa Gln	tcc Ser	atg Met 240	att Ile	ggt Gly	gca Ala	ggt Gly	cct Pro 245	atg Met	agt Ser	ggc Gly	agg Arg	acg Thr 250	ttg Leu	aaa Lys	gaa Glu	770
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Pro Glu Thr Val Ala His Asn Gly Arg Ile Leu Tyr Leu Asp Phe His
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ccc gtg cgc cgt ggg gat caa gat tta ggc tac gtg gta acc atc cgc 914
 Pro Val Arg Arg Gly Asp Gln Asp Leu Gly Tyr Val Val Thr Ile Arg
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gat cgt acc gac atc att gaa ctc agt gaa cgc ctc gac tct gtg cgc 962
 Asp Arg Thr Asp Ile Ile Glu Leu Ser Glu Arg Leu Asp Ser Val Arg
 305 310 315

acc atg acc cac gca ctc cgc gcc cag cgc cac gag ttt gcc aac cgc 1010
 Thr Met Thr His Ala Leu Arg Ala Gln Arg His Glu Phe Ala Asn Arg
 320 325 330

atc cac acc gca aca ggg ctt atc gac gcc ggc cgc gtc cac gac gcg 1058
 Ile His Thr Ala Thr Gly Leu Ile Asp Ala Gly Arg Val His Asp Ala
 335 340 345

gca gag ttt cta ggc gat ata tcc cgc aac ggg gga cag tca cat cca 1106
 Ala Glu Phe Leu Gly Asp Ile Ser Arg Asn Gly Gly Gln Ser His Pro
 350 355 360 365

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agt act gct tct att tcc gca tct gaa aag ggc gtt agt ctg cgc atc 1202
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 400 405 410

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 Ala Thr Ile Leu Gly Asn Leu Ile Asn Asn Ala Ile Asp Ala Ala Val
 415 420 425

gca ggt gaa gcc cca cgg tgg att gag ctt acg ttg atg gat gat gcc 1346
 Ala Gly Glu Ala Pro Arg Trp Ile Glu Leu Thr Leu Met Asp Asp Ala
 430 435 440 445

gat acg ctg gtc att tct gtt gca gat tct ggt cct gga atc cca gag 1394
 Asp Thr Leu Val Ile Ser Val Ala Asp Ser Gly Pro Gly Ile Pro Glu
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ggc gtg gat gta ttt gcc aca gcc acc cag ata gga gac tct gaa gat 1442
 Gly Val Asp Val Phe Ala Thr Ala Thr Gln Ile Gly Asp Ser Glu Asp
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aat gaa cgc acc cac ggg cat ggc att ggt cta aaa ctg tgc cgg gct 1490
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ttg gct aga tca cat ggt ggc gat gtc tgg gtg att gat aga gga acc 1538
 Leu Ala Arg Ser His Gly Gly Asp Val Trp Val Ile Asp Arg Gly Thr
 495 500 505

gaa gat ggc gct gta ttt gga gtg aaa cta ccg gga gta atg gag 1583
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515

520

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1606

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<213> Corynebacterium glutamicum

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Ala Leu Asp Thr Gln Thr Gly Ala Asn Pro Ser Ala Glu Glu Leu Ala
 50 55 60

Asp Gly Asp Ile Gln Ala Val Ala Gln Ala Ala Asn Glu Arg Thr Gly
 65 70 75 80

Ala Leu Phe Val Val Ile Thr Asp Gly Leu Gly Ile Arg Leu Ser His
 85 90 95

Pro Asp Glu Glu Arg Leu Gly Glu Gln Val Ser Thr Ser Phe Glu Ala
 100 105 110

Ala Met Arg Gly Glu Glu Thr Met Ala Trp Glu Thr Gly Thr Leu Gly
 115 120 125

Ala Ser Ala Arg Ala Lys Val Pro Ile Phe Ala Pro Asp Ser Ser Val
 130 135 140

Pro Val Gly Glu Val Ser Val Gly Phe Glu Arg Asp Ser Val Tyr Ser
 145 150 155 160

Arg Leu Pro Met Phe Leu Ala Ala Leu Ala Leu Ile Ser Val Leu Gly
 165 170 175

Ile Leu Ile Gly Val Gly Val Ala Met Gly Met Arg Arg Arg Trp Glu
 180 185 190

Arg Val Thr Leu Gly Leu Gln Pro Glu Glu Leu Val Thr Leu Val Gln
 195 200 205

Asn Gln Thr Ala Val Ile Asp Gly Ile Asp Glu Gly Val Leu Ala Leu
 210 215 220

Ser Pro Asn Gly Thr Ile Gly Val His Asn Glu Gln Ala Gln Ser Met
 225 230 235 240

Ile Gly Ala Gly Pro Met Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu
 245 250 255

Asp Leu Gly Leu Asp Gly Val Val Leu His Gly Gln His Pro Glu Thr
 260 265 270

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His	Ala	Leu	Arg	Ala	Gln	Arg	His	Glu	Phe	Ala	Asn	Arg	Ile	His	Thr	
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Ala	Thr	Gly	Leu	Ile	Asp	Ala	Gly	Arg	Val	His	Asp	Ala	Ala	Glu	Phe	
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Thr	Leu	Ile	Leu	Gly	Thr	Val	Lys	Asp	Pro	Glu	Asp	Val	Ala	Thr	Ile	
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 Asn Ala Ile Asp Ala Ala Val Ala Gly Glu Ala Pro Arg Trp Ile Glu
 260 265 270

ctt acg ttg atg gat gat gcc gat acg ctg gtc att tct gtt gca gat 864
 Leu Thr Leu Met Asp Asp Ala Asp Thr Leu Val Ile Ser Val Ala Asp
 275 280 285

tct ggt cct gga atc cca gag ggc gtg gat gta ttt gcc aca gcc acc 912
 Ser Gly Pro Gly Ile Pro Glu Gly Val Asp Val Phe Ala Thr Ala Thr
 290 295 300

cag ata gga gac tct gaa gat aat gaa cgc acc cac ggg cat ggc att 960
 Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg Thr His Gly His Gly Ile
 305 310 315 320

ggt cta aaa ctg tgc cgg gct ttg gct aga tca cat ggt ggc gat gtc 1008
 Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg Ser His Gly Gly Asp Val
 325 330 335

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 Trp Val Ile Asp Arg Gly Thr Glu Asp Gly Ala Val Phe Gly Val Lys
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Asp Gly Ile Asp Glu Gly Val Leu Ala Leu Ser Pro Asn Gly Thr Ile
 50 55 60

Gly Val His Asn Glu Gln Ala Gln Ser Met Ile Gly Ala Gly Pro Met
 65 70 75 80

Ser Gly Arg Thr Leu Lys Glu Leu Gly Leu Asp Leu Gly Leu Asp Gly
 85 90 95

Val Val Leu His Gly Gln His Pro Glu Thr Val Ala His Asn Gly Arg
 100 105 110

Ile Leu Tyr Leu Asp Phe His Pro Val Arg Arg Gly Asp Gln Asp Leu
 115 120 125

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Gly Tyr Val Val Thr Ile Arg Asp Arg Thr Asp Ile Ile Glu Leu Ser
 130 135 140
 Glu Arg Leu Asp Ser Val Arg Thr Met Thr His Ala Leu Arg Ala Gln
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 Arg His Glu Phe Ala Asn Arg Ile His Thr Ala Thr Gly Leu Ile Asp
 165 170 175
 Ala Gly Arg Val His Asp Ala Ala Glu Phe Leu Gly Asp Ile Ser Arg
 180 185 190
 Asn Gly Gly Gln Ser His Pro Leu Ile Gly Ser Ala His Leu Asn Glu
 195 200 205
 Ala Phe Leu Ser Ser Phe Leu Ser Thr Ala Ser Ile Ser Ala Ser Glu
 210 215 220
 Lys Gly Val Ser Leu Arg Ile Asn Ser Asp Thr Leu Ile Leu Gly Thr
 225 230 235 240
 Val Lys Asp Pro Glu Asp Val Ala Thr Ile Leu Gly Asn Leu Ile Asn
 245 250 255
 Asn Ala Ile Asp Ala Ala Val Ala Gly Glu Ala Pro Arg Trp Ile Glu
 260 265 270
 Leu Thr Leu Met Asp Asp Ala Asp Thr Leu Val Ile Ser Val Ala Asp
 275 280 285
 Ser Gly Pro Gly Ile Pro Glu Gly Val Asp Val Phe Ala Thr Ala Thr
 290 295 300
 Gln Ile Gly Asp Ser Glu Asp Asn Glu Arg Thr His Gly His Gly Ile
 305 310 315 320
 Gly Leu Lys Leu Cys Arg Ala Leu Ala Arg Ser His Gly Gly Asp Val
 325 330 335
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 Leu Pro Gly Val Met Glu
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<223> RXA00129

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Val Leu Gly Ser Ile
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ttc acc gca tca gct gtc gtg atg atc ctt ttg ggg ctg ggc atg ctg 163
Phe Thr Ala Ser Ala Val Val Met Ile Leu Leu Gly Leu Gly Met Leu
10 15 20

act gta ttc acc caa cgg ttg gtg gat cag aaa atc gat att gcg agc 211
Thr Val Phe Thr Gln Arg Leu Val Asp Gln Lys Ile Asp Ile Ala Ser
25 30 35

tcc gaa atc gac cgc gcc cgc gtc atc gtc gaa gag caa atc acc gca 259
Ser Glu Ile Asp Arg Ala Arg Val Ile Val Glu Glu Gln Ile Thr Ala
40 45 50

tcc ggc gcc tca aca tcg gtg cag gcg cga gtg aac tct gcc cgc gct 307
Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val Asn Ser Ala Arg Ala
55 60 65

gcg ctc tcc agc ttg ggt acc agc ggc ggt aca gaa acc aac gcc gcc 355
Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr Glu Thr Asn Ala Ala
70 75 80 85

tac gat cca gtc gtg ttg gtg aac aac gat gac ctg gtg gtc tct ccc 403
Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp Leu Val Val Ser Pro
90 95 100

gag ggt tac caa atc cca gaa cgt ctg cga tac ttc gtc tct gag aac 451
Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr Phe Val Ser Glu Asn
105 110 115

caa gtc tcg tat cag ttc tcc agc atc gac caa ggc gac gga tcg tcc 499
Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln Gly Asp Gly Ser Ser
120 125 130

tac caa gcg ctc atc atc gga acg ccc acg gaa agc gac atc ccg aac 547
Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu Ser Asp Ile Pro Asn
135 140 145

ctc cag gtg tat ctg gtg ttc tcc atg gaa agc gac gaa tcc tct ctt 595
Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser Asp Glu Ser Ser Leu
150 155 160 165

gct ctc atg cga gga ctc ctc tca gct gca ctg ctg atc gtg gtg gtg 643
Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu Leu Ile Val Val Val
170 175 180

ctg ctg gtc ggt atc gca tgg cta gcc acc caa cag gtc acc gcg ccg 691
Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln Gln Val Thr Ala Pro
185 190 195

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Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe Ala Gln Gly Lys Leu
200 205 210

cgt gaa cgc atg gtg gtg gaa ggc gaa gac gag atg gcc cgc ctg gcg 787
Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu Met Ala Arg Leu Ala
215 220 225

gtg tcc ttc aac gcg atg gcc gaa tcg ctg tcc gcg cag atc acc aaa 835
Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser Ala Gln Ile Thr Lys

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cac gaa ttg cgc aca ccg ctg aca acg His Glu Leu Arg Thr Pro Leu Thr Thr	265	gtg cgc atg gct gct gat cta Val Arg Met Ala Ala Asp Leu	275	931
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caa ctg atg aac agg gag ttg gac cga Gln Leu Met Asn Arg Glu Leu Asp Arg	295	ttc gag tcg ctg ctg agc gat Phe Glu Ser Leu Leu Ser Asp	305	1027
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gcg ctt cac gat gtc cgc atc cca gtg Ala Leu His Asp Val Arg Ile Pro Val	330	cga tcg gca ttg gaa caa gta Arg Ser Ala Leu Glu Gln Val	335	1123
caa cac ttg gcc acc gag ctg gat gtg Gln His Leu Ala Thr Glu Leu Asp Val	345	gaa ttg ctt gtt aat ttg ccc Glu Leu Leu Val Asn Leu Pro	350	1171
gaa gaa gcg atc aac att caa ggc gat Glu Glu Ala Ile Asn Ile Gln Gly Asp	360	tcc agg cgc atc gaa aga atc Ser Arg Arg Ile Glu Arg Ile	370	1219
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gtt gag ttg aaa gtt gcc gac aac gtg Val Glu Leu Lys Val Ala Asp Asn Val	390	gac gca gta gcg atc gtt gtt Asp Ala Val Ala Ile Val Val	400	1315
att gat cac gcc gtc gcc ctg aaa cct Ile Asp His Gly Val Gly Leu Lys Pro	410	gga caa gac gaa ttg gtg ttc Gly Gln Asp Glu Leu Val Phe	415	1363
aac aga ttc tgg cga gcc gac cct tcg Asn Arg Phe Trp Arg Ala Asp Pro Ser	425	gcg gtc cgc cat tct ggt gcc Arg Val Arg His Ser Gly Gly	430	1411
acc gcc ctg ggt ctt gcg att tct cgc Thr Gly Leu Gly Leu Ala Ile Ser Arg	440	gaa gat gcg atg ctt cat gga Glu Asp Ala Met Leu His Gly	445	1459
gga aac ctt gat gcg gcg gga acg atc Gly Asn Leu Asp Ala Ala Gly Thr Ile	455	ggt gtt ggt tcc att ttc cgt Gly Val Gly Ser Ile Phe Arg	465	1507
ttg gtc ttg cct aaa gaa ccg cat gga Leu Val Leu Pro Lys Glu Pro His Gly	470	aat tat cgt gaa gca ccg atc Asn Tyr Arg Glu Ala Pro Ile	480	1555

ccg ttg atc get cca gag aca ccg tgg gaa ggg gag cag cag 1597
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 35 40 45
 Glu Gln Ile Thr Ala Ser Gly Ala Ser Thr Ser Val Gln Ala Arg Val
 50 55 60
 Asn Ser Ala Arg Ala Ala Leu Ser Ser Leu Gly Thr Ser Gly Gly Thr
 65 70 75 80
 Glu Thr Asn Ala Ala Tyr Asp Pro Val Val Leu Val Asn Asn Asp Asp
 85 90 95
 Leu Val Val Ser Pro Glu Gly Tyr Gln Ile Pro Glu Arg Leu Arg Tyr
 100 105 110
 Phe Val Ser Glu Asn Gln Val Ser Tyr Gln Phe Ser Ser Ile Asp Gln
 115 120 125
 Gly Asp Gly Ser Ser Tyr Gln Ala Leu Ile Ile Gly Thr Pro Thr Glu
 130 135 140
 Ser Asp Ile Pro Asn Leu Gln Val Tyr Leu Val Phe Ser Met Glu Ser
 145 150 155 160
 Asp Glu Ser Ser Leu Ala Leu Met Arg Gly Leu Leu Ser Ala Ala Leu
 165 170 175
 Leu Ile Val Val Val Leu Leu Val Gly Ile Ala Trp Leu Ala Thr Gln
 180 185 190
 Gln Val Thr Ala Pro Val Arg Ser Ala Ser Arg Ile Ala Glu Arg Phe
 195 200 205
 Ala Gln Gly Lys Leu Arg Glu Arg Met Val Val Glu Gly Glu Asp Glu
 210 215 220
 Met Ala Arg Leu Ala Val Ser Phe Asn Ala Met Ala Glu Ser Leu Ser
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 Ala Gln Ile Thr Lys Leu Glu Glu Tyr Gly Asn Leu Gln Arg Gln Phe
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				Met	Gln Ser Ser Leu	5
gat cgt gtg tcg gaa acc gga cgc aat gag ctc gat gtt gaa acc ctt				1		163
Asp Arg Val Ser	Glu Thr Gly Arg Asn	Glu Leu Asp	Val Glu Thr Leu			20
	10		15			
gtg aag aag ggg aat caa ccg ggc atg agc tat cgc aac agt atc						211
Val Lys Lys Gly Asn Gln Pro Gly Ala			Met Ser Tyr Arg Asn Ser Ile			35
	25		30			
cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc						259
His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala						50
	40		45			
cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg						307
Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val						65
	55		60			
tgg ggt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc						355
Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser						85
	70		75			80
cac gcc atg cag ctg gcc tgg ctg ttt gtg ctg acg ctg gtg tgg att						403
His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile						95
	90					100
ttt atg gtg ccg atc gtg ccc gtg tcc att tat ctg ctg ttc ccg ctg						451
Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu						105
	105		110			115
ttt ttc ctc tat cta cag gtg atg cct gac gtg aga gcc att att gcg						499
Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala						120
	120		125			130
att ttg ggt gcg aca gcg att gcg att gcc agc cag tat tcc gtg ggg						547
Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly						135
	140					145
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Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr						150
	155					160
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Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu						170
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aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg						691
Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala						185
	185					190
gtg acg gaa cga aat gcg ggt att gct gcg gaa cgt caa cgt att gcg						739
Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala						200
	200					205
cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg						787
His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met						215
	215					220

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 Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu
 230 235 240 245
 aag cca aag gag gcg atc gtg aag aag atg cgc ctt gcc cga caa aca 883
 Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
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 gcc tcc gac aat ctc agt gag gct cgc gcg atg att gcg gcg ttg caa 931
 Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met Ile Ala Leu Gln
 265 270 275
 ccg gca gcg ctg tct aaa acc tcc ttg gaa gca gca ctt cac cgc gtc 979
 Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
 280 285 290
 aca gaa ccg ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat 1027
 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
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 gtt cgc caa ctg ccc atg aaa act gaa gcc acc ctt ctg cga att gct 1075
 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala
 310 315 320 325
 caa ggt gcg atc gga aat gtg gcg aaa cat tca gag gcg aaa aac tgc 1123
 Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys
 330 335 340
 cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt 1171
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 Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala
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 ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa 1267
 Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Gln Arg Ala Met Glu
 375 380 385
 ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg 1315
 Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala
 390 395 400 405
 gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg 1363
 Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala
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 ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta 1411
 Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu
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<213> *Corynebacterium glutamicum*

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35 40 45

Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys
50 55 60

Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys
65 70 75 80

Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu
85 90 95

Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr
100 105 110

Leu Leu Phe Pro Leu Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val
115 120 125

Arg Gly Ile Ile Ala Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser
130 135 140

Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val
145 150 155 160

Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp
165 170 175

Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr
180 185 190

Arg Ser Gln Leu Ala Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu
195 200 205

Arg Gln Arg Ile Ala His Glu Ile His Asp Thr Val Ala Gln Gly Leu
210 215 220

Ser Ser Ile Gln Met Leu Leu His Val Ser Glu Gln Glu Ile Leu Val
225 230 235 240

Ala Glu Met Glu Glu Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg
245 250 255

Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met
260 265 270

Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala
275 280 285

Ala Leu His Arg Val Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile
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				1				5	
gat cgt gtg tcg gaa acc gga cgc aat gag ctg gat gtt gaa acc ctt									163
Asp Arg Val Ser Glu Thr Gly Arg Asn Glu Leu Asp Val Glu Thr Leu									
gtg aag aag ggg aat caa ccg gcc gcg atg agc tat cgc aac agt atc									211
Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser Tyr Arg Asn Ser Ile									
cac att ttg aca gcc tcg ctg ctg gtc gtg ggg ttg gga gct tcc gcc									259
His Ile Leu Thr Ala Ser Leu Leu Val Val Gly Leu Gly Ala Ser Ala									
cgc ctg acg ctg ccg atg ttt gcg ctg tcg tgc gtg ctg ttg ttt gtg									307
Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys Val Leu Leu Phe Val									
tgg qgt ttt ctg tac ttc tat gga tca acc aaa cgc gta gat ttg agc									355

Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys Arg Val Asp Leu Ser
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 His Gly Met Gln Leu Gly Trp Leu Phe Val Leu Thr Leu Val Trp Ile
 90 95 100
 ttt atg gtg cgc atc gtg ccc gtg tcc att tat ctg ctg ttc cgc ctg 451
 Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr Leu Leu Phe Pro Leu
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 Phe Phe Leu Tyr Leu Gln Val Met Pro Asp Val Arg Gly Ile Ile Ala
 120 125 130
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 Ile Leu Gly Ala Thr Ala Ile Ala Ile Ala Ser Gln Tyr Ser Val Gly
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 Leu Thr Phe Gly Gly Val Met Gly Pro Val Val Ser Ala Ile Val Thr
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 gtg gct att gat tac gcg ttc cgc acg ttg tgg cgg gtg aat aat gaa 643
 Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp Arg Val Asn Asn Glu
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 aag cag gaa ttg att gat cag ttg att gaa act cgc tcc cag ctg gcg 691
 Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr Arg Ser Gln Leu Ala
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 Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu Arg Gln Arg Ile Ala
 200 205 210
 cat gaa att cat gac acg gtc gcc cag gga ctc tcc tcc att caa atg 787
 His Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln Met
 215 220 225
 ctg ctg cat gtc tct gaa cag gag att ctc gtt gct gag atg gaa gag 835
 Leu Leu His Val Ser Glu Gln Glu Ile Leu Val Ala Glu Met Glu Glu
 230 235 240 245
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 Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg Leu Ala Arg Gln Thr
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 265 270 275
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 Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala Ala Leu His Arg Val
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 aca gaa cgc ttg ttg ggt att aat ttt gtg att tct gtc gac ggt gat 1027
 Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile Ser Val Asp Gly Asp
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 Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr Leu Leu Arg Ile Ala

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Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser Glu Ala Lys Asn Cys	330	335	340	
cac gtg aca cta acc tac gaa gac aca gaa gta cgc ctt gat gtg gtt				1171
His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val Arg Leu Asp Val Val	345	350	355	
gat gac ggt gtg ggt ttt gag cct tcg gaa gtg tcc agt acc ccc gct				1219
Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val Ser Ser Thr Pro Ala	360	365	370	
ggc ctt ggc cat atc ggc tta acc gca ttg cag cag cgt gcg atg gaa				1267
Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln Arg Ala Met Glu	375	380	385	
ttg cac ggc gaa gtt ata gtg gaa tct gca tat ggg cag ggt act gcg				1315
Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr Gly Gln Gly Thr Ala	390	395	400	405
gta tct gca gca ttg ccg gtg gag cca cca gag ggg ttt gtc ggg gcg				1363
Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu Gly Phe Val Gly Ala	410	415	420	
ccg gtt ttg gca gat tcg gac tca agt gct aca ggc gag gtt gaa cta				1411
Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr Gly Glu Val Glu Leu	425	430	435	
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Asp Val Glu Thr Leu Val Lys Lys Gly Asn Gln Pro Gly Ala Met Ser	20	25	30	
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Leu Gly Ala Ser Ala Arg Leu Thr Leu Pro Met Phe Ala Leu Ser Cys	50	55	60	
Val Leu Leu Phe Val Trp Gly Phe Leu Tyr Phe Tyr Gly Ser Thr Lys	65	70	75	80
Arg Val Asp Leu Ser His Gly Met Gln Leu Gly Trp Leu Phe Val Leu	85	90	95	
Thr Leu Val Trp Ile Phe Met Val Pro Ile Val Pro Val Ser Ile Tyr	100	105	110	

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 115 120 125
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 130 135 140
 Gln Tyr Ser Val Gly Leu Thr Phe Gly Gly Val Met Gly Pro Val Val
 145 150 155 160
 Ser Ala Ile Val Thr Val Ala Ile Asp Tyr Ala Phe Arg Thr Leu Trp
 165 170 175
 Arg Val Asn Asn Glu Lys Gln Glu Leu Ile Asp Gln Leu Ile Glu Thr
 180 185 190
 Arg Ser Gln Leu Ala Val Thr Glu Arg Asn Ala Gly Ile Ala Ala Glu
 195 200 205
 Arg Gln Arg Ile Ala His Glu Ile His Asp Thr Val Ala Gln Gly Leu
 210 215 220
 Ser Ser Ile Gln Met Leu Leu His Val Ser Glu Gln Glu Ile Leu Val
 225 230 235 240
 Ala Glu Met Glu Glu Lys Pro Lys Glu Ala Ile Val Lys Lys Met Arg
 245 250 255
 Leu Ala Arg Gln Thr Ala Ser Asp Asn Leu Ser Glu Ala Arg Ala Met
 260 265 270
 Ile Ala Ala Leu Gln Pro Ala Ala Leu Ser Lys Thr Ser Leu Glu Ala
 275 280 285
 Ala Leu His Arg Val Thr Glu Pro Leu Leu Gly Ile Asn Phe Val Ile
 290 295 300
 Ser Val Asp Gly Asp Val Arg Gln Leu Pro Met Lys Thr Glu Ala Thr
 305 310 315 320
 Leu Leu Arg Ile Ala Gln Gly Ala Ile Gly Asn Val Ala Lys His Ser
 325 330 335
 Glu Ala Lys Asn Cys His Val Thr Leu Thr Tyr Glu Asp Thr Glu Val
 340 345 350
 Arg Leu Asp Val Val Asp Asp Gly Val Gly Phe Glu Pro Ser Glu Val
 355 360 365
 Ser Ser Thr Pro Ala Gly Leu Gly His Ile Gly Leu Thr Ala Leu Gln
 370 375 380
 Gln Arg Ala Met Glu Leu His Gly Glu Val Ile Val Glu Ser Ala Tyr
 385 390 395 400
 Gly Gln Gly Thr Ala Val Ser Ala Ala Leu Pro Val Glu Pro Pro Glu
 405 410 415
 Gly Phe Val Gly Ala Pro Val Leu Ala Asp Ser Asp Ser Ser Ala Thr
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Gly Glu Val Glu Leu Ser Ser Pro Thr Asp Asp Glu
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<223> RXA00006

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Met Val Asp Phe Asp
1 5
acc atc gca gcc cga ctt gtc acc gaa aca gaa gaa gca atc atc tac 163
Thr Ile Ala Ala Arg Leu Val Thr Glu Thr Glu Glu Ala Ile Ile Tyr
10 15 20
gcc acc cgc gat gga ata atc aga ctc tgg aac ggc ggc tcc gag aaa 211
Ala Thr Arg Asp Gly Ile Ile Arg Leu Trp Asn Gly Gly Ser Glu Lys
25 30 35
ctc ttt gga tac acg gcc ggc gaa gcc ctt gga aaa tca ctc gac atc 259
Leu Phe Gly Tyr Thr Ala Gly Glu Ala Leu Gly Lys Ser Leu Asp Ile
40 45 50
atc att ccc gaa aaa cac cgc aag gcc cac tgg gac gga tgg gat cgc 307
Ile Ile Pro Glu Lys His Arg Lys Ala His Trp Asp Gly Trp Asp Arg
55 60 65
gtc atg gaa tcc gcc gaa act cgc tat ggc tcc gaa cgc ctt aac gtt 355
Val Met Glu Ser Gly Glu Thr Arg Tyr Gly Ser Glu Pro Leu Asn Val
70 75 80 85
cca ggc att cgt gcc gat gga tcc aaa atg tct ttg gaa ttc tcc atc 403
Pro Gly Ile Arg Ala Asp Gly Ser Lys Met Ser Leu Glu Phe Ser Ile
90 95 100
acc atc ctg aag gac gat tcc gga aaa atc gaa ggc gtt gca gct ttt 451
Thr Ile Leu Lys Asp Asp Ser Gly Lys Ile Glu Gly Val Ala Ala Phe
105 110 115
ctc cgc gat gtc acc gcc aat tgg gat gag aaa aag gcc ctg cgg atc 499
Leu Arg Asp Val Thr Ala Asn Trp Asp Glu Lys Lys Ala Leu Arg Ile
120 125 130
cga atc aaa gag ttg gaa cgc caa atc gag ggc cat taaggagatt 545
Arg Ile Lys Glu Leu Glu Arg Gln Ile Glu Gly His
135 140 145
cttgggtgcg cgg 558

<210> 36

gtt gcg gtg cgc aga gct gaa aac acc att gtc cgc tca gct aag ccc 211
Val Ala Val Arg Arg Ala Glu Asn Thr Ile Val Arg Ser Ala Lys Pro
25 30 35

gca ttc tca gtt gag gaa ctt tcg gag atc ctg gag tca cat tct att	259
Ala Phe Ser Val Glu Glu Leu Ser Glu Ile Leu Glu Ser His Ser Ile	
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cgc ctg gag ctg gag ccg atc cta gaa ctt gaa aca ggt cgg gtg ggt	307
Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu Thr Gly Arg Val Gly	
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gca gcc gaa ggt ctg ctg cga atc aac ttg gat ggc acc gat gtt cct	355
Ala Ala Glu Glu Gly Leu Leu Arg Ile Asn Leu Asp Gly Thr Asp Val Pro	
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75	
80	
90	
95	
100	
ctt gat atc gca gtc atg aga gaa gga att aat cat att gag agg ctg	451
Leu Asp Ile Ala Val Met Arg Glu Gly Ile Asn His Ile Glu Arg Leu	
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110	
115	
aga gct gtg tgt ccg act ttc agc ctc gct ttg aat ctg tcg ggc tat	499
Arg Ala Val Cys Pro Thr Phe Ser Leu Ala Leu Asn Leu Ser Gly Tyr	
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125	
130	
135	
140	
145	
gct cgc gat ctg cca agg gga tca att agg ttt gag att act gag acc	595
Ala Arg Asp Leu Pro Arg Gly Ser Ile Arg Phe Glu Ile Thr Glu Thr	
150	
155	
160	
165	
gct ccg att gaa gac att gac gcg gca aaa gag ttt gtg cag atg ttg	643
Ala Pro Ile Glu Asp Ile Asp Ala Ala Glu Phe Val Gln Met Leu	
170	
175	
180	
aaa gat ttt ggc ttc cac atc gta atc gat gac ttt ggc gca gga cat	691
Lys Asp Phe Gly Phe His Ile Val Ile Asp Asp Phe Gly Ala Gly His	
185	
190	
195	
gag cct tat caa tat cta aag aag ttc gac ttt agc gtg ctg aag att	739
Glu Pro Tyr Gln Tyr Leu Lys Lys Phe Phe Ser Phe Val Leu Lys Ile	
200	
205	
210	
215	
220	
225	
230	
235	
240	
245	
250	
255	
260	
265	
270	
275	
att gat gaa ttt ata gct act tat ctc gag acg aac caa acc gct acc	979

Ile Asp Glu Phe Ile Ala Thr Tyr Leu Glu Thr Asn Gln Thr Ala Thr
 280 285 290

tgg ggg taggaagaat atgaaaaaga aga
 Trp Gly
 295

1008

<210> 38
 <211> 295
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 38
 Val Asn Pro Phe Ile Leu Ala Asp Gln Leu Leu Tyr Asp Ala Lys His
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Ala Gly Arg Asn Arg Val Ala Val Arg Arg Ala Glu Asn Thr Ile Val
 20 25 30

Arg Ser Ala Lys Pro Ala Phe Ser Val Glu Glu Leu Ser Glu Ile Leu
 35 40 45

Glu Ser His Ser Ile Arg Leu Glu Leu Gln Pro Ile Leu Glu Leu Glu
 50 55 60

Thr Gly Arg Val Gly Ala Ala Glu Gly Leu Leu Arg Ile Asn Leu Asp
 65 70 75 80

Gly Thr Asp Val Pro Thr Gly Gln Phe Val Gln Ser Val Glu Gln Ala
 85 90 95

Gly Leu Ala Pro Lys Leu Asp Ile Ala Val Met Arg Glu Gly Ile Asn
 100 105 110

His Ile Glu Arg Leu Arg Ala Val Cys Pro Thr Phe Ser Leu Ala Leu
 115 120 125

Asn Leu Ser Gly Tyr Ser Leu Ser Ser Ala Lys Ile Arg Glu Glu Leu
 130 135 140

Arg Ala Glu Phe Arg Ala Arg Asp Leu Pro Arg Gly Ser Ile Arg Phe
 145 150 155 160

Glu Ile Thr Glu Thr Ala Pro Ile Glu Asp Ile Asp Ala Ala Lys Glu
 165 170 175

Phe Val Gln Met Leu Lys Asp Phe Gly Phe His Ile Val Ile Asp Asp
 180 185 190

Phe Gly Ala Gly His Glu Pro Tyr Gln Tyr Leu Lys Lys Phe Asp Phe
 195 200 205

Ser Val Leu Lys Ile Ala Gly Glu Phe Ile Glu Gly Met Val Thr Asn
 210 215 220

Arg Val Asp Arg Ser Ile Val Glu Ser Ile Ala Gln Leu Ala Lys Asp
 225 230 235 240

Glu Glu Met Glu Thr Val Ala Glu Phe Val Ser Ser Lys Glu Ile Leu
 245 250 255

gtt gcc ggg ccc gga att gca ctt tcg acg ccg ctg gta cta aat att 547

	Val	Ala	Gly	Pro	Gly	Ile	Ala	Leu	Ser	Thr	Pro	Leu	Val	Leu	Asn	Ile	
	135						140					145					
cac	cg	tca	gca	tgg	cg	gag	ttc	gca	gtt	gtt	atc	ata	gct	acg	gtc		595
His	Arg	Ser	Ala	Trp	Arg	Glu	Phe	Ala	Val	Val	Ile	Ile	Ala	Thr	Val		
150					155					160					165		
gga	gtg	ctg	gcg	ctc	att	ttc	gga	ttt	gct	gtg	gat	ctt	ccg	acg	gtc		643
Gly	Val	Leu	Ala	Leu	Ile	Phe	Gly	Phe	Ala	Val	Asp	Leu	Pro	Thr	Val		
				170					175					180			
tac	ttg	gca	atg	ttg	cca	ttg	tat	tgg	agt	gca	acc	cgt	ctt	cca	gtg		691
Tyr	Leu	Ala	Met	Leu	Pro	Leu	Tyr	Tyr	Ser	Ala	Thr	Arg	Leu	Pro	Val		
			185					190					195				
ctt	tta	gcc	gtt	ctt	cat	gcg	gtg	ttt	act	tca	gca	ata	gtc	gta	att		739
Leu	Leu	Ala	Val	Leu	His	Ala	Val	Phe	Thr	Ser	Ala	Ile	Val	Val	Ile		
		200					205					210					
ctg	tat	ttc	cta	tta	ggt	acc	gga	tct	ttt	gcg	att	acg	gat	gaa	tcc		787
Leu	Tyr	Phe	Leu	Leu	Gly	Thr	Gly	Ser	Phe	Ala	Ile	Thr	Asp	Glu	Ser		
		215				220					225						
ata	ctg	gtg	cag	gca	acg	aca	att	cag	ctt	ttt	gtt	ctg	atg	tgt	atc		835
Ile	Leu	Val	Gln	Ala	Thr	Thr	Ile	Gln	Leu	Phe	Val	Leu	Met	Cys	Ile		
230					235						240				245		
ttg	ttg	tcg	cta	gtt	gtg	tca	acg	aca	gtc	cag	cag	aca	tca	gca	ctg		883
Leu	Leu	Ser	Leu	Val	Val	Ser	Thr	Thr	Val	Gln	Gln	Thr	Ser	Ala	Leu		
				250					255						260		
gtt	gaa	gag	cta	gag	gtg	gta	gcg	aag	acc	ctt	cct	gat	gcg	ctt	ttt		931
Val	Glu	Glu	Leu	Glu	Val	Val	Ala	Lys	Thr	Leu	Pro	Asp	Ala	Leu	Phe		
			265					270					275				
atc	gta	aac	aaa	aat	gga	aca	gca	ttt	cct	gtt	aac	gca	ggc	gcg	aaa		979
Ile	Val	Asn	Lys	Asn	Gly	Thr	Ala	Phe	Pro	Val	Asn	Ala	Gly	Ala	Lys		
			280				285					290					
aat	ttc	gtc	aag	caa	tca	ccg	gat	ggg	cat	tat	tcc	atg	ccg	aaa	cta		1027
Asn	Phe	Val	Lys	Gln	Ser	Pro	Asp	Gly	His	Tyr	Ser	Met	Pro	Lys	Leu		
		295				300						305					
cag	aat	ata	gac	ggt	gaa	ccc	atg	gat	gag	aaa	gaa	agt	ccg	agc	agt		1075
Gln	Asn	Ile	Asp	Gly	Glu	Pro	Met	Asp	Glu	Lys	Glu	Ser	Pro	Ser	Ser		
310					315						320				325		
atg	gcc	ttg	cgt	gga	caa	ggt	gtc	gaa	gga	gta	tta	gcc	aag	tta	ggt		1123
Met	Ala	Leu	Arg	Gly	Gln	Gly	Val	Glu	Gly	Val	Leu	Ala	Lys	Leu	Gly		
				330					335						340		
gaa																	

ggc cga gga aaa gtg tta tcg cgg gtg tca agt aaa gta tcg gcg gga 2035
 Gly Arg Gly Lys Val Leu Ser Arg Val Ser Ser Lys Val Ser Ala Gly
 630 635 640 645

cgc tct ttt ctg atg ctc gtg ccc aag gtg tgaatccatt cattcttgct 2085
 Arg Ser Phe Leu Met Leu Val Pro Lys Val
 650 655

gat 2088

<210> 40

<211> 655

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 40

Val Val Ala Arg Asp Leu Gln Lys Leu Glu Lys Leu Arg Leu Ile Cys
 1 5 10 15

Gly Tyr Val Phe Leu Val Pro Ala Ile Tyr Leu His Phe Phe Ala Glu
 20 25 30

Thr Ser Leu Arg Gly Val Ile Leu Ala Gly Ile Ala His Ala Ile Ala
 35 40 45

Gly Pro Gly Val Ala Leu Val Met Ala Phe Met Glu Asn Ala Gln Leu
 50 55 60

Pro Glu Leu Leu Arg Lys Arg His Ala Phe Ala Pro Phe Ser His Ile
 65 70 75 80

Arg Leu Pro Gly Asp Val Phe Arg Leu Leu Val Ala Gly Ile Val Met
 85 90 95

Val Ala Ile Ser Lys Leu Ile Val Ile Leu Ala Tyr Ala Leu Ala Asp
 100 105 110

Leu Pro Tyr Ser Phe Thr Leu Tyr Leu Thr Met Ala Leu Arg Asp Leu
 115 120 125

Thr Gly Ile Ile Val Val Ala Gly Pro Gly Ile Ala Leu Ser Thr Pro
 130 135 140

Leu Val Leu Asn Ile His Arg Ser Ala Trp Arg Glu Phe Ala Val Val
 145 150 155 160

Ile Ile Ala Thr Val Gly Val Leu Ala Leu Ile Phe Gly Phe Ala Val
 165 170 175

Asp Leu Pro Thr Val Tyr Leu Ala Met Leu Pro Leu Tyr Trp Ser Ala
 180 185 190

Thr Arg Leu Pro Val Leu Leu Ala Val Leu His Ala Val Phe Thr Ser
 195 200 205

Ala Ile Val Val Ile Leu Tyr Phe Leu Leu Gly Thr Gly Ser Phe Ala
 210 215 220

Ile Thr Asp Glu Ser Ile Leu Val Gln Ala Thr Thr Ile Gln Leu Phe

225	230	235	240
Val Leu Met Cys	Ile Leu Leu Ser	Leu Val Val Ser	Thr Thr Val Gln
245		250	255
Gln Thr Ser Ala	Leu Val Glu Glu	Leu Glu Val Val	Ala Lys Thr Leu
260		265	270
Pro Asp Ala Leu	Phe Ile Val Asn	Lys Asn Gly Thr	Ala Phe Pro Val
275		280	285
Asn Ala Gly Ala	Lys Asn Phe Val	Lys Gln Ser Pro	Asp Gly His Tyr
290		295	300
Ser Met Pro Lys	Leu Gln Asn Ile	Asp Gly Glu Pro	Met Asp Glu Lys
305	310	315	320
Glu Ser Pro Ser	Ser Met Ala Leu	Arg Gly Gln Gly	Val Glu Gly Val
	325	330	335
Leu Ala Lys Leu	Gly Glu Val Leu	Gly Glu Asp Pro	Asp Leu Ala Arg
	340	345	350
Arg Ile Phe Glu	Ile Ser Ala Ser	Pro Met Tyr Leu	Arg Gly Glu Thr
	355	360	365
Glu Pro Gly His	Ala Leu Val Ile	Trp His Asp Ser	Thr Asn Glu Tyr
	370	375	380
Tyr Thr Met Gln	Gln Leu Thr Leu	Ala Tyr Glu Glu	Ser Arg Leu Leu
	385	390	395
Phe Glu Lys Ala	Pro Gln Gly Ile	Ala Met Leu Asp	Pro Ser Gly Glu
	405	410	415
Ile Val Met Ala	Asn Arg Ser Phe	Gly Asp Leu Val	Gly Thr Thr Pro
	420	425	430
Val Arg Leu Leu	Gly Arg Asn Leu	Glu Asp Phe Gly	Val Glu Glu Gly
	435	440	445
Thr Met Glu Tyr	Val Thr Pro Val	Leu Ser Asp Pro	Glu Ala Val Val
	450	455	460
His Leu Asp Arg	Ser Leu Glu Thr	Leu Arg Gly Lys	Gln Lys Asn Val
	465	470	475
Ala Met Ser Phe	Ser Ser Met Gly	Asn Val Gly Gly	Arg Ile Gly Thr
	485	490	495
Leu Leu Val Asn	Val Val Asp Val	Thr Glu Arg Gln	Glu Leu Ile Glu
	500	505	510
Leu Val Glu His	Leu Ala Asp His	Asp Ser Leu Thr	Gly Leu Val Asn
	515	520	525
Arg Arg Arg Leu	Glu Ser Asp Ile	Glu Glu Leu Ile	Leu Lys Asn Glu
	530	535	540
Arg Asp Ser Thr	Asp Ser Ala Leu	Leu Leu Leu Leu	Asp Leu Asp Tyr
	545	550	555
			560

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Lys Glu Val Asn Asp Ser Leu Gly His Glu Ala Gly Asp Gln Leu Leu
565 570 575

Ile Glu Phe Ala Glu Ile Leu Lys Asp Ser Val Arg Asp Ser Asp Ile
580 585 590

Val Gly Arg Ile Gly Gly Asp Glu Phe Val Ile Val Leu Pro Asp Thr
595 600 605

Asp Arg Asp Gly Ala Glu Ala Ile Gly Ile Arg Ile Ile Glu Leu Val
610 615 620

Asn Gln His Phe Lys Gly Arg Gly Lys Val Leu Ser Arg Val Ser Ser
625 630 635 640

Lys Val Ser Ala Gly Arg Ser Phe Leu Met Leu Val Pro Lys Val
645 650 655

<210> 41

<211> 1239

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1216)

<223> RXA02669

<400> 41

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tcgacaccat ccgaggtggt ggctaccgga tggccttcaa atg aca gcc ctc atc 115
Met Thr Ala Leu Ile
1 5

cca gct cgc cac agc ctg act ttt cgt ctg ctc acc gcg cag ctt gct 163
Pro Ala Arg His Ser Leu Thr Phe Arg Leu Leu Thr Ala Gln Leu Ala
10 15 20

gtg gtg ttg atc agt ctg ctg gcc gcc ctg att gtg gct gcc ttg gta 211
Val Val Leu Ile Ser Leu Leu Ala Ala Leu Ile Val Ala Ala Leu Val
25 30 35

ggg cct gca att ttc aat tct cac ctg gat ctt tcc ggc ccg att gat 259
Gly Pro Ala Ile Phe Asn Ser His Leu Asp Leu Ser Gly Pro Ile Asp
40 45 50

ccc cgc cag acg gat ttc cac att cag gag gcc tac ccg gac gcc aat 307
Pro Arg Gln Thr Asp Phe His Ile Gln Glu Ala Tyr Arg Asp Ala Asn
55 60 65

tac att gcc ctc gca gcg gca ctt ccc acc gca gtg ttg agc tcc att 355
Tyr Ile Ala Leu Ala Ala Ala Leu Pro Thr Ala Val Leu Ser Ser Ile
70 75 80 85

ggg gtg agt ttt tgg ctt tcc cac cgc ctg ggc cag ccg ttg tgg cga 403
Gly Val Ser Phe Trp Leu Ser His Arg Leu Gly Gln Pro Leu Trp Arg
90 95 100

000000 1239 000000

ctg tcc cgg gct gca act gcc atg agc tcc ggc gac tac cag gtg cgc 451
 Leu Ser Arg Ala Ala Thr Ala Met Ser Ser Gly Asp Tyr Gln Val Arg
 105 110 115

gta ccc att tcc gat gtg gat aaa gag gtc gct gct cta tct ctc gcc 499
 Val Pro Ile Ser Asp Val Asp Lys Glu Val Ala Ala Leu Ser Leu Ala
 120 125 130

ttc aat tcc atg gcg gat cag ctc gaa cac aca gaa gaa ctc cgc cga 547
 Phe Asn Ser Met Ala Asp Gln Leu Glu His Thr Glu Glu Leu Arg Arg
 135 140 145

aac atg ctc tcc gat cta tcc cat gaa atg aac act ccc ctt tcc gtc 595
 Asn Met Leu Ser Asp Leu Ser His Glu Met Asn Thr Pro Leu Ser Val
 150 155 160 165

ctc ctt gtt tat gtc gac ggt ttg cag gac ggc atg gtg gag tgg gac 643
 Leu Leu Val Tyr Val Asp Gly Leu Gln Asp Gly Met Val Glu Trp Asp
 170 175 180

gcc gac acc cac gca gtt ttc gcc gag caa ctt ggc cgg ctt tcc cgc 691
 Ala Asp Thr His Ala Val Phe Ala Glu Gln Leu Gly Arg Leu Ser Arg
 185 190 195

ctc aca tca gat ctt gat gat gtc tct aga gcc caa gaa cac cgc ttc 739
 Leu Thr Ser Asp Leu Asp Asp Val Ser Arg Ala Gln Glu His Arg Phe
 200 205 210

gac ctg gtc tac agc acc gtc gcc atc ggt ggt ctc att cac aat gcc 787
 Asp Leu Val Tyr Ser Thr Val Ala Ile Gly Gly Leu Ile His Asn Ala
 215 220 225

gcc gga gcc gcc gca ggt tcc tac caa gaa aaa ggc gtg gcc ctg gaa 835
 Ala Gly Ala Ala Ala Gly Ser Tyr Gln Glu Lys Gly Val Ala Leu Glu
 230 235 240 245

gta aca ggc agc gat tcc acc gaa ctc atc cgc gtt gat agc caa cgc 883
 Val Thr Gly Ser Asp Ser Thr Glu Leu Ile Arg Val Asp Ser Gln Arg
 250 255 260

ttc gcc caa gtc atg gcc aac ctc ttc tcc aac gcc ttg cgg cac acc 931
 Phe Ala Gln Val Met Ala Asn Leu Phe Ser Asn Ala Leu Arg His Thr
 265 270 275

ccc gcc ggt ggg aaa gtt cac gtc cgc gtc ctg cgt caa ggc gtg gga 979
 Pro Ala Gly Gly Lys Val His Val Arg Val Leu Arg Gln Gly Val Gly
 280 285 290

acc atc gtc atc gaa gtc ata gac aac ggc gaa gga atc gcc cct gaa 1027
 Thr Ile Val Ile Glu Val Ile Asp Asn Gly Glu Gly Ile Ala Pro Glu
 295 300 305

cac gta aaa tac gtt ttc gaa cgc tac ttc cgc gcc aaa cga tcc gac 1075
 His Val Lys Tyr Val Phe Glu Arg Tyr Phe Arg Ala Lys Arg Ser Asp
 310 315 320 325

tcc gac gac caa tcc ggc tcc gga atc ggc ctc acc atc tcc cgc gca 1123
 Ser Asp Asp Gln Ser Gly Ser Gly Ile Gly Leu Thr Ile Ser Arg Ala
 330 335 340

ctc atc gaa gcg caa ggt ggc aca cta acc gca gaa tcc gct ggc ctg 1171

Leu Ile Glu Ala Gln Gly Gly Thr Leu Thr Ala Glu Ser Ala Gly Leu
345 350 355

ggc aaa ggc gcg aaa ttt acc atc cga cta ccc ctt tta agc aaa 1216
Gly Lys Gly Ala Lys Phe Thr Ile Arg Leu Pro Leu Leu Ser Lys
360 365 370

taaaaaaatt gcttttcgac gct 1239

<210> 42

<211> 372

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

Met Thr Ala Leu Ile Pro Ala Arg His Ser Leu Thr Phe Arg Leu Leu
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Thr Ala Gln Leu Ala Val Val Leu Ile Ser Leu Leu Ala Ala Leu Ile
20 25 30

Val Ala Ala Leu Val Gly Pro Ala Ile Phe Asn Ser His Leu Asp Leu
35 40 45

Ser Gly Pro Ile Asp Pro Arg Gln Thr Asp Phe His Ile Gln Glu Ala
50 55 60

Tyr Arg Asp Ala Asn Tyr Ile Ala Leu Ala Ala Ala Leu Pro Thr Ala
65 70 75 80

Val Leu Ser Ser Ile Gly Val Ser Phe Trp Leu Ser His Arg Leu Gly
85 90 95

Gln Pro Leu Trp Arg Leu Ser Arg Ala Ala Thr Ala Met Ser Ser Gly
100 105 110

Asp Tyr Gln Val Arg Val Pro Ile Ser Asp Val Asp Lys Glu Val Ala
115 120 125

Ala Leu Ser Leu Ala Phe Asn Ser Met Ala Asp Gln Leu Glu His Thr
130 135 140

Glu Glu Leu Arg Arg Asn Met Leu Ser Asp Leu Ser His Glu Met Asn
145 150 155 160

Thr Pro Leu Ser Val Leu Leu Val Tyr Val Asp Gly Leu Gln Asp Gly
165 170 175

Met Val Glu Trp Asp Ala Asp Thr His Ala Val Phe Ala Glu Gln Leu
180 185 190

Gly Arg Leu Ser Arg Leu Thr Ser Asp Leu Asp Asp Val Ser Arg Ala
195 200 205

Gln Glu His Arg Phe Asp Leu Val Tyr Ser Thr Val Ala Ile Gly Gly
210 215 220

Leu Ile His Asn Ala Ala Gly Ala Ala Ala Gly Ser Tyr Gln Glu Lys
225 230 235 240

Gly Val Ala Leu Glu Val Thr Gly Ser Asp Ser Thr Glu Leu Ile Arg
245 250 255

Val Asp Ser Gln Arg Phe Ala Gln Val Met Ala Asn Leu Phe Ser Asn
260 265 270

Ala Leu Arg His Thr Pro Ala Gly Gly Lys Val His Val Arg Val Leu
275 280 285

Arg Gln Gly Val Gly Thr Ile Val Ile Glu Val Ile Asp Asn Gly Glu
290 295 300

Gly Ile Ala Pro Glu His Val Lys Tyr Val Phe Glu Arg Tyr Phe Arg
305 310 315 320

Ala Lys Arg Ser Asp Ser Asp Asp Gln Ser Gly Ser Gly Ile Gly Leu
325 330 335

Thr Ile Ser Arg Ala Leu Ile Glu Ala Gln Gly Gly Thr Leu Thr Ala
340 345 350

Glu Ser Ala Gly Leu Gly Lys Gly Ala Lys Phe Thr Ile Arg Leu Pro
355 360 365

Leu Leu Ser Lys
370

<210> 43

<211> 1380

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101) .. (1357)

<223> RXN01211

<400> 43

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ctgcagccga cgggattaag gcagctaaca ttgagacacg atg aat aaa gat ttc 115
Met Asn Lys Asp Phe
1 5

tgg acc gca ggc tgg acc gcc cgc tgg ttt tgc cgc ggg gtt tcc ctt 163
 Trp Thr Ala Gly Trp Thr Ala Arg Trp Phe Ser Arg Gly Val Ser Leu
 10 15 20

ttg gcc agc cca gtt acc gcc cca ctg aac tct tgg cgg aga ttg cct 211
Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser Trp Arg Arg Leu Pro
25 30 35

aac ttg gcc aag tac acc ctc tac acc agg gtg tgc ttg caa gcg atc 259
Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val Ser Leu Gln Ala Ile
40 45 50

ccc gtg gtg ttg ctg tcg gcg tat ttc ctg ggc atc gta gct aat gca 307
Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly Ile Val Ala Asn Ala
55 60 65

ggc acc ctg aat ccc tca ttt gtg tgg ctg ctg ggt ttc tgg gtc atc 355
 Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Gly Phe Ser Val Ile 85
 70 75 80

ctt tta ata gtg acg gta ttg gtt tat gaa tat cag cca tgg ctg aat 403
 Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr Gln Pro Ser Leu Asn 100
 90 95 100

tct cat cct agg cgc agc gta cag cgg ttc ttc acc ggg ttg gtg 451
 Ser His Pro Arg Ser Val Gln Pro Phe Phe Phe Thr Gly Leu Val 115
 105 110 115

ctc aac gtt tta ggc gtt gtg gtg tct gtg gtg ctt caa att cgg ggc 499
 Leu Asn Val Leu Gly Val Val Val Ser Val Val Leu Gln Ile Pro Gly 130
 120 125 130

tta aac atg tgg gac aac acc cga gca act gcc ctt att ttc act ctt 547
 Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala Leu Ile Phe Thr Leu 145
 135 140 145

acc tgc gta ttt ctg ctt tgg atc gcc tac att cgg tgg atg aat tac 595
 Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile Pro Trp Met Asn Tyr 165
 150 155 160 165

cga tgg gtt tgg ctg atc gca atg tct gca gtg ttg tgg tgg acc agc 643
 Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val Leu Trp Trp Trp Ser 180
 170 175 180

aca acg act gat tat tta agt gca ttg tgg gtg gtt atc cgg cca ctc 691
 Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val Val Ile Pro Pro Leu 195
 185 190 195

atg gca gga acc gtc cga ctt tcc gta tgg acc gtc gat gtc atg aaa 739
 Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr Val Asp Val Met Lys 210
 200 205 210

gag gtt gag cgt tcc cgc gaa ttg gaa gcc tcc ctc cgc gtc acc gaa 787
 Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser Leu Arg Val Thr Glu 225
 215 220 225

gaa cgc ctt cgt ttc gcc cag gaa ctc cac gac act tta gga caa cac 835
 Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp Thr Leu Gly Gln His 245
 230 235 240 245

ctg gcg gca atg tcc gtg aaa tca gaa ctg gcg ctt gcc ctg gcg aaa 883
 Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala Leu Ala Leu Ala Lys 260
 250 255 260

cgc ggc gac gac cgc ctc gaa aac gag ctg cgt gag ctc caa aaa ctc 931
 Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg Glu Leu Gln Lys Leu 275
 265 270 275

acc cgc acc tcc atg tgg gaa atg cgc gac gtc gtc tcc gcc tac cgc 979
 Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val Val Ser Gly Tyr Arg 290
 280 285 290

acc gtc aac ctc gcc acg gaa atc gag ggc gct aaa agt ttg ctt gcc 1027
 Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala Lys Ser Leu Leu Ala 305
 295 300 305

gac gcc cac atc cac ctt tcc gtc atc ggc acc acg tcc cag gtg tca 1075

Asp Ala His Ile His Leu Ser Val Ile Gly Thr Thr Ser Gln Val Ser
 310 315 320 325

ccc gct cac cga gaa ctg tgc gcg tgg ctt gtc cgg gaa gcc acc aca 1123
 Pro Ala His Arg Glu Leu Cys Ala Trp Leu Thr Thr Thr
 330 335 340

aac att ctg cgc cac tct gat gca acg gat gcc acc ctc acg ttg agc 1171
 Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala Thr Leu Thr Leu Ser
 345 350 355

agc aca gag gtg cgc atg gac aac aat ggt gtg aac aag gac atc ggc 1219
 Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val Asn Lys Asp Ile Gly
 360 365 370

aga ctc tct ggt ctc agc gcc ctg cgc tca cga gcg gaa tca gcc gga 1267
 Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg Ala Glu Ser Ala Gly
 375 380 385

atg acg ctc att gtg tcc cgc gaa gac gac cag ttc agc gtc cgc atg 1315
 Met Thr Leu Ile Val Ser Arg Glu Asp Asp Gln Phe Ser Val Arg Met
 390 395 400 405

ctc att aat gca cct gca aat aca cct gca gaa aag gaa gct 1357
 Leu Ile Asn Ala Pro Ala Asn Thr Pro Ala Glu Lys Glu Ala
 410 415

taaatgattt ccatttccat cgc 1380

<210> 44
 <211> 419
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 44
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 20 25 30

Trp Arg Arg Leu Pro Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val
 35 40 45

Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly
 50 55 60

Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu
 65 70 75 80

Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr
 85 90 95

Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe
 100 105 110

Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val
 115 120 125

Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala

130 135 140
 Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile
 145 150 155 160
 Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val
 165 170 175
 Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val
 180 185 190
 Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr
 195 200 205
 Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser
 210 215 220
 Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp
 225 230 235 240
 Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala
 245 250 255
 Leu Ala Leu Ala Lys Arg Gly Asp Asp Arg Leu Glu Asn Glu Leu Arg
 260 265 270
 Glu Leu Gln Lys Leu Thr Arg Thr Ser Met Ser Glu Met Arg Asp Val
 275 280 285
 Val Ser Gly Tyr Arg Thr Val Asn Leu Ala Thr Glu Ile Glu Gly Ala
 290 295 300
 Lys Ser Leu Leu Ala Asp Ala His Ile His Leu Ser Val Ile Gly Thr
 305 310 315 320
 Thr Ser Gln Val Ser Pro Ala His Arg Glu Leu Cys Ala Trp Leu Val
 325 330 335
 Arg Glu Ala Thr Thr Asn Ile Leu Arg His Ser Asp Ala Thr Asp Ala
 340 345 350
 Thr Leu Thr Leu Ser Ser Thr Glu Val Arg Met Asp Asn Asn Gly Val
 355 360 365
 Asn Lys Asp Ile Gly Arg Leu Ser Gly Leu Ser Ala Leu Arg Ser Arg
 370 375 380
 Ala Glu Ser Ala Gly Met Thr Leu Ile Val Ser Arg Glu Asp Asp Gln
 385 390 395 400
 Phe Ser Val Arg Met Leu Ile Asn Ala Pro Ala Asn Thr Pro Ala Glu
 405 410 415
 Lys Glu Ala

<210> 45
 <211> 895
 <212> DNA
 <213> Corynebacterium glutamicum

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 Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr Val Asp Val Met Lys
 200 205 210

gag gtt gag cgt tcc cgc gaa ttg gaa gcc tcc ctc cgc gtc acc gaa 787
 Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser Leu Arg Val Thr Glu
 215 220 225

gaa cgc ctt cgt ttc gcc cag gaa ctc cac gac act tta gga caa cac 835
 Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp Thr Leu Gly Gln His
 230 235 240 245

ctg gcg gca atg tcc gtg aaa tca gaa ctg gcg ctt gcc ctg gcg aaa 883
 Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala Leu Ala Leu Lys
 250 255 260

cgc ggc gac gac 895
 Arg Gly Asp Asp
 265

<210> 46

<211> 265

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 46

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Arg Gly Val Ser Leu Leu Ala Ser Pro Val Thr Ala Pro Leu Asn Ser
 20 25 30

Trp Arg Arg Leu Pro Asn Leu Ala Lys Tyr Thr Leu Tyr Thr Arg Val
 35 40 45

Ser Leu Gln Ala Ile Pro Val Val Leu Leu Ser Ala Tyr Phe Leu Gly
 50 55 60

Ile Val Ala Asn Ala Gly Thr Leu Asn Pro Ser Phe Val Trp Leu Leu
 65 70 75 80

Gly Phe Ser Val Ile Leu Leu Ile Val Thr Val Leu Val Tyr Glu Tyr
 85 90 95

Gln Pro Ser Leu Asn Ser His Pro Arg Arg Ser Val Gln Pro Phe Phe
 100 105 110

Phe Thr Gly Leu Val Leu Asn Val Leu Gly Val Val Val Ser Val Val
 115 120 125

Leu Gln Ile Pro Gly Leu Asn Met Ser Asp Asn Thr Arg Ala Thr Ala
 130 135 140

Leu Ile Phe Thr Leu Thr Cys Val Phe Leu Leu Ser Ile Ala Tyr Ile
 145 150 155 160

Pro Trp Met Asn Tyr Arg Trp Val Trp Leu Ile Ala Met Ser Ala Val
 165 170 175

Leu Trp Trp Thr Ser Thr Thr Thr Asp Tyr Leu Ser Ala Leu Trp Val

180	185	190
Val Ile Pro Pro Leu Met Ala Gly Thr Val Arg Leu Ser Val Trp Thr		
195	200	205
Val Asp Val Met Lys Glu Val Glu Arg Ser Arg Glu Leu Glu Ala Ser		
210	215	220
Leu Arg Val Thr Glu Glu Arg Leu Arg Phe Ala Gln Glu Leu His Asp		
225	230	235
Thr Leu Gly Gln His Leu Ala Ala Met Ser Val Lys Ser Glu Leu Ala		
245	250	255
Leu Ala Leu Ala Lys Arg Gly Asp Asp		
260	265	

<210> 47
 <211> 529
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <223> RXA01248

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 Met Ala Asp Arg Thr
 1 5

ccg acc acc gcc acg ccc ccg ggg cgg gtg ctg gtc gtc gat gat gaa 163
 Pro Thr Thr Ala Thr Pro Pro Gly Arg Val Leu Val Val Asp Asp Glu
 10 15 20

caa ccc ctg gct cag atg gtg gcc tcc tac ctc atc cgg gcc gcc ttc 211
 Gln Pro Leu Ala Gln Met Val Ala Ser Tyr Leu Ile Arg Ala Gly Phe
 25 30 35

gac acc cgc cag gcg cac acc ggc acc cag gcc gtg gac gag gcc cgt 259
 Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala Val Asp Glu Ala Arg
 40 45 50

cgc ttt tcc ccc gat gtt gtg gtg ctg gat ctg ggg ctg ccc gaa ctc 307
 Arg Phe Ser Pro Asp Val Val Leu Asp Leu Gly Leu Pro Glu Leu
 55 60 65

gac ggc ctg gag gtg tgc cga cgg atc cgc acc ttc tgc gac tgc tac. 355
 Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr Phe Ser Asp Cys Tyr
 70 75 80 85

atc ctc atg ctc acc gcg cgt ggc agc gag gac gac aag atc agc ggt 403
 Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp Asp Lys Ile Ser Gly
 90 95 100

ttg acc ctg ggg gcg gat gac tac atc acc aaa cct ttt agc atc cgg 451
 Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys Pro Phe Ser Ile Arg

105 110 115 499
 gaa ctg gtg acc cgg gtg cat gcg gtg ctg cgc cgc ccg cgc acc agc
 Glu Leu Val Thr Arg Val His Ala Val Leu Arg Arg Pro Arg Thr Ser
 120 125 130

acc acc cca ccg cag gtg acc acc ccc ttg 529
 Thr Thr Pro Pro Gln Val Thr Thr Pro Leu
 135 140

<210> 48
 <211> 143
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 48
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Val Val Asp Asp Glu Gln Pro Leu Ala Gln Met Val Ala Ser Tyr Leu
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Ile Arg Ala Gly Phe Asp Thr Arg Gln Ala His Thr Gly Thr Gln Ala
 35 40 45

Val Asp Glu Ala Arg Arg Phe Ser Pro Asp Val Val Val Leu Asp Leu
 50 55 60

Gly Leu Pro Glu Leu Asp Gly Leu Glu Val Cys Arg Arg Ile Arg Thr
 65 70 75 80

Phe Ser Asp Cys Tyr Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Asp
 85 90 95

Asp Lys Ile Ser Gly Leu Thr Leu Gly Ala Asp Asp Tyr Ile Thr Lys
 100 105 110

Pro Phe Ser Ile Arg Glu Leu Val Thr Arg Val His Ala Val Leu Arg
 115 120 125

Arg Pro Arg Thr Ser Thr Thr Pro Pro Gln Val Thr Thr Pro Leu
 130 135 140

<210> 49
 <211> 846
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(823)
 <223> RXA02668

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 tggttgtaat caggaaacag aaaaggccat acttgaaacc atg acg aac ccc tcc 115
 Met Thr Asn Pro Ser
 1 5

ccc gcg cta aat gaa acc ctt tcc ggc agg gtg ctg atc gtt gaa gat 163
 Pro Ala Leu Asn Glu Thr Leu Ser Gly Arg Val Leu Ile Val Glu Asp
 10 15 20

gag cgc cct ctt gct cgc atg att tcc ctt tat tta agc aaa gcg ggt 211
 Glu Arg Pro Leu Ala Arg Met Ile Ser Leu Tyr Leu Ser Lys Ala Gly
 25 30 35

ttc gat acc acc acg atc cac gac ggc gcc gct gct cca gat aag gtc 259
 Phe Asp Thr Thr Thr Ile His Asp Gly Ala Ala Ala Pro Asp Lys Val
 40 45 50

gct cac ctg cgc ccc gac gtg gtc att ttg gat ctt ggg ctg cct ggt 307
 Ala His Leu Arg Pro Asp Val Val Ile Leu Asp Leu Gly Leu Pro Gly
 55 60 65

ctt gat ggt ttg gaa gtg tgc aaa cgc atc cgc gcg ttc acc gat tgc 355
 Leu Asp Gly Leu Glu Val Cys Lys Arg Ile Arg Ala Phe Thr Asp Cys
 70 75 80 85

tac atc cta atg ctc acc gcc agg ggt tca gag cgg gat cgg att aca 403
 Tyr Ile Leu Met Leu Thr Ala Arg Gly Ser Glu Arg Asp Arg Ile Thr
 90 95 100

ggt ttg gaa att ggg gct gat gat tac atc acc aag cgg ttt aat atc 451
 Gly Leu Glu Ile Gly Ala Asp Asp Tyr Ile Thr Lys Pro Phe Asn Ile
 105 110 115

cgc gaa ctt gtc att cgt atc cag tca gta atg cgt cgc cct cga aaa 499
 Arg Glu Leu Val Ile Arg Ile Gln Ser Val Met Arg Arg Pro Arg Lys
 120 125 130

atc gat gaa acc atc caa aat ggt ttg acc ttg act tat ggc cac att 547
 Ile Asp Glu Thr Ile Gln Asn Gly Leu Thr Leu Thr Tyr Gly His Ile
 135 140 145

gag ctg gac acc ttg gcg cat gaa gtc act gtc aaa gcc gtt ggg gtg 595
 Glu Leu Asp Thr Leu Ala His Glu Val Thr Val Lys Gly Val Gly Val
 150 155 160 165

aca ctg acc cgc aca gaa ttt gag ctg ctt caa gcc ctc atg cac aaa 643
 Thr Leu Thr Arg Thr Glu Phe Glu Leu Leu Gln Ala Leu Met His Lys
 170 175 180

ccg gga gag gca gtg tct agg cgt gat ttg gtc agc caa gtg tgg gat 691
 Pro Gly Glu Ala Val Ser Arg Arg Asp Leu Val Ser Gln Val Trp Asp
 185 190 195

acc acc tgg gtt ggc gat gaa cgc atc gtt gac gtg cac att gga aat 739
 Thr Thr Trp Val Gly Asp Glu Arg Ile Val Asp Val His Ile Gly Asn
 200 205 210

ctg cgc cgc aag ctg gaa gca cct gcg ccg ggt tca cac ttc atc gac 787
 Leu Arg Arg Lys Leu Glu Ala Pro Ala Pro Gly Ser His Phe Ile Asp
 215 220 225

acc atc cga ggt gtt ggc tac cgg atg gcc ttc aaa tgacagccct 833
 Thr Ile Arg Gly Val Gly Tyr Arg Met Ala Phe Lys
 230 235 240

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846

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<212> PRT
<213> Corynebacterium glutamicum
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		20						25					30				
Leu	Ser	Lys	Ala	Gly	Phe	Asp	Thr	Thr	Thr	Ile	His	Asp	Gly	Ala	Ala		
		35					40					45					
Ala	Pro	Asp	Lys	Val	Ala	His	Leu	Arg	Pro	Asp	Val	Val	Ile	Leu	Asp		
	50					55					60						
Leu	Gly	Leu	Pro	Gly	Leu	Asp	Gly	Leu	Glu	Val	Cys	Lys	Arg	Ile	Arg		
	65				70					75					80		
Ala	Phe	Thr	Asp	Cys	Tyr	Ile	Leu	Met	Leu	Thr	Ala	Arg	Gly	Ser	Glu		
			85						90					95			
Arg	Asp	Arg	Ile	Thr	Gly	Leu	Glu	Ile	Gly	Ala	Asp	Asp	Tyr	Ile	Thr		
			100					105					110				
Lys	Pro	Phe	Asn	Ile	Arg	Glu	Leu	Val	Ile	Arg	Ile	Gln	Ser	Val	Met		
		115					120					125					
Arg	Arg	Pro	Arg	Lys	Ile	Asp	Glu	Thr	Ile	Gln	Asn	Gly	Leu	Thr	Leu		
		130				135					140						
Thr	Tyr	Gly	His	Ile	Glu	Leu	Asp	Thr	Leu	Ala	His	Glu	Val	Thr	Val		
				150						155					160		
Lys	Gly	Val	Gly	Val	Thr	Leu	Thr	Arg	Thr	Glu	Phe	Glu	Leu	Leu	Gln		
			165						170					175			
Ala	Leu	Met	His	Lys	Pro	Gly	Glu	Ala	Val	Ser	Arg	Arg	Asp	Leu	Val		
			180					185					190				
Ser	Gln	Val	Trp	Asp	Thr	Thr	Trp	Val	Gly	Asp	Glu	Arg	Ile	Val	Asp		
		195					200					205					
Val	His	Ile	Gly	Asn	Leu	Arg	Lys	Leu	Glu	Ala	Pro	Ala	Pro	Gly			
		210				215				220							
Ser	His	Phe	Ile	Asp	Thr	Ile	Arg	Gly	Val	Gly	Tyr	Arg	Met	Ala	Phe		
				230						235					240		
Lys																	

<210>	51
<211>	819
<212>	DNA

Tyr Val Leu Arg Glu Thr Ala Pro
225 230

<210> 53
<211> 1488
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1465)
<223> RXA02631

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tgggcctgcc cctaccgaaa gtgatgactc cgacgggtca atg tcg ttg cgt tgg 115
Met Ser Leu Arg Trp 5
1

cgc ttg gct ttg ctg agc gcc act ttg gta gct ttc gcc gtt ggt gtt 163
Arg Leu Ala Leu Leu Ser Ala Thr Leu Val Ala Phe Ala Val Gly Val
10 15 20

att act gtt gct gca tat tgg tct gtc tcc agc tat gtc acc aac tca 211
Ile Thr Val Ala Ala Tyr Trp Ser Val Ser Ser Tyr Val Thr Asn Ser
25 30 35

atc gat cgt gat ctg gaa aaa caa gcg gat gca atg ctt gga cga gcc 259
Ile Asp Arg Asp Leu Glu Lys Gln Ala Asp Ala Met Leu Gly Arg Ala
40 45 50

agt gaa gcg gga ttc tat gca acc gca gaa acc gaa att gct ctg tta 307
Ser Glu Ala Gly Phe Tyr Ala Thr Ala Glu Thr Glu Ile Ala Leu Leu
55 60 65

ggg gaa tat gcc agt gac act cga atc gcc tta atc cca cct ggg tgg 355
Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu Ile Pro Pro Gly Trp
70 75 80 85

gaa tac gtc atc ggt gaa tcc ata tca ctg cct gat tca gat ttc ctt 403
Glu Tyr Val Ile Gly Glu Ser Ile Ser Leu Pro Asp Ser Asp Phe Leu
90 95 100

aag agt aaa gaa gcg ggg aaa cag atc ctc gta aca agt gct gag cgc 451
Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val Thr Ser Ala Glu Arg
105 110 115

att ctc atg aaa cga gat agc tcg ggc aca gtg gtg gtt ttt gct aaa 499
Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val Val Phe Ala Lys
120 125 130

gat atg gtg gat acc gat cgg cag ctc acg gtg ctt ggc gtc att ctc 547
Asp Met Val Asp Thr Asp Arg Gln Leu Thr Val Leu Gly Val Ile Leu
135 140 145

ttg atc att ggc ggc agt ggt gtt ttg gcg tcg att ctg ctt ggt ttc 595
Leu Ile Ile Gly Gly Ser Gly Val Leu Ala Ser Ile Leu Leu Gly Phe
150 155 160 165

atc att gcg aag gag ggg ctg aaa cca ctg tca aag ctg cag cgt gcc 643
 ile ile ala lys glu gly leu lys pro leu ser lys leu gln arg ala
 170 175 180

gtc gaa gag atc gaa cga act gat gag ctt cgt gcg att ccc gtg gtg 691
 val glu glu ile glu arg thr asp glu leu arg ala ile pro val val
 185 190 195

gga aat gat gag ttc gct aag ttg act cgt agt ttc aat gac atg ctc 739
 gly asn asp glu phe ala lys leu thr arg ser phe asn asp met leu
 200 205 210

aag gca ctg cgg gag tot cgt acc cgg caa tct cag ttg gtg gca gat 787
 lys ala leu arg glu ser arg thr arg gln ser gln leu val ala asp
 215 220 225

gca gga cac gag ctg aaa act cca ctg acc tca atg cgg aca aat att 835
 ala gly his glu leu lys thr pro leu thr ser met arg thr asn ile
 230 235 240 245

gaa ttg ctg ttg atg gca acc aac agt gga gga tcg gga atc ccc aag 883
 glu leu leu leu met ala thr asn ser gly gly ser gly ile pro lys
 250 255 260

gaa gaa ttg gat ggc ctt cag cgt gat gta ttg gcg cag atg acc gaa 931
 glu glu leu asp gly leu gln arg asp val leu ala gln met thr glu
 265 270 275

atg tct gat ttg att ggt gat ctt gtt gat ctt gcg cgt gaa gaa acc 979
 met ser asp leu ile gly asp leu val asp leu ala arg glu glu thr
 280 285 290

gcc gaa acg tca agc att gta gat ctc aac caa gtg ttg gaa att gcg 1027
 ala glu thr ser ser ile val asp leu asn gln val leu glu ile ala
 295 300 305

ctt gac cga atg gaa agc cgt cgc atg acg gtg cgg ata gat gtt tcc 1075
 leu asp arg met glu ser arg arg met thr val arg ile asp val ser
 310 315 320 325

gag act gtg gat tgg aaa ctg ctg ggc gat gat ttt tcc tta acc agg 1123
 glu thr val asp trp lys leu leu gly asp asp phe ser leu thr arg
 330 335 340

gca tta gta aat gtt ttg gat aat gcc att aaa tgg tcg cct gag aat 1171
 ala leu val asn val leu asp asn ala ile lys trp ser pro glu asn
 345 350 355

ggc att gtt cga gtg tcg atg tca cag atc gac aaa gca acg gtc cgc 1219
 gly ile val arg val ser met ser gln ile asp lys ala thr val arg
 360 365 370

att gtt att gat gat tca ggg cct gga att gct gaa aaa gaa cga gga 1267
 ile val ile asp asp ser gly pro gly ile ala glu lys glu arg gly
 375 380 385

tta gtt ttg gaa cgg ttc tat cgc gcc gtc agc tcc cgt tcc atg ccg 1315
 leu val leu glu arg phe tyr arg ala val ser ser arg ser met pro
 390 395 400 405

gga tcg gga tta ggt ctt gcc atc gtg aat cag gtt gtg aat cgg cat 1363
Gly Ser Gly Leu Gly Leu Ala Ile Val Asn Gln Val Val Asn Arg His
410 415 420

ggt ggc caa ctc gtt gtg ggt gaa tca gat gat ggc gga acg aga atc 1411
Gly Gly Gln Leu Val Val Gly Glu Ser Asp Asp Gly Gly Thr Arg Ile
425 430 435

act att gat ttg cca ggg gaa ccc att cgc agc ggg ttc gaa aat gtc 1459
Thr Ile Asp Leu Pro Gly Glu Pro Ile Arg Ser Gly Phe Glu Asn Val
440 445 450

gat gat taaaccacta aagagctcac agg 1488
Asp Asp
455

<210> 54

<211> 455

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 54

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Phe Ala Val Gly Val Ile Thr Val Ala Ala Tyr Trp Ser Val Ser Ser
20 25 30

Tyr Val Thr Asn Ser Ile Asp Arg Asp Leu Glu Lys Gln Ala Asp Ala
35 40 45

Met Leu Gly Arg Ala Ser Glu Ala Gly Phe Tyr Ala Thr Ala Glu Thr
50 55 60

Glu Ile Ala Leu Leu Gly Glu Tyr Ala Ser Asp Thr Arg Ile Ala Leu
65 70 75 80

Ile Pro Pro Gly Trp Glu Tyr Val Ile Gly Glu Ser Ile Ser Leu Pro
85 90 95

Asp Ser Asp Phe Leu Lys Ser Lys Glu Ala Gly Lys Gln Ile Leu Val
100 105 110

Thr Ser Ala Glu Arg Ile Leu Met Lys Arg Asp Ser Ser Gly Thr Val
115 120 125

Val Val Phe Ala Lys Asp Met Val Asp Thr Asp Arg Gln Leu Thr Val
130 135 140

Leu Gly Val Ile Leu Leu Ile Ile Gly Gly Ser Gly Val Leu Ala Ser
145 150 155 160

Ile Leu Leu Gly Phe Ile Ile Ala Lys Glu Gly Leu Lys Pro Leu Ser
165 170 175

Lys Leu Gln Arg Ala Val Glu Glu Ile Glu Arg Thr Asp Glu Leu Arg
180 185 190

Ala Ile Pro Val Val Gly Asn Asp Glu Phe Ala Lys Leu Thr Arg Ser
195 200 205

Phe Asn Asp Met Leu Lys Ala Leu Arg Glu Ser Arg Thr Arg Gln Ser
 210 215 220
 Gln Leu Val Ala Asp Ala Gly His Glu Leu Lys Thr Pro Leu Thr Ser
 225 230 235 240
 Met Arg Thr Asn Ile Glu Leu Leu Leu Met Ala Thr Asn Ser Gly Gly
 245 250 255
 Ser Gly Ile Pro Lys Glu Glu Leu Asp Gly Leu Gln Arg Asp Val Leu
 260 265 270
 Ala Gln Met Thr Glu Met Ser Asp Leu Ile Gly Asp Leu Val Asp Leu
 275 280 285
 Ala Arg Glu Glu Thr Ala Glu Thr Ser Ser Ile Val Asp Leu Asn Gln
 290 295 300
 Val Leu Glu Ile Ala Leu Asp Arg Met Glu Ser Arg Arg Met Thr Val
 305 310 315 320
 Arg Ile Asp Val Ser Glu Thr Val Asp Trp Lys Leu Leu Gly Asp Asp
 325 330 335
 Phe Ser Leu Thr Arg Ala Leu Val Asn Val Leu Asp Asn Ala Ile Lys
 340 345 350
 Trp Ser Pro Glu Asn Gly Ile Val Arg Val Ser Met Ser Gln Ile Asp
 355 360 365
 Lys Ala Thr Val Arg Ile Val Ile Asp Asp Ser Gly Pro Gly Ile Ala
 370 375 380
 Glu Lys Glu Arg Gly Leu Val Leu Glu Arg Phe Tyr Arg Ala Val Ser
 385 390 395 400
 Ser Arg Ser Met Pro Gly Ser Gly Leu Gly Leu Ala Ile Val Asn Gln
 405 410 415
 Val Val Asn Arg His Gly Gly Gln Leu Val Val Gly Glu Ser Asp Asp
 420 425 430
 Gly Gly Thr Arg Ile Thr Ile Asp Leu Pro Gly Glu Pro Ile Arg Ser
 435 440 445
 Gly Phe Glu Asn Val Asp Asp
 450 455

<210> 55

<211> 789

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(766)

<223> RXA00609

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Met Ser Lys Ile Leu
1 5
ctc gct gaa gat gac gcc ggc atc gca gat ttc atc gtt cgt ggc ctc 163
Leu Ala Glu Asp Asp Ala Gly Ile Ala Asp Phe Ile Val Arg Gly Leu
10 15 20
atc cgc gaa ggc ttc gaa tgc gag gtc acc gaa tcc ggc gcc gaa gct 211
Ile Arg Glu Gly Phe Glu Cys Glu Val Thr Glu Ser Gly Ala Glu Ala
25 30 35
ttc gcc cgc gca cat tcc ggc gat ttc gat ctc atg gtt tta gac ctc 259
Phe Ala Arg Ala His Ser Gly Asp Phe Asp Leu Met Val Leu Asp Leu
40 45 50
ggc ctc ccc cac atg gac ggc acg gat gtc cta gag caa tta aga aat 307
Gly Leu Pro His Met Asp Gly Thr Asp Val Leu Glu Leu Arg Asn
55 60 65
ctg cag gtc acg cta cct atc att gtg ctc acg gca cgc acc aac atc 355
Leu Gln Val Thr Leu Pro Ile Ile Val Leu Thr Ala Arg Thr Asn Ile
70 75 80 85
gag gac cgc ctc cgc acc ctc gag ggc ggc gcc gac gat tac atg ccc 403
Glu Asp Arg Leu Arg Thr Leu Glu Gly Gly Ala Asp Asp Tyr Met Pro
90 95 100
aaa cca ttc caa ttc gca gaa tta ctg gcc cgc atc aaa ctc cgc ctc 451
Lys Pro Phe Gln Phe Ala Glu Leu Leu Ala Arg Ile Lys Leu Arg Leu
105 110 115
gcc aaa cac act cct cag gaa acg ccg acc gat gcg cgc gtg cta cga 499
Ala Lys His Thr Pro Gln Glu Thr Pro Thr Asp Ala Arg Val Leu Arg
120 125 130
aac ggc gat ttg gag ctc gat ctt cgt acc cag cgt gtg ctc atc gac 547
Asn Gly Asp Leu Glu Leu Asp Leu Arg Thr Gln Arg Val Leu Ile Asp
135 140 145
ggc tcc tgg cac gac ctt tcc cgc cgc gaa gtc gat ctg ctc gaa acc 595
Gly Ser Trp His Asp Leu Ser Arg Arg Glu Val Asp Leu Leu Glu Thr
150 155 160 165
ctc atg cga cac cca ggg caa atc ctc tcc cga gtc caa ctc ctc cga 643
Leu Met Arg His Pro Gly Gln Ile Leu Ser Arg Val Gln Leu Leu Arg
170 175 180
ctg gtg tgg gac atg gat tgg gac ccc ggc tca aac gtg gtg gac gta 691
Leu Val Trp Asp Met Asp Trp Asp Pro Gly Ser Asn Val Val Asp Val
185 190 195
tat atc cgc gcg ttg agg aag aaa atc ggt gcc cat cgg gtc gaa acc 739
Tyr Ile Arg Ala Leu Arg Lys Lys Ile Gly Ala His Arg Val Glu Thr
200 205 210
atc cga gga tct ggc tac cgg ctg cgc taactgcaga acgagaccaa 786
Ile Arg Gly Ser Gly Tyr Arg Leu Arg
215 220

ccc gaa gaa ctc cgc gcc aac aca cca att ttg cac gac gga gta agc 787
 Pro Glu Glu Leu Arg Ala Asn Thr Pro Ile Leu His Asp Gly Val Ser
 215 220 225

cca ata gaa ctg cct ggg gat acc tgg caa gaa caa ttc atc gaa ggc 835
 Pro Ile Glu Leu Pro Gly Asp Thr Trp Gln Glu Gln Phe Ile Glu Gly
 230 235 240 245

tac gat ctc ctc gtt ccc gca atg ggc aaa gcg aaa tcc ctg caa ggc 883
 Tyr Asp Leu Leu Val Pro Ala Met Gly Lys Ala Lys Ser Leu Gln Gly
 250 255 260

gaa gcc atc cga att gcc gga cga gta tcc aac gaa ttt cac ggc aac 931
 Glu Ala Ile Arg Ile Ala Gly Arg Val Ser Asn Glu Phe His Gly Asn
 265 270 275

ggt ggc gtc aac tgg gac aaa gac ttc aaa cgc atg gcc aaa tct ctc 979
 Gly Gly Val Asn Trp Asp Lys Asp Phe Lys Arg Met Ala Lys Ser Leu
 280 285 290

aac cac att tgt gag cag ggc gtt cct ttg ggt gag cca gaa tta gaa 1027
 Asn His Ile Cys Glu Gln Gly Val Pro Leu Gly Glu Pro Glu Leu Glu
 295 300 305

gaa ctg gct gcg gcc gtt aaa tca gtg cgc aaa gga gaa ccc acc gag 1075
 Glu Leu Ala Ala Ala Val Lys Ser Val Arg Lys Gly Glu Pro Thr Glu
 310 315 320 325

gag gag atc gac acc ctt cca cgg ttg gcc acc aaa tgg gtc gca caa 1123
 Glu Glu Ile Asp Thr Leu Pro Arg Leu Ala Thr Lys Trp Val Ala Gln
 330 335 340

aac cca caa ccg ctg cca ctg gga gag gtt gac tac aag cgc 1165
 Asn Pro Gln Pro Leu Pro Leu Gly Glu Val Asp Tyr Lys Arg
 345 350 355

tgaacgttga gtttgagttt ggt 1188

<210> 58
 <211> 355
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 58
 Met Ala Arg Lys Leu Lys Asp Lys Leu Pro Arg Ser Phe Asp Lys Ile
 1 5 10 15

Val Glu Ser Gly Asp Phe Asp Ala Phe Lys Glu Val Phe Thr Glu Arg
 20 25 30

Ala Leu Asp Ala Lys Asn Arg His Gly Asn Thr Ala Leu His Met Arg
 35 40 45

Gly Val Pro Glu Glu Phe Lys Ile Trp Met Leu Asp Gln Gly Leu Asp
 50 55 60

Val Asp Ile Arg Asn Glu Asp Gly Asp Thr Pro Leu His Val His Ser
 65 70 75 80

His Asp Trp Asn Leu Ser Pro Asp Phe Leu Leu Lys Arg Gly Ala Asp

85										90					95				
Val	Cys	Ala	Val	Asn	Asn	Glu	Gly	Glu	Ser	Val	Ala	Tyr	Ser	Ala	Ala				
			100						105					110					
Phe	Phe	Pro	Glu	Asn	Leu	Lys	Lys	Leu	Ile	Asp	Ala	Gly	Ala	Asp	Pro				
		115					120						125						
Tyr	Ser	Arg	Ala	Asn	Asp	Gly	Thr	Thr	Pro	Leu	Met	Arg	Val	Ile	Arg				
		130				135					140								
Ser	Ala	Asp	Thr	Gly	Gln	Ile	Ile	Glu	Leu	Ala	Glu	Ile	Thr	Lys	Leu				
		145			150				155					160					
Leu	Ser	Gly	Thr	Glu	Phe	Thr	Asp	Ala	Glu	Phe	Arg	Glu	Thr	Gln	Glu				
			165					170						175					
Arg	Ile	Ile	Ala	Met	Gly	Glu	Arg	Phe	Glu	Asp	Val	Arg	Glu	Val	Tyr				
			180				185						190						
Asn	Glu	Glu	Ser	Val	Asp	Gln	Ala	Ser	Ala	Asp	Met	Ile	Trp	Leu	Tyr				
			195				200				205								
Asp	Arg	Phe	Asp	Ile	Pro	Glu	Glu	Leu	Arg	Ala	Asn	Thr	Pro	Ile	Leu				
		210			215						220								
His	Asp	Gly	Val	Ser	Pro	Ile	Glu	Leu	Pro	Gly	Asp	Thr	Trp	Gln	Glu				
		225			230				235					240					
Gln	Phe	Ile	Glu	Gly	Tyr	Asp	Leu	Leu	Val	Pro	Ala	Met	Gly	Lys	Ala				
			245					250						255					
Lys	Ser	Leu	Gln	Gly	Glu	Ala	Ile	Arg	Ile	Ala	Gly	Arg	Val	Ser	Asn				
		260					265						270						
Glu	Phe	His	Gly	Asn	Gly	Gly	Val	Asn	Trp	Asp	Lys	Asp	Phe	Lys	Arg				
		275					280						285						
Met	Ala	Lys	Ser	Leu	Asn	His	Ile	Cys	Glu	Gln	Gly	Val	Pro	Leu	Gly				
		290				295					300								
Glu	Pro	Glu	Leu	Glu	Glu	Leu	Ala	Ala	Ala	Val	Lys	Ser	Val	Arg	Lys				
		305			310				315					320					
Gly	Glu	Pro	Thr	Glu	Glu	Glu	Ile	Asp	Thr	Leu	Pro	Arg	Leu	Ala	Thr				
			325						330					335					
Lys	Trp	Val	Ala	Gln	Asn	Pro	Gln	Pro	Leu	Pro	Leu	Gly	Glu	Val	Asp				
		340					345						350						
Tyr	Lys	Arg																	
		355																	

<210> 59

<211> 1530

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1507)

<223> RXA01827

<400> 59

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tgcccgagct gtgcttcagg cagccggagg atttttaaaat atg agt caa gaa gac 115
 Met Ser Gln Glu Asp
 1 5

atc act gga aaa gat cga ctc caa gaa ctc atc ggc gct gat tat cgt 163
 Ile Thr Gly Lys Asp Arg Leu Gln Glu Leu Ile Gly Ala Asp Tyr Arg
 10 15 20

ctg cag tgg atc atc gga cac ggt ggc atg tcc acc gta tgg ctc gca 211
 Leu Gln Trp Ile Ile Gly His Gly Gly Met Ser Thr Val Trp Leu Ala
 25 30 35

gat gat tgg gtc aat gat cgc gaa gta gcc atc aag gta ctg cgc ccg 259
 Asp Asp Val Val Asn Asp Arg Glu Val Ala Ile Lys Val Leu Arg Pro
 40 45 50

gaa ttt tcc gac aac cag gag ttc ttg aac cgt ttc cgc aat gaa gcg 307
 Glu Phe Ser Asp Asn Gln Glu Phe Leu Asn Arg Phe Arg Asn Glu Ala
 55 60 65

caa gcg gct gag aat atc gat tct gaa cac gtg gtg gcc acc tat gac 355
 Gln Ala Ala Glu Asn Ile Asp Ser Glu His Val Val Ala Thr Tyr Asp
 70 75 80 85

tac cgt gag gtt cca gac cct gct ggg cat act ttc tgc ttc atc gtc 403
 Tyr Arg Glu Val Pro Asp Pro Ala Gly His Thr Phe Cys Phe Ile Val
 90 95 100

atg gaa ttt gtc cgc ggt gaa tgc ctt gcg gat ctt cta gag cgc gaa 451
 Met Glu Phe Val Arg Gly Glu Ser Leu Ala Asp Leu Leu Glu Arg Glu
 105 110 115

ggc aga ctg ccg gaa gac ctg gct ctt gat gtg atg gaa cag gcg gca 499
 Gly Arg Leu Pro Glu Asp Leu Ala Leu Asp Val Met Glu Gln Ala Ala
 120 125 130

cat ggt ttg tgc gtg att cac cgg atg gac atg gtg cac cgc gat atc 547
 His Gly Leu Ser Val Ile His Arg Met Asp Met Val His Arg Asp Ile
 135 140 145

aag ccg ggc aac atg ctg atc aca gcc aat ggc att gtg aag atc acg 595
 Lys Pro Gly Asn Met Leu Ile Thr Ala Asn Gly Ile Val Lys Ile Thr
 150 155 160 165

gac ttt ggt atc gct aag gct gcc gct gct gtg cct ttg acc cgc acc 643
 Asp Phe Gly Ile Ala Lys Ala Ala Ala Val Pro Leu Thr Arg Thr
 170 175 180

ggc atg gtg gtg ggt act gct caa tat gtt tca cct gag caa gcc cag 691
 Gly Met Val Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Gln Ala Gln
 185 190 195

ggc aag gaa gtc acc gcg gct tct gat att tat tct ctc ggt gtg gtc 739
 Gly Lys Glu Val Thr Ala Ala Ser Asp Ile Tyr Ser Leu Gly Val Val
 200 205 210

000000-000000

ggc tat gag atg atg gct ggc cgc cgc cgc ttc act gga gat tct tcg 787
 Gly Tyr Glu Met Met Ala Gly Arg Arg Pro Phe Thr Gly Asp Ser Ser
 215 220 225

gtg tct gtg gcg atc gcg cac atc aac caa gct ccg ccg cag atg ccc 835
 Val Ser Val Ala Ile Ala His Ile Asn Gln Ala Pro Pro Gln Met Pro
 230 235 240 245

acc agc att tcg gca cag act cgc gag ttg att ggc att gcg ttg cgc 883
 Thr Ser Ile Ser Ala Gln Thr Arg Glu Ile Gly Ile Ala Leu Arg
 250 255 260

aag gat ccg ggt cgc cgt ttc cct gat gga aat gaa atg gcg cta gct 931
 Lys Asp Pro Gly Arg Arg Phe Pro Asp Gly Asn Glu Met Ala Leu Ala
 265 270 275

gtt tct gct gtg cgc ctt ggc aag cgc cgc cct caa ccg cgc acg agc 979
 Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro Gln Pro Arg Thr Ser
 280 285 290

gcg atg atg gcg cag gcg gag gcg ccg tcg cca agc gaa tca acg gcg 1027
 Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro Ser Glu Ser Thr Ala
 295 300 305

atg ctg ggc agg gtg gcc cgc cct gca aca atc acc caa gaa gcg gcc 1075
 Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile Thr Gln Glu Ala Ala
 310 315 320 325

ccg aaa cgc ggt tcc ggc att ggc att ggt ctg ttc atc gca gct ttg 1123
 Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu Phe Ile Ala Ala Leu
 330 335 340

ctt gcc gtg att att ggc gcg gtg atc tat gcg ggc acc acc gga att 1171
 Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala Gly Thr Thr Gly Ile
 345 350 355

ttg ttc aac gac act ccg gaa gaa acc acc aca cct gaa acc att acg 1219
 Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr Pro Glu Thr Ile Thr
 360 365 370

gaa aca tac acc cca acc gtg gag gaa acc acc tct cag tgg gta ccg 1267
 Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr Thr Ser Gln Trp Val Pro
 375 380 385

cca acg cct cca aca ccg tca aca ttc acc gaa cct gaa aca act tca 1315
 Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu Pro Glu Thr Thr Ser
 390 395 400 405

cac cgt ccg acg aca agt gaa gag agc aca tcc gag gaa cca acc acg 1363
 His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser Glu Glu Pro Thr Thr
 410 415 420

gaa gct cca aca agt agc cga act gtg cct caa atc cct acc tct aca 1411
 Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln Ile Pro Thr Ser Thr
 425 430 435

cct agg acg agt gct agc gtt cca gtt gag act aat gca ccg gct gat 1459
 Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr Asn Ala Pro Ala Asp
 440 445 450

gat tta atc gac gcc gta aat ggc cta ttg gat gta gga gga gcg cag 1507
 Asp Leu Ile Asp Ala Val Asn Gly Leu Leu Asp Val Gly Gly Ala Gln
 455 460 465

tgaccttcgt gatcgatgat cgc 1530

<210> 60

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

Met Ser Gln Glu Asp Ile Thr Gly Lys Asp Arg Leu Gln Glu Leu Ile
 1 5 10 15

Gly Ala Asp Tyr Arg Leu Gln Trp Ile Ile Gly His Gly Gly Met Ser
 20 25 30

Thr Val Trp Leu Ala Asp Asp Val Val Asn Asp Arg Glu Val Ala Ile
 35 40 45

Lys Val Leu Arg Pro Glu Phe Ser Asp Asn Gln Glu Phe Leu Asn Arg
 50 55 60

Phe Arg Asn Glu Ala Gln Ala Ala Glu Asn Ile Asp Ser Glu His Val
 65 70 75 80

Val Ala Thr Tyr Asp Tyr Arg Glu Val Pro Asp Pro Ala Gly His Thr
 85 90 95

Phe Cys Phe Ile Val Met Glu Phe Val Arg Gly Glu Ser Leu Ala Asp
 100 105 110

Leu Leu Glu Arg Glu Gly Arg Leu Pro Glu Asp Leu Ala Leu Asp Val
 115 120 125

Met Glu Gln Ala Ala His Gly Leu Ser Val Ile His Arg Met Asp Met
 130 135 140

Val His Arg Asp Ile Lys Pro Gly Asn Met Leu Ile Thr Ala Asn Gly
 145 150 155 160

Ile Val Lys Ile Thr Asp Phe Gly Ile Ala Lys Ala Ala Ala Val
 165 170 175

Pro Leu Thr Arg Thr Gly Met Val Val Gly Thr Ala Gln Tyr Val Ser
 180 185 190

Pro Glu Gln Ala Gln Gly Lys Glu Val Thr Ala Ala Ser Asp Ile Tyr
 195 200 205

Ser Leu Gly Val Val Gly Tyr Glu Met Met Ala Gly Arg Arg Pro Phe
 210 215 220

Thr Gly Asp Ser Ser Val Ser Val Ala Ile Ala His Ile Asn Gln Ala
 225 230 235 240

Pro Pro Gln Met Pro Thr Ser Ile Ser Ala Gln Thr Arg Glu Leu Ile
 245 250 255

Gly Ile Ala Leu Arg Lys Asp Pro Gly Arg Arg Phe Pro Asp Gly Asn
260 265 270

Glu Met Ala Leu Ala Val Ser Ala Val Arg Leu Gly Lys Arg Pro Pro
275 280 285

Gln Pro Arg Thr Ser Ala Met Met Ala Gln Ala Glu Ala Pro Ser Pro
290 295 300

Ser Glu Ser Thr Ala Met Leu Gly Arg Val Ala Arg Pro Ala Thr Ile
305 310 315 320

Thr Gln Glu Ala Ala Pro Lys Arg Gly Ser Gly Ile Gly Ile Gly Leu
325 330 335

Phe Ile Ala Ala Leu Leu Ala Val Ile Ile Gly Ala Val Ile Tyr Ala
340 345 350

Gly Thr Thr Gly Ile Leu Phe Asn Asp Thr Pro Glu Glu Thr Thr Thr
355 360 365

Pro Glu Thr Ile Thr Glu Thr Tyr Thr Pro Thr Val Glu Glu Thr Thr
370 375 380

Ser Gln Trp Val Pro Pro Thr Pro Pro Thr Arg Ser Thr Phe Thr Glu
385 390 395 400

Pro Glu Thr Thr Ser His Arg Pro Thr Thr Ser Glu Glu Ser Thr Ser
405 410 415

Glu Glu Pro Thr Thr Glu Ala Pro Thr Ser Ser Arg Thr Val Pro Gln
420 425 430

Ile Pro Thr Ser Thr Pro Arg Thr Ser Ala Ser Val Pro Val Glu Thr
435 440 445

Asn Ala Pro Ala Asp Asp Leu Ile Asp Ala Val Asn Gly Leu Leu Asp
450 455 460

Val Gly Gly Ala Gln
465

<210> 61

<211> 1254

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> RXA00813

<400> 61

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taagctcagc atgcgacgcg gtcctcgagg aggtggcggc atg act gac att gat 115
Met Thr Asp Ile Asp
1 5

ctg gtg gtg gaa aac gtc caa agg att atc gcc acc aaa gag aca ccg 163

Gly Arg Arg Leu Asp Asp Ala Gln Pro Phe Ala Asp Gly Arg Ile Thr
 115 120
 Arg Asp Asp Gly Ser Val Leu Arg Ile His Ala Val Leu Ala Pro Leu
 130 135 140
 Ala Glu Ser Gly Thr Cys Ile Ser Val Arg Val Leu Arg Gln Ala Arg
 145 150 155 160
 Leu Ser Leu Asp Asp Leu Ile Gln Ser Gly Thr Val Pro Glu Asp Ile
 165 170 175
 Ala Pro Ala Leu Arg Asn Ile Ile Asn Gln Arg Arg Ser Phe Leu Val
 180 185 190
 Val Gly Gly Thr Gly Thr Gly Lys Thr Thr Leu Leu Ser Ala Met Leu
 195 200 205
 Thr Glu Val Pro Ala Asp Gln Arg Ile Ile Cys Ile Glu Asp Thr Ala
 210 215 220
 Glu Leu His Pro Gly His Pro Ser Thr Ile Asn Leu Val Ser Arg Gln
 225 230 235 240
 Ala Asn Val Glu Gly Ala Gly Ala Val Ser Met Ala Asp Leu Leu Lys
 245 250 255
 Gln Ser Leu Arg Met Arg Pro Asp Arg Ile Val Val Gly Glu Ile Arg
 260 265 270
 Gly Ala Glu Val Val Asp Leu Leu Ala Ala Met Asn Thr Gly His Asp
 275 280 285
 Gly Gly Ala Gly Thr Ile His Ala Asn Ser Ile Ser Glu Val Pro Ala
 290 295 300
 Arg Met Glu Ala Leu Ala Ala Thr Gly Gly Leu Asp Arg Met Ala Leu
 305 310 315 320
 His Ser Gln Leu Ala Ala Ala Val Asp Ile Val Leu Val Met Lys His
 325 330 335
 Thr Pro Phe Gly Arg Arg Leu Ala Gln Leu Gly Val Leu Arg Gly Asn
 340 345 350
 Pro Val Thr Thr Gln Val Val Trp Asp Leu Asp His Gly Met His Glu
 355 360 365
 Gly Ser Glu Glu Ala Trp Phe Met Pro
 370 375

<210> 63

<211> 2061

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2038)

<223> RXA01826

<400> 63

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tcgacgcctg aaatggccta ttgtagttag gaggagcgca gtg acc ttc gtg atc 115
 Val Thr Phe Val Ile
 1 5

gct gat cgc tat gaa ctg gat gcc gtc atc ggc tcc ggt gcc atg agc 163
 Ala Asp Arg Tyr 10 Glu Leu Asp Ala Val Ile Gly Ser Gly Gly Met Ser 20

gag gtg ttc gcg gcc acc gac acg ctg att ggt cgg gag gtc gcg gta 211
 Glu Val Phe 25 Ala Thr Asp Thr 30 Leu Ile Gly Arg Glu Val Ala Val 35

aag atg ctg cgc atc gac ctt gcg aaa gat ccc aat ttc cga gaa cgc 259
 Lys Met Leu Arg Ile Asp Leu Ala Lys Asp Pro Asn Phe Arg Glu Arg 40 45 50

ttc cgc agg gaa gcc caa aac tcc gga agg ttg agc cac tct tcg atc 307
 Phe Arg Arg Glu Ala Gln Asn Ser Gly Arg Leu Ser His Ser Ser Ile 55 60 65

gtc gct gtt ttt gac acc gcc gaa gta gac aaa gac gcc acc tct gtt 355
 Val Ala Val Phe Asp Thr Gly Glu Val Asp Lys Asp Gly Thr Ser Val 70 75 80 85

ccc tac att gtg atg gaa cgc gtg cag ggt cga aac ctg cgc gaa gtt 403
 Pro Tyr Ile Val Met Glu Arg Val Gln Gly Arg Asn Leu Arg Glu Val 90 95 100

gtc acc gaa gac gcc gta ttc acc cca gtt gag gca gcc aac atc ctg 451
 Val Thr Glu Asp Gly Val Phe Thr Pro Val Glu Ala Ala Asn Ile Leu 105 110 115

atc cct gtg tgt gaa gcg ctg cag gca tcc cat gac gcc gcc att att 499
 Ile Pro Val Cys Glu Ala Leu Gln Ala Ser His Asp Ala Gly Ile Ile 120 125 130

cac cgc gat gtg aaa ccc gcc aac atc atg atc acc aac acc ggt gcc 547
 His Arg Asp Val Lys Pro Ala Asn Ile Met Ile Thr Asn Thr Gly Gly 135 140 145

gtg aaa gtc atg gac ttc gcc atc gcc cgc gcg gtc aac gat tcc acc 595
 Val Lys Val Met Asp Phe Gly Ile Ala Arg Ala Val Asn Asp Ser Thr 150 155 160 165

tcc gcc atg act caa acc tcc gca gtc atc gcc acc gcc cag tac ctg 643
 Ser Ala Met Thr Gln Thr Ser Ala Val Ile Gly Thr Ala Gln Tyr Leu 170 175 180

tcc cct gag cag gcc cgc gcc aaa ccc gcc gat gcg cgt tcc gat att 691
 Ser Pro Glu Gln Ala Arg Gly Lys Pro Ala Asp Ala Arg Ser Asp Ile 185 190 195

tac gcc acc gcc tgc gtc atg tac gaa tta gtc acc ggt aag cca cct 739
 Tyr Ala Thr Gly Cys Val Met Tyr Glu Leu Val Thr Gly Lys Pro Pro 200 205 210

ttt gaa ggc gag tcc cct ttc gcc gtg gcc tac caa cac gtc cag gaa Phe Glu Gly Glu Ser Pro Phe Ala Val Ala Tyr Gln His Val Gln Glu 215 220 225	787
gac ccc acc cct cct tcg gat ttc atc gcg gac ctc acc ccg acc tct Asp Pro Thr Pro Pro Ser Asp Phe Ile Ala Asp Leu Thr Pro Thr Ser 230 235 240 245	835
gct gtc aac gtg gat gcc gtg gta ctc acc gcc atg gca aaa cac ccc Ala Val Asn Val Asp Ala Val Val Leu Thr Ala Met Ala Lys His Pro 250 255 260	883
gcc gac cgc tac caa aca gcc tcc gaa atg gcc gct gac ctg ggc cgg Ala Asp Arg Tyr Gln Thr Ala Ser Glu Met Ala Ala Asp Leu Gly Arg 265 270 275	931
cta tcc cgc aat gca gtc tcc cat gcc gca cgc gcg cat gta gaa aca Leu Ser Arg Asn Ala Val Ser His Ala Ala Arg Ala His Val Glu Thr 280 285 290	979
gaa gaa acc cca gaa gag ccc gaa act cgc ttc tcg acg cgc acc tcc Glu Glu Thr Pro Glu Glu Pro Glu Thr Arg Phe Ser Thr Arg Thr Ser 295 300 305	1027
acc caa gtg gcc ccc gcc gca gcc gtg gct gcg gcc agt acg ggg tca Thr Gln Val Ala Pro Ala Ala Gly Val Ala Ala Ser Thr Gly Ser 310 315 320 325	1075
ggg tct tct tcg cgt aaa cgt gga tcc aga ggc ctc acc gcc ctg gcc Gly Ser Ser Ser Arg Lys Arg Gly Ser Arg Gly Leu Thr Ala Leu Ala 330 335 340	1123
atc gtg tta tcc cta ggt gtc gtc ggc gtt gcc ggt gcc ttc acc tac Ile Val Leu Ser Leu Gly Val Val Gly Val Ala Gly Ala Phe Thr Tyr 345 350 355	1171
gac tac ttt gcc aac agc tcc tcc act gca acc agc gcg atc ccc aat Asp Tyr Phe Ala Asn Ser Ser Thr Ala Thr Ser Ala Ile Pro Asn 360 365 370	1219
gtg gaa ggc ctc ccg cag caa gaa gct ctc aca gaa ctt caa gca gca Val Glu Gly Leu Pro Gln Gln Glu Ala Leu Thr Glu Leu Gln Ala Ala 375 380 385	1267
gga ttt gtt gtc aac atc gtc gaa gaa gcc agc gcc gac gtc gcc gaa Gly Phe Val Val Asn Ile Val Glu Glu Ala Ser Ala Asp Val Ala Glu 390 395 400 405	1315
ggc ctc gtc atc cga gca aac cca agc gtt gga tcc gaa atc cgc caa Gly Leu Val Ile Arg Ala Asn Pro Ser Val Gly Ser Glu Ile Arg Gln 410 415 420	1363
ggg gcc acc gtc acc atc acc gtg tcc acc gcc cga gaa atg atc aac Gly Ala Thr Val Thr Ile Thr Val Ser Thr Gly Arg Glu Met Ile Asn 425 430 435	1411
atc cca gac gtc tcc gcc atg aca ctt gag gac gcc gcc cgc gcc ctc Ile Pro Asp Val Ser Gly Met Thr Leu Glu Asp Ala Ala Arg Ala Leu 440 445 450	1459
gaa gac gtt ggt ctc ata ctc aac caa aac gtt cgg gaa gaa acc tcc	1507

Glu Asp Val Gly Leu Ile Leu Asn Gln Asn Val Arg Glu Glu Thr Ser
 455 460 465

gac gac gtc gaa tct ggc ctc gtc atc gac caa aac ccc gaa gcc ggc 1555
 Asp Asp Val Glu Ser Gly Leu Val Ile Asp Gln Asn Pro Glu Ala Gly
 470 475 480 485

caa gaa gta gtc gtg ggt tcc tct gta tct cta acc atg tct tca ggc 1603
 Gln Glu Val Val Val Gly Ser Ser Val Ser Leu Thr Met Ser Ser Gly
 490 495 500

acc gag agc atc cga gtg ccc aac ctc acc ggc atg aac tgg tca caa 1651
 Thr Glu Ser Ile Arg Val Pro Asn Leu Thr Gly Met Asn Trp Ser Gln
 505 510 515

gca gaa caa aac ctc atc tcc atg ggc ttt aac ccc aca gct tcc tac 1699
 Ala Glu Gln Asn Leu Ile Ser Met Gly Phe Asn Pro Thr Ala Ser Tyr
 520 525 530

tta gac agc agc gaa cca gaa ggc gaa gtc ctc tca gtt tcc agc caa 1747
 Leu Asp Ser Ser Glu Pro Glu Gly Glu Val Leu Ser Val Ser Ser Gln
 535 540 545

gga act gaa cta ccc aag ggt tca tcc atc aca gtg gaa gtc tcc aac 1795
 Gly Thr Glu Leu Pro Lys Gly Ser Ser Ile Thr Val Glu Val Ser Asn
 550 555 560 565

ggc atg ctc atc caa gcc ccc gat ctc gcc cgc atg tcc acc gaa cag 1843
 Gly Met Leu Ile Gln Ala Pro Asp Leu Ala Arg Met Ser Thr Glu Gln
 570 575 580

gcc atc agt gcc ctc cgc gct gct ggc tgg acc gcc cca gat caa tcc 1891
 Ala Ile Ser Ala Leu Arg Ala Ala Gly Trp Thr Ala Pro Asp Gln Ser
 585 590 595

ctg atc gtc ggc gac ccc atc cac acc gca gcc ctc gtg gat caa aac 1939
 Leu Ile Val Gly Asp Pro Ile His Thr Ala Ala Leu Val Asp Gln Asn
 600 605 610

aaa atc gga ttc caa tcc cca acc cct gca acc ctc ttc cgc aaa gac 1987
 Lys Ile Gly Phe Gln Ser Pro Thr Pro Ala Thr Leu Phe Arg Lys Asp
 615 620 625

gcc caa gtg caa gtg cga ctc ttc gaa ttc gat ctc gct gca ctc gtg 2035
 Ala Gln Val Gln Val Arg Leu Phe Glu Phe Asp Leu Ala Ala Leu Val
 630 635 640 645

caa tagccaacaa ggaaccgctc aag 2061
 Gln

<210> 64

<211> 646

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

Val Thr Phe Val Ile Ala Asp Arg Tyr Glu Leu Asp Ala Val Ile Gly
 1 5 10 15

Ser Gly Gly Met Ser Glu Val Phe Ala Ala Thr Asp Thr Leu Ile Gly
 20 25 30
 Arg Glu Val Ala Val Lys Met Leu Arg Ile Asp Leu Ala Lys Asp Pro
 35 40 45
 Asn Phe Arg Glu Arg Phe Arg Arg Glu Ala Gln Asn Ser Gly Arg Leu
 50 55 60
 Ser His Ser Ser Ile Val Ala Val Phe Asp Thr Gly Glu Val Asp Lys
 65 70 75 80
 Asp Gly Thr Ser Val Pro Tyr Ile Val Met Glu Arg Val Gln Gly Arg
 85 90 95
 Asn Leu Arg Glu Val Val Thr Glu Asp Gly Val Phe Thr Pro Val Glu
 100 105 110
 Ala Ala Asn Ile Leu Ile Pro Val Cys Glu Ala Leu Gln Ala Ser His
 115 120 125
 Asp Ala Gly Ile Ile His Arg Asp Val Lys Pro Ala Asn Ile Met Ile
 130 135 140
 Thr Asn Thr Gly Gly Val Lys Val Met Asp Phe Gly Ile Ala Arg Ala
 145 150 155 160
 Val Asn Asp Ser Thr Ser Ala Met Thr Gln Thr Ser Ala Val Ile Gly
 165 170 175
 Thr Ala Gln Tyr Leu Ser Pro Glu Gln Ala Arg Gly Lys Pro Ala Asp
 180 185 190
 Ala Arg Ser Asp Ile Tyr Ala Thr Gly Cys Val Met Tyr Glu Leu Val
 195 200 205
 Thr Gly Lys Pro Pro Phe Glu Gly Glu Ser Pro Phe Ala Val Ala Tyr
 210 215 220
 Gln His Val Gln Glu Asp Pro Thr Pro Pro Ser Asp Phe Ile Ala Asp
 225 230 235 240
 Leu Thr Pro Thr Ser Ala Val Asn Val Asp Ala Val Val Leu Thr Ala
 245 250 255
 Met Ala Lys His Pro Ala Asp Arg Tyr Gln Thr Ala Ser Glu Met Ala
 260 265 270
 Ala Asp Leu Gly Arg Leu Ser Arg Asn Ala Val Ser His Ala Ala Arg
 275 280 285
 Ala His Val Glu Thr Glu Glu Thr Pro Glu Glu Pro Glu Thr Arg Phe
 290 295 300
 Ser Thr Arg Thr Ser Thr Gln Val Ala Pro Ala Ala Gly Val Ala Ala
 305 310 315 320
 Ala Ser Thr Gly Ser Gly Ser Ser Ser Arg Lys Arg Gly Ser Arg Gly
 325 330 335
 Leu Thr Ala Leu Ala Ile Val Leu Ser Leu Gly Val Val Gly Val Ala

340	345	350
Gly Ala Phe Thr Tyr Asp Tyr Phe Ala Asn Ser Ser Ser Thr Ala Thr 355 360 365		
Ser Ala Ile Pro Asn Val Glu Gly Leu Pro Gln Gln Glu Ala Leu Thr 370 375 380		
Glu Leu Gln Ala Ala Gly Phe Val Val Asn Ile Val Glu Glu Ala Ser 385 390 395 400		
Ala Asp Val Ala Glu Gly Leu Val Ile Arg Ala Asn Pro Ser Val Gly 405 410 415		
Ser Glu Ile Arg Gln Gly Ala Thr Val Thr Ile Thr Val Ser Thr Gly 420 425 430		
Arg Glu Met Ile Asn Ile Pro Asp Val Ser Gly Met Thr Leu Glu Asp 435 440 445		
Ala Ala Arg Ala Leu Glu Asp Val Gly Leu Ile Leu Asn Gln Asn Val 450 455 460		
Arg Glu Glu Thr Ser Asp Asp Val Glu Ser Gly Leu Val Ile Asp Gln 465 470 475 480		
Asn Pro Glu Ala Gly Gln Glu Val Val Val Gly Ser Ser Val Ser Leu 485 490 495		
Thr Met Ser Ser Gly Thr Glu Ser Ile Arg Val Pro Asn Leu Thr Gly 500 505 510		
Met Asn Trp Ser Gln Ala Glu Gln Asn Leu Ile Ser Met Gly Phe Asn 515 520 525		
Pro Thr Ala Ser Tyr Leu Asp Ser Ser Glu Pro Glu Gly Glu Val Leu 530 535 540		
Ser Val Ser Ser Gln Gly Thr Glu Leu Pro Lys Gly Ser Ser Ile Thr 545 550 555 560		
Val Glu Val Ser Asn Gly Met Leu Ile Gln Ala Pro Asp Leu Ala Arg 565 570 575		
Met Ser Thr Glu Gln Ala Ile Ser Ala Leu Arg Ala Ala Gly Trp Thr 580 585 590		
Ala Pro Asp Gln Ser Leu Ile Val Gly Asp Pro Ile His Thr Ala Ala 595 600 605		
Leu Val Asp Gln Asn Lys Ile Gly Phe Gln Ser Pro Thr Pro Ala Thr 610 615 620		
Leu Phe Arg Lys Asp Ala Gln Val Gln Val Arg Leu Phe Glu Phe Asp 625 630 635 640		
Leu Ala Ala Leu Val Gln 645		

<211> 2271

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (2248)

<223> RXA02699

<400> 65

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ggacaggtat cggattgaaa ctccgattgc cgggggtggt atg tct acc gtg tac 115
Met Ser Thr Val Tyr
1 5

agg tgc ctt gat ctt cgt tta gga cgt tcc atg gcg ctt aaa gtc atg 163
Arg Cys Leu Asp Leu Arg Leu Gly Arg Ser Met Ala Leu Lys Val Met
10 15 20

gaa gaa gat ttc gtt gat gat ccc att ttc cgg cag cgt tcc cgt agg 211
Glu Glu Asp Phe Val Asp Asp Pro Ile Phe Arg Gln Arg Ser Arg Arg
25 30 35

gaa gct cgg tca atg gcg cag cta aat cat cca aat ttg gtc aat gtg 259
Glu Ala Arg Ser Met Ala Gln Leu Asn His Pro Asn Leu Val Asn Val
40 45 50

tat gat ttt tcc gct act gac ggt ttg gtg tat ctg gtg atg gag tta 307
Tyr Asp Phe Ser Ala Thr Asp Gly Leu Val Tyr Leu Val Met Glu Leu
55 60 65

atc act ggt ggc acc ttg cgt gag ttg ctg gct gag cgg gga cct atg 355
Ile Thr Gly Gly Thr Leu Arg Glu Leu Leu Ala Glu Arg Gly Pro Met
70 75 80 85

ccc ccg cat gct gct gtg ggc gtt atg cgt ggg gtg ctc acg ggt ctc 403
Pro Pro His Ala Ala Val Gly Val Met Arg Gly Val Leu Thr Gly Leu
90 95 100

gcg gct gcc cac cgg gcg ggc atg gtg cac cgg gat atc aag cct gac 451
Ala Ala Ala His Arg Ala Gly Met Val His Arg Asp Ile Lys Pro Asp
105 110 115

aac gtg ttg atc aat agt gat cac cag gtg aaa ctg tct gat ttc ggc 499
Asn Val Leu Ile Asn Ser Asp His Gln Val Lys Leu Ser Asp Phe Gly
120 125 130

ttg gtt cga gcg gct cac gcc ggc cag tct cag gac aat cag att gtg 547
Leu Val Arg Ala Ala His Ala Gly Gln Ser Gln Asp Asn Gln Ile Val
135 140 145

ggc acg gtg gct tat ctt tcc cct gag cag gtt gag ggc ggt gag atc 595
Gly Thr Val Ala Tyr Leu Ser Pro Glu Gln Val Glu Gly Gly Glu Ile
150 155 160 165

ggg ccg gcc agc gac gtg tat tcg gca ggc att gtg ctc ttt gag ctg 643
 Gly Pro Ala Ser Asp Val Tyr Ser Ala Gly Ile Val Leu Phe Glu Leu
 170 175 180

ctc aca ggc acc acg cct ttt tgg ggc gag gat gat ctc gac cat gca 691

Leu Thr Gly Thr Thr Pro Phe Ser Gly Glu Asp Asp Leu Asp His Ala
 185 190 195
 tac gcc cgc ctt acg gaa gtc gtg ccg gca ccg agt tcg ctt atc gac 739
 Tyr Ala Arg Leu Thr Glu Val Val Pro Ala Pro Ser Ser Leu Ile Asp
 200 205 210
 ggc gtc ccc tcc ctc atc gat gag ctt gtc gcg aca gct acc tcc att 787
 Gly Val Pro Ser Leu Ile Asp Glu Leu Val Ala Thr Ala Thr Ser Ile
 215 220 225
 aat cct gag gat cgt ttc gat gat tct gga gag ttt ttg tcc gca ctg 835
 Asn Pro Glu Asp Arg Phe Asp Asp Ser Gly Glu Phe Leu Ser Ala Leu
 230 235 240 245
 gaa gat gtc gca aca gag ttg agc ttg ccg gct ttc ccg gtc cct gtg 883
 Glu Asp Val Ala Thr Glu Leu Ser Leu Pro Ala Phe Arg Val Pro Val
 250 255 260
 ccg gtt aat tcc gca gcc aat agg gct aat gcc cag gtc ccg gat gct 931
 Pro Val Asn Ser Ala Ala Asn Arg Ala Asn Ala Gln Val Pro Asp Ala
 265 270 275
 cag cca act gat atg ttt acc acc cat atc ccc aag act cct gag cct 979
 Gln Pro Thr Asp Met Phe Thr Thr His Ile Pro Lys Thr Pro Glu Pro
 280 285 290
 gat cac act gcg atc att ccg gtg gcc tca gca aat gag acg tcg att 1027
 Asp His Thr Ala Ile Ile Pro Val Ala Ser Ala Asn Glu Thr Ser Ile
 295 300 305
 ctg cct gcg caa aac atg gca caa aat atg gcg cag aat ccg ctg caa 1075
 Leu Pro Ala Gln Asn Met Ala Gln Asn Met Ala Gln Asn Pro Leu Gln
 310 315 320 325
 cct ccg gaa cct gat ttc gcc ccg gag cca cct ccg gac aca gcg ctg 1123
 Pro Pro Glu Pro Asp Phe Ala Pro Glu Pro Pro Pro Asp Thr Ala Leu
 330 335 340
 aat att caa gat caa gag ctt gcg cgc gcc gat gag cca gaa att aat 1171
 Asn Ile Gln Asp Gln Glu Leu Ala Arg Ala Asp Glu Pro Glu Ile Asn
 345 350 355
 acc gtc agc aat cgt tcc aaa ttg aag ctg acg ttg tgg tca att ttc 1219
 Thr Val Ser Asn Arg Ser Lys Leu Lys Leu Thr Leu Trp Ser Ile Phe
 360 365 370
 gtg gtc gca gtg atc gct gct gtt gct gtt gcc ggt tgg tgg ttc ggt 1267
 Val Val Ala Val Ile Ala Ala Val Ala Val Gly Gly Trp Trp Phe Gly
 375 380 385
 tca gcc cgt tac ggt gag att ccg cag gtg ttg gcc atg gat gag gtc 1315
 Ser Gly Arg Tyr Gly Glu Ile Pro Gln Val Leu Gly Met Asp Glu Val
 390 395 400 405
 cag gca gta gct gtt gta gag gaa gct ggt ttc gtg gca gtg gct gaa 1363
 Gln Ala Val Ala Val Val Glu Glu Ala Gly Phe Val Ala Val Ala Glu
 410 415 420
 cct cag tat gac aat gag gtt ccc act ggt tcg att att ggg act gaa 1411
 Pro Gln Tyr Asp Asn Glu Val Pro Thr Gly Ser Ile Ile Gly Thr Glu

425										430					435					
cct	tct	ttt	ggt	gag	cgc	ctt	cct	cgc	ggc	gag	gat	gtt	tct	gtc	ctc	1459				
Pro	Ser	Phe	Gly	Glu	Arg	Leu	Pro	Arg	Gly	Glu	Asp	Val	Ser	Val	Leu					
440										445	450									
gtc	tct	caa	ggg	cgt	ccc	gtg	gtg	ccg	gat	ctt	agc	gag	gat	cga	tcc	1507				
Val	Ser	Gln	Gly	Arg	Pro	Val	Val	Pro	Asp	Leu	Ser	Glu	Asp	Arg	Ser					
455										460	465									
tta	agc	acc	gtt	cgt	gaa	gag	ttg	gaa	cag	arg	acg	ttc	gtc	tggt	gtt	1555				
Leu	Ser	Thr	Val	Arg	Glu	Glu	Leu	Glu	Gln	Arg	Thr	Phe	Val	Trp	Val					
470										475	480					485				
gat	ggc	cca	ggt	gaa	tat	tct	gac	gat	gtt	cca	gaa	gga	caa	gta	gtt	1603				
Asp	Gly	Pro	Gly	Glu	Tyr	Ser	Asp	Asp	Val	Pro	Glu	Gly	Gln	Val	Val					
490										495	500									
tct	ttt	aca	ccg	tcg	tca	ggc	acg	cag	ctt	gat	gtt	ggg	gaa	acc	gtg	1651				
Ser	Phe	Thr	Ser	Ser	Ser	Gly	Thr	Gln	Leu	Asp	Val	Gly	Glu	Thr	Val					
505										510	515									
cag	atc	cat	ttg	agc	cga	ggc	ccc	gcc	ccg	gtt	gag	att	cct	gat	gtc	1699				
Gln	Ile	His	Leu	Ser	Arg	Gly	Pro	Ala	Pro	Val	Glu	Ile	Pro	Asp	Val					
520										525	530									
tct	ggc	atg	gga	gtg	gat	cag	gca	aca	cgt	gtg	ttg	gag	cgc	gca	ggt	1747				
Ser	Gly	Met	Gly	Val	Asp	Gln	Ala	Thr	Arg	Val	Leu	Glu	Arg	Ala	Gly					
535										540	545									
ttg	agc	gtc	gag	cgt	act	gaa	gaa	ggc	ttt	gat	gct	gag	aca	cca	aat	1795				
Leu	Ser	Val	Glu	Arg	Thr	Glu	Glu	Gly	Phe	Asp	Ala	Glu	Thr	Pro	Asn					
550										555	560					565				
ggt	gat	gtc	tac	ggg	act	tcg	ccc	aag	gta	tct	act	gag	gtc	aag	cgc	1843				
Gly	Asp	Val	Tyr	Gly	Thr	Ser	Pro	Lys	Val	Ser	Thr	Glu	Val	Lys	Arg					
570										575	580									
gga	acc	tct	gtt	gtg	ctg	cag	gtg	tcc	aat	gct	att	tcg	gta	ccg	gat	1891				
Gly	Thr	Ser	Val	Val	Leu	Gln	Val	Ser	Asn	Ala	Ile	Ser	Val	Pro	Asp					
585										590	595									
gtg	gtg	ggt	atg	acc	aag	gac	gaa	gcc	acc	gcg	gcg	ctt	gcg	gaa	gaa	1939				
Val	Val	Gly	Met	Thr	Lys	Asp	Glu	Ala	Thr	Ala	Ala	Leu	Ala	Glu	Glu					
600										605	610									
gga	ttg	gtc	gtg	gcg	tcg	aca	agc	att	att	cct	ggt	gag	gcg	gcg	agc	1987				
Gly	Leu	Val	Val	Ala	Ser	Thr	Ser	Ile	Ile	Pro	Gly	Glu	Ala	Ala	Ser					
615										620	625									
tcc	gct	gac	gcc	gtc	gtg	acc	gtc	gag	cct	gaa	tcc	ggc	agc	cgc	gtt	2035				
Ser	Ala	Asp	Ala	Val	Val	Thr	Val	Glu	Pro	Glu	Ser	Gly	Ser	Arg	Val					
630										635	640					645				
gat	cca	gcg	cat	ccg	cag	gtc	agc	ctc	ggg	tta	gct	ggg	gag	att	caa	2083				
Asp	Pro	Ala	His	Pro	Gln	Val	Ser	Leu	Gly	Leu	Ala	Gly	Glu	Ile	Gln					
650										655	660									
gtt	cca	agc	gtg	gtt	gga	cgt	aag	gtt	agc	gat	gct	cga	agc	att	ctg	2131				
Val	Pro	Ser	Val	Val	Gly	Arg	Lys	Val	Ser	Asp	Ala	Arg	Ser	Ile	Leu					
665										670	675									

gaa gaa gcc ggt tta acg ctg aca act gat gcg gac gac aac gat cga 2179
 Glu Glu Ala Gly Leu Thr Leu Thr Asp Ala Asp Asp Asn Asp Arg
 680 685 690

att tat agt caa acc cct cgt gca cgc agc gaa gtc tcg gta ggg gga 2227
 Ile Tyr Ser Gln Thr Pro Arg Ala Arg Ser Glu Val Ser Val Gly Gly
 695 700 705

gaa gtt aca gta agg gcg ttt tagtggttcc ctogttgcag caa 2271
 Glu Val Thr Val Arg Ala Phe
 710 715

<210> 66

<211> 716

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Met Ser Thr Val Tyr Arg Cys Leu Asp Leu Arg Leu Gly Arg Ser Met
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Ala Leu Lys Val Met Glu Glu Asp Phe Val Asp Asp Pro Ile Phe Arg
 20 25 30

Gln Arg Ser Arg Arg Glu Ala Arg Ser Met Ala Gln Leu Asn His Pro
 35 40 45

Asn Leu Val Asn Val Tyr Asp Phe Ser Ala Thr Asp Gly Leu Val Tyr
 50 55 60

Leu Val Met Glu Leu Ile Thr Gly Gly Thr Leu Arg Glu Leu Leu Ala
 65 70 75 80

Glu Arg Gly Pro Met Pro Pro His Ala Ala Val Gly Val Met Arg Gly
 85 90 95

Val Leu Thr Gly Leu Ala Ala Ala His Arg Ala Gly Met Val His Arg
 100 105 110

Asp Ile Lys Pro Asp Asn Val Leu Ile Asn Ser Asp His Gln Val Lys
 115 120 125

Leu Ser Asp Phe Gly Leu Val Arg Ala Ala His Ala Gly Gln Ser Gln
 130 135 140

Asp Asn Gln Ile Val Gly Thr Val Ala Tyr Leu Ser Pro Glu Gln Val
 145 150 155 160

Glu Gly Gly Glu Ile Gly Pro Ala Ser Asp Val Tyr Ser Ala Gly Ile
 165 170 175

Val Leu Phe Glu Leu Leu Thr Gly Thr Thr Pro Phe Ser Gly Glu Asp
 180 185 190

Asp Leu Asp His Ala Tyr Ala Arg Leu Thr Glu Val Val Pro Ala Pro
 195 200 205

Ser Ser Leu Ile Asp Gly Val Pro Ser Leu Ile Asp Glu Leu Val Ala
 210 215 220

Thr Ala Thr Ser Ile Asn Pro Glu Asp Arg Phe Asp Asp Ser Gly Glu
 225 230 235 240
 Phe Leu Ser Ala Leu Glu Asp Val Ala Thr Glu Leu Ser Leu Pro Ala
 245 250 255
 Phe Arg Val Pro Val Pro Val Asn Ser Ala Ala Asn Arg Ala Asn Ala
 260 265 270
 Gln Val Pro Asp Ala Gln Pro Thr Asp Met Phe Thr Thr His Ile Pro
 275 280 285
 Lys Thr Pro Glu Pro Asp His Thr Ala Ile Ile Pro Val Ala Ser Ala
 290 295 300
 Asn Glu Thr Ser Ile Leu Pro Ala Gln Asn Met Ala Gln Asn Met Ala
 305 310 315 320
 Gln Asn Pro Leu Gln Pro Pro Glu Pro Asp Phe Ala Pro Glu Pro Pro
 325 330 335
 Pro Asp Thr Ala Leu Asn Ile Gln Asp Gln Glu Leu Ala Arg Ala Asp
 340 345 350
 Glu Pro Glu Ile Asn Thr Val Ser Asn Arg Ser Lys Leu Lys Leu Thr
 355 360 365
 Leu Trp Ser Ile Phe Val Val Ala Val Ile Ala Ala Val Ala Val Gly
 370 375 380
 Gly Trp Trp Phe Gly Ser Gly Arg Tyr Gly Glu Ile Pro Gln Val Leu
 385 390 395 400
 Gly Met Asp Glu Val Gln Ala Val Ala Val Val Glu Glu Ala Gly Phe
 405 410 415
 Val Ala Val Ala Glu Pro Gln Tyr Asp Asn Glu Val Pro Thr Gly Ser
 420 425 430
 Ile Ile Gly Thr Glu Pro Ser Phe Gly Glu Arg Leu Pro Arg Gly Glu
 435 440 445
 Asp Val Ser Val Leu Val Ser Gln Gly Arg Pro Val Val Pro Asp Leu
 450 455 460
 Ser Glu Asp Arg Ser Leu Ser Thr Val Arg Glu Glu Leu Glu Gln Arg
 465 470 475 480
 Thr Phe Val Trp Val Asp Gly Pro Gly Glu Tyr Ser Asp Asp Val Pro
 485 490 495
 Glu Gly Gln Val Val Ser Phe Thr Pro Ser Ser Gly Thr Gln Leu Asp
 500 505 510
 Val Gly Glu Thr Val Gln Ile His Leu Ser Arg Gly Pro Ala Pro Val
 515 520 525
 Glu Ile Pro Asp Val Ser Gly Met Gly Val Asp Gln Ala Thr Arg Val
 530 535 540

Leu Glu Arg Ala Gly Leu Ser Val Glu Arg Thr Glu Glu Gly Phe Asp
545 550 555 560

Ala Glu Thr Pro Asn Gly Asp Val Tyr Gly Thr Ser Pro Lys Val Ser
565 570 575

Thr Glu Val Lys Arg Gly Thr Ser Val Val Leu Gln Val Ser Asn Ala
580 585 590

Ile Ser Val Pro Asp Val Val Gly Met Thr Lys Asp Glu Ala Thr Ala
595 600 605

Ala Leu Ala Glu Glu Gly Leu Val Val Ala Ser Thr Ser Ile Ile Pro
610 615 620

Gly Glu Ala Ala Ser Ser Ala Asp Ala Val Val Thr Val Glu Pro Glu
625 630 635 640

Ser Gly Ser Arg Val Asp Pro Ala His Pro Gln Val Ser Leu Gly Leu
645 650 655

Ala Gly Glu Ile Gln Val Pro Ser Val Val Gly Arg Lys Val Ser Asp
660 665 670

Ala Arg Ser Ile Leu Glu Glu Ala Gly Leu Thr Leu Thr Thr Asp Ala
675 680 685

Asp Asp Asn Asp Arg Ile Tyr Ser Gln Thr Pro Arg Ala Arg Ser Glu
690 695 700

Val Ser Val Gly Gly Glu Val Thr Val Arg Ala Phe
705 710 715

<210> 67

<211> 549

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(526)

<223> RXA00319

<400> 67

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aattgttttc gtatgcaccg gaaacatttg ccgatccccc atg tcg gaa gtc atc 115
Met Ser Glu Val Ile
1 5

gcg aag gca aaa gcg gaa gaa gct ggc ttg gaa gac aac gtc att ttc 163
Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu Asp Asn Val Ile Phe
10 15 20

tcc tcc tgt ggc atg ggc aat tgg cac gtt ggc caa cct gct gac aag 211
Ser Ser Cys Gly Met Gly Asn Trp His Val Gly Gln Pro Ala Asp Lys
25 30 35

cga gct ctc gcg gaa ctg aaa tca gcc ggt tac aac ggc gac acc cac 259
Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr Asn Gly Asp Thr His

40	45	50	
cgc gca gca caa ctt ggt ccc gag cac atg cgc gca gat ctc ttc gtc			307
Arg Ala Ala Gln Leu Gly	Pro Glu His Met Arg	Ala Asp Leu Phe Val	
55	60	65	
gcg cta gat tcc ggc cac gcc ggt gag ctc gcc gca acg ggt gtt ccc			355
Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala Ala Thr Gly Val Pro			
70	75	80	85
aac gac aaa atc cgc ctc atg cgt tcc ttc gac cca gag tcc aac ccc			403
Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp Pro Glu Ser Asn Pro			
90	95	100	
acc gac gat gtc gca gac cct tac tac gcc aca tcc cag gat ttc gtg			451
Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr Ser Gln Asp Phe Val			
105	110	115	
ctc acc cgt gaa aac atc gaa gat gct atg ccg gcc ctt ttg gag tgg			499
Leu Thr Arg Glu Asn Ile Glu Asp Ala Met Pro Gly Leu Leu Glu Trp			
120	125	130	
gtc aga gat cac atc cgc act gat tct taggtctttg agctaaaaag			546
Val Arg Asp His Ile Arg Thr Asp Ser			
135	140		
tcc			549
 <210> 68			
<211> 142			
<212> PRT			
<213> Corynebacterium glutamicum			
 <400> 68			
Met Ser Glu Val Ile Ala Lys Ala Lys Ala Glu Glu Ala Gly Leu Glu			
1	5	10	15
Asp Asn Val Ile Phe Ser Ser Cys Gly Met Gly Asn Trp His Val Gly			
20	25	30	
Gln Pro Ala Asp Lys Arg Ala Leu Ala Glu Leu Lys Ser Ala Gly Tyr			
35	40	45	
Asn Gly Asp Thr His Arg Ala Ala Gln Leu Gly Pro Glu His Met Arg			
50	55	60	
Ala Asp Leu Phe Val Ala Leu Asp Ser Gly His Ala Gly Glu Leu Ala			
65	70	75	80
Ala Thr Gly Val Pro Asn Asp Lys Ile Arg Leu Met Arg Ser Phe Asp			
85	90	95	
Pro Glu Ser Asn Pro Thr Asp Asp Val Ala Asp Pro Tyr Tyr Gly Thr			
100	105	110	
Ser Gln Asp Phe Val Leu Thr Arg Glu Asn Ile Glu Asp Ala Met Pro			
115	120	125	
Gly Leu Leu Glu Trp Val Arg Asp His Ile Arg Thr Asp Ser			
130	135	140	

	170		175		180	
cag cta att cca gct att cgt ttg att gct tct tat ttg aac aaa gca						691
Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser Tyr Leu Asn Lys Ala						
	185		190		195	

ctg gag tct gcg taatggcgag gaagtatcgg gtg		726
Leu Glu Ser Ala		
	200	

<210> 70
 <211> 201
 <212> PRT
 <213> Corynebacterium glutamicum

Met Ser Asn Ser Phe Thr Ile Leu Thr Val Cys Thr Gly Asn Ile Cys			
1	5	10	15
Arg Ser Pro Leu Ala Lys Gln Leu Leu Glu Leu Glu Leu Pro Gly Ala			
	20	25	30
Asp Ile Ile Arg Val Asp Ser Ala Gly Val Gln Ala Met Val Asp Ser			
	35	40	45
Pro Met Pro Glu Gln Ser Leu Glu Ile Ala Arg Lys Gln Gly Ile Glu			
	50	55	60
Asn Pro Glu Glu His Arg Ala Lys Gln Ile Thr Glu Glu Leu Val Asn			
	65	70	75
Gln Ser Asp Leu Ile Leu Ala Met Asp Arg Gly His Arg Lys Ser Ile			
	85	90	95
Val Gln Leu Ser Pro Arg Ala Thr Arg Lys Val Phe Thr Val Val Asp			
	100	105	110
Leu Ala Arg Leu Ile Glu Ala Thr Thr Asp Ala Asp Leu Gln Glu Glu			
	115	120	125
Leu Asn Leu Ala Gly Asp Ser Val Ile Asp Arg Leu His Ala Thr Val			
	130	135	140
Glu Ala Ala Arg Leu Ser Arg Ser Glu Leu Asn Pro Leu Asp Asn Leu			
	145	150	155
Ala Asp Glu Asp Ile Val Asp Pro Tyr Gly Lys Ser Gln Ser Val Tyr			
	165	170	175
Glu Ala Ser Ala Ser Gln Leu Ile Pro Ala Ile Arg Leu Ile Ala Ser			
	180	185	190
Tyr Leu Asn Lys Ala Leu Glu Ser Ala			
	195	200	

<210> 71
 <211> 1476
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1453)

<223> RXA01830

<400> 71

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 Met Leu Lys Leu Lys
 1 5

tat gcg gtg gca tct gac cga ggg tta gtg cgc ggg aac aat gag gat 163
 Tyr Ala Val Ala Ser Asp Arg Gly Leu Val Arg Gly Asn Asn Glu Asp
 10 15 20

tcc gct tac get ggc cgc cat ttg ttg gcg ctg gct gat ggt atg ggc 211
 Ser Ala Tyr Ala Gly Pro His Leu Leu Ala Leu Ala Asp Gly Met Gly
 25 30 35

ggc cat gct gct ggt gag atc gct tcc caa acc atg atc aac cat ttg 259
 Gly His Ala Ala Gly Glu Ile Ala Ser Gln Thr Met Ile Asn His Leu
 40 45 50

cgt gcg ctt gat gtt gat cct ggt gat aac gat atg ttg gcg ctg gtg 307
 Arg Ala Leu Asp Val Asp Pro Gly Asp Asn Asp Met Leu Ala Leu Val
 55 60 65

ggc atg gtg gca ggc gaa gcc aac gcg gcg att gct gag ggc atc gcc 355
 Gly Met Val Ala Gly Glu Ala Asn Ala Ala Ile Ala Glu Gly Ile Ala
 70 75 80 85

gaa gac ccg gcg cgc gac ggc atg ggc act acg ttg acg gcg ttc atg 403
 Glu Asp Pro Ala Arg Asp Gly Met Gly Thr Thr Leu Thr Ala Phe Met
 90 95 100

ttt aac ggg cgt gac ctg gca atg tgc cac gtc ggc gat agt cgt ggt 451
 Phe Asn Gly Arg Asp Leu Ala Met Cys His Val Gly Asp Ser Arg Gly
 105 110 115

tat gtg ctt cgc gac gat aag ttg gta cag gtt aca gtc gac gat act 499
 Tyr Val Leu Arg Asp Asp Lys Leu Val Gln Val Thr Val Asp Asp Thr
 120 125 130

ttt gtg cag tcg ttg gtc gct gag ggc aag ctt gat cca gaa gat gtt 547
 Phe Val Gln Ser Leu Val Ala Glu Gly Lys Leu Asp Pro Glu Asp Val
 135 140 145

tca act cac cct cag cgt tct ttg att ctg aag gct tac acc ggc cat 595
 Ser Thr His Pro Gln Arg Ser Leu Ile Leu Lys Ala Tyr Thr Gly His
 150 155 160 165

cct gtg gag ccc act ctg gag caa ttc ccg gcc ttg cct ggg gat cgt 643
 Pro Val Glu Pro Thr Leu Glu Gln Phe Pro Ala Leu Pro Gly Asp Arg
 170 175 180

ttg ttg ttg tgc tct gat ggt cta tca gat ccg gtt aca cac tcc acg 691
 Leu Leu Leu Cys Ser Asp Gly Leu Ser Asp Pro Val Thr His Ser Thr
 185 190 195

att gaa gaa aca gtg cgt gta ggc acc cgg cag gat gcg tcc acc aag 739
 ile Glu Glu Thr Val Arg Val Gly Thr Pro Gln Asp Ala Ser Thr Lys
 200 205 210

ttg gtg gag ttg gcg ctg cgt tct ggc ggt cgg gac aat gtg acg gtc 787
 Leu Val Glu Leu Ala Leu Arg Ser Gly Gly Pro Asp Asn Val Thr Val
 215 220 225

att gtg gcc gat gtt gta gaa gtc acc gag gcg gaa gca gca gcg gaa 835
 ile Val Ala Asp Val Val Glu Val Thr Glu Ala Glu Ala Ala Glu
 230 235 240 245

gca tca gtg cct gtc acg gct ggt gcg ctc aat ggt gag cag cct gaa 883
 Ala Ser Val Pro Val Thr Ala Gly Ala Leu Asn Gly Glu Gln Pro Glu
 250 255 260

gat cgg cgg cct gat acc gct gcg gga cgc gct gcg gcg atc aca cgg 931
 Asp Pro Arg Pro Asp Thr Ala Ala Gly Arg Ala Ala Ala Ile Thr Arg
 265 270 275

cga gct caa gtg att gat cgg gca cca aag ata tct gat gct gga acg 979
 Arg Ala Gln Val Ile Asp Pro Ala Pro Lys Ile Ser Asp Ala Gly Thr
 280 285 290

gag gat att ccc aca att gag gag cca cca gag aaa agt tcc agc aaa 1027
 Glu Asp Ile Pro Thr Ile Glu Glu Pro Pro Glu Lys Ser Ser Ser Lys
 295 300 305

ctt gcg gta ttg atc gta gcc ctg gtc atc ctc atc ggt gta gtt gcc 1075
 Leu Ala Val Leu Ile Val Ala Leu Val Ile Leu Ile Gly Val Val Ala
 310 315 320 325

gca gga tgg tgg ggc tac tcc cgt att gac agc act ttt tac gtc gcg 1123
 Ala Gly Trp Trp Gly Tyr Ser Arg Ile Asp Ser Thr Phe Tyr Val Ala
 330 335 340

gtc aat gat gag gaa gcc atc acc gtg gaa cac ggt gtg gat tac cgc 1171
 Val Asn Asp Glu Glu Ala Ile Thr Val Glu His Gly Val Asp Tyr Arg
 345 350 355

atc ttt ggc aag gat tta cat tcg caa ttc cag gtg gcg tgc ctg aat 1219
 Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln Val Ala Cys Leu Asn
 360 365 370

gaa gct ggc acc ttg tca ctc aag gaa tcc tgt gaa aac ggt acg tct 1267
 Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys Glu Asn Gly Thr Ser
 375 380 385

ttc aaa ttg gat gat tta ccg gca tct gtt cgc ggt agt gtc gca gga 1315
 Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg Gly Ser Val Ala Gly
 390 395 400 405

tta ccg tct ggg tcg tat gac gag gtc cag gcg caa atg caa cgg ctg 1363
 Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala Gln Met Gln Arg Leu
 410 415 420

gct gct caa gct ttg cca gtg tgc gtg aac tta gaa gta aca acc ggt 1411
 Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu Glu Val Thr Thr Gly
 425 430 435

ggc gat aga aac gaa ccc gga gtc aat tgt agg gag gtc tca 1453

Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg Glu Val Ser
 440 445 450

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1476

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 <212> PRT
 <213> Corynebacterium glutamicum

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 Ala Asp Gly Met Gly Gly His Ala Ala Gly Glu Ile Ala Ser Gln Thr
 35 40 45
 Met Ile Asn His Leu Arg Ala Leu Asp Val Asp Pro Gly Asp Asn Asp
 50 55 60
 Met Leu Ala Leu Val Gly Met Val Ala Gly Glu Ala Asn Ala Ala Ile
 65 70 75 80
 Ala Glu Gly Ile Ala Glu Asp Pro Ala Arg Asp Gly Met Gly Thr Thr
 85 90 95
 Leu Thr Ala Phe Met Phe Asn Gly Arg Asp Leu Ala Met Cys His Val
 100 105 110
 Gly Asp Ser Arg Gly Tyr Val Leu Arg Asp Asp Lys Leu Val Gln Val
 115 120 125
 Thr Val Asp Asp Thr Phe Val Gln Ser Leu Val Ala Glu Gly Lys Leu
 130 135 140
 Asp Pro Glu Asp Val Ser Thr His Pro Gln Arg Ser Leu Ile Leu Lys
 145 150 155 160
 Ala Tyr Thr Gly His Pro Val Glu Pro Thr Leu Glu Gln Phe Pro Ala
 165 170 175
 Leu Pro Gly Asp Arg Leu Leu Leu Cys Ser Asp Gly Leu Ser Asp Pro
 180 185 190
 Val Thr His Ser Thr Ile Glu Glu Thr Val Arg Val Gly Thr Pro Gln
 195 200 205
 Asp Ala Ser Thr Lys Leu Val Glu Leu Ala Leu Arg Ser Gly Gly Pro
 210 215 220
 Asp Asn Val Thr Val Ile Val Ala Asp Val Val Glu Val Thr Glu Ala
 225 230 235 240
 Glu Ala Ala Ala Glu Ala Ser Val Pro Val Thr Ala Gly Ala Leu Asn
 245 250 255
 Gly Glu Gln Pro Glu Asp Pro Arg Pro Asp Thr Ala Ala Gly Arg Ala

260	265	270
Ala Ala Ile Thr Arg Arg Ala Gln Val Ile Asp Pro Ala Pro Lys Ile 275 280 285		
Ser Asp Ala Gly Thr Glu Asp Ile Pro Thr Ile Glu Glu Pro Pro Glu 290 295 300		
Lys Ser Ser Ser Lys Leu Ala Val Leu Ile Val Ala Leu Val Ile Leu 305 310 315 320		
Ile Gly Val Val Ala Ala Gly Trp Trp Gly Tyr Ser Arg Ile Asp Ser 325 330 335		
Thr Phe Tyr Val Ala Val Asn Asp Glu Glu Ala Ile Thr Val Glu His 340 345 350		
Gly Val Asp Tyr Arg Ile Phe Gly Lys Asp Leu His Ser Gln Phe Gln 355 360 365		
Val Ala Cys Leu Asn Glu Ala Gly Thr Leu Ser Leu Lys Glu Ser Cys 370 375 380		
Glu Asn Gly Thr Ser Phe Lys Leu Asp Asp Leu Pro Ala Ser Val Arg 385 390 395		
Gly Ser Val Ala Gly Leu Pro Ser Gly Ser Tyr Asp Glu Val Gln Ala 405 410 415		
Gln Met Gln Arg Leu Ala Ala Gln Ala Leu Pro Val Cys Val Asn Leu 420 425 430		
Glu Val Thr Thr Gly Gly Asp Arg Asn Glu Pro Gly Val Asn Cys Arg 435 440 445		
Glu Val Ser 450		
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tcgtaccggt gagcgcgcg g aagcagccct ttaaaaaactt atg aat aat cca gcc	115	
	Met Asn Asn Pro Ala	
	1 5	
cag ctg cgc caa gat act gaa aag gaa gtc ctg gcg ttg ctg ggc tct	163	
Gln Leu Arg Gln Asp Thr Glu Lys Glu Val Leu Ala Leu Leu Gly Ser		
	10 15 20	
ttg gtt tta ccc gcc ggc acc gcg ctt gcc gcc acc gga tct ttg gcc	211	

Leu	Val	Leu	Pro	Ala	Gly	Thr	Ala	Leu	Ala	Ala	Thr	Gly	Ser	Leu	Ala	
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agg	tcc	gaa	ctc	acg	ccg	tat	tcc	gat	tgg	gac	ctc	att	ttg	atc	cat	259
Arg	Ser	Glu	Leu	Thr	Pro	Tyr	Ser	Asp	Leu	Asp	Leu	Ile	Leu	Ile	His	
		40					45					50				
cca	cca	gga	gcc	acc	ccg	gat	ggc	gtg	gag	gat	ttg	tgg	tac	ccg	att	307
Pro	Pro	Gly	Ala	Thr	Pro	Asp	Gly	Val	Glu	Asp	Leu	Trp	Tyr	Pro	Ile	
		55				60					65					
tgg	gac	gca	aaa	aag	cgt	ctc	gac	tac	tcc	gtg	cgc	acc	cca	gat	gag	355
Trp	Asp	Ala	Lys	Lys	Arg	Leu	Asp	Tyr	Ser	Val	Arg	Thr	Pro	Asp	Glu	
		70			75					80					85	
tgt	gtg	gct	atg	att	tct	gcg	gat	tcc	act	gca	gcc	ctt	gcc	atg	ctt	403
Cys	Val	Ala	Met	Ile	Ser	Ala	Asp	Ser	Thr	Ala	Ala	Leu	Ala	Met	Leu	
				90					95					100		
gac	ctg	cgg	ttt	gtc	gct	ggc	gat	gag	gat	ctg	tgt	gcc	aaa	acg	cgc	451
Asp	Leu	Arg	Phe	Val	Ala	Gly	Asp	Glu	Asp	Leu	Cys	Ala	Lys	Thr	Arg	
			105					110					115			
cgg	cgc	atc	gtg	gag	aag	tgg	cgc	cag	gaa	ctc	aac	aaa	aac	ttc	gat	499
Arg	Arg	Ile	Val	Glu	Lys	Trp	Arg	Gln	Glu	Leu	Asn	Lys	Asn	Phe	Asp	
				120			125					130				
gcc	gtt	gtg	gac	acc	gcg	att	gcc	cgt	tgg	cgc	cgc	tcc	gga	ccc	gtc	547
Ala	Val	Val	Asp	Thr	Ala	Ile	Ala	Arg	Trp	Arg	Arg	Ser	Gly	Pro	Val	
				135			140					145				
gtg	gca	atg	acg	cgg	cca	gat	ctt	aaa	cac	ggc	agg	gga	ggg	ctg	cgc	595
Val	Ala	Met	Thr	Arg	Pro	Asp	Leu	Lys	His	Gly	Arg	Gly	Gly	Leu	Arg	
					155					160					165	
gat	ttc	gaa	ctg	atc	aag	gcc	ctc	gcg	ctc	ggc	cac	cta	tgc	aac	ctt	643
Asp	Phe	Glu	Leu	Ile	Lys	Ala	Leu	Ala	Leu	Gly	His	Leu	Cys	Asn	Leu	
				170					175					180		
cca	cag	ctt	gat	gcg	caa	cac	cag	ctg	ctt	ctc	gac	gcc	cgc	acc	ttg	691
Pro	Gln	Leu	Asp	Ala	Gln	His	Gln	Leu	Leu	Leu	Asp	Ala	Arg	Thr	Leu	
				185				190					195			
ctg	cac	gtc	cac	gcg	cga	cgc	tcc	cgc	gac	gtc	ctt	gac	ccc	gaa	ttt	739
Leu	His	Val	His	Ala	Arg	Arg	Ser	Arg	Asp	Val	Leu	Asp	Pro	Glu	Phe	
			200				205					210				
gcg	gtg	gat	gtg	gcc	atg	gat	ttg	ggc	ttt	gtt	gac	cgc	tat	cac	ctg	787
Ala	Val	Asp	Val	Ala	Met	Asp	Leu	Gly	Phe	Val	Asp	Arg	Tyr	His	Leu	
				215		220					225					
ggc	cgg	gag	atc	gcc	gat	gca	gcc	cgc	gcc	att	gat	gat	ggc	ctg	acc	835
Gly	Arg	Glu	Ile	Ala	Asp	Ala	Ala	Arg	Ala	Ile						

265	270	275	
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gca ctt cca ctt cga gtg Ala Leu Pro Leu Arg Val 295	gcc gca gcc gca gca Ala Ala Ala Ala 300	acc acc gga ctt ccg Thr Thr Gly Leu Pro 305	1027
gtg gca gaa tca acc tgg gtt Val Ala Glu Ser Thr Trp 310	cga ctt aat gaa tgc Val Arg Leu Asn Glu 315	ccg cca ctt cct Pro Pro Leu Pro 320	1075
gag cca tgg cct gcc aat gca Glu Pro Trp Pro Ala Asn 330	gca gca ggg gac ttc ttt Ala Ala Gly Asp Phe 335	gac ttc cgg att ctc tcc Arg Ile Leu Ser 340	1123
agt ccg aaa aac tca cgc cga Ser Pro Lys Asn Ser Arg 345	gtg gtg aaa aat atg gat Val Val Lys Asn Met 350	cgc cac gga Asp Arg His Gly 355	1171
ttg tgg tgc cgt ttt gtt cca Leu Trp Ser Arg Phe Val 360	gaa tgg gac cgc atc Glu Trp Asp Arg Ile 365	aaa ggg ctt atg Lys Gly Leu Met 370	1219
ccc cgt gaa ccc agc cat att Pro Arg Glu Pro Ser His 375	tcc acc atc gat gaa cat Ser Thr Ile Asp Glu 380	agg ctt aac His Ser Leu Asn 385	1267
act gtt gca gga tgt gcg cta Thr Val Ala Gly Cys Ala 390	gaa act gtg acc gtc cgc Leu Glu Thr Val Thr 395	cgc ccc gat Ala Arg Pro Asp 400	1315
ctt tta gtt ttg gga gcc ttg Leu Leu Val Leu Gly Ala 410	tac cac gac att ggc aag His Asp Ile Gly Lys 415	ggc ttc ccg Gly Phe Pro 420	1363
cgt cca cac gaa caa gta ggt Arg Pro His Glu Gln Val 425	gca gag atg gtg gcg agg Ala Glu Met Val Ala 430	gct gca agc Ala Ala Ser 435	1411
cgc atg gga ttg aac ctt cgc Arg Met Gly Leu Asn Leu 440	gat cgt gcc agc gtg caa Arg Asp Arg Ala Ser 445	acg ctg gtc Gln Thr Leu Val 450	1459
gcc gag cac acc gcg gtg gcc Ala Glu His Thr Ala Val 455	aaa atc gcc gcg cgc ctt Lys Ile Ala Ala Arg 460	gat ccc tcc Leu Asp Pro Ser 465	1507
tcg gag ggc gcc gtc gat aag Ser Glu Gly Ala Val Asp 470	ctg ctt gat gct gtt agg Lys Leu Leu Asp Ala 475	tat gac ctg Tyr Asp Leu 480	1555
gtg aca ttg aat ctg ctt gag Val Thr Leu Asn Leu Leu 490	gtg cta aca gaa gct gat Glu Val Leu Thr Glu 495	gcg aaa gcc Ala Lys Ala 500	1603
acg ggg cct ggc gtg tgg acg Thr Gly Pro Gly Val Trp 505	gcg cgt ttg gag cat gcg Ala Ala Leu Glu His 510	ctg cgg att Ala Arg Ile 515	1651

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gtg tgc aag cgt gcg cgt gat cgc ctc acc gat att cgc cgc gtt gcg 1699
Val Cys Lys Arg Ala Arg Asp Arg Leu Thr Asp Ile Arg Pro Val Ala
520 525 530

ccg atg att gcg cca cgt agt gaa att ggt ttg gtg gaa cgc gat ggc 1747
Pro Met Ile Ala Pro Arg Ser Glu Ile Gly Leu Val Glu Arg Asp Gly
535 540 545

gtg ttc aca gtg caa tgg cac ggc gaa gac tta cat cgg att ctt ggc 1795
Val Phe Thr Val Gln Trp His Gly Glu Asp Leu His Arg Ile Leu Gly
550 555 560

gta att tat gcc aaa gga tgg aca atc acc gcg cgc cgc atg ctg gcc 1843
Val Ile Tyr Ala Lys Gly Trp Thr Ile Thr Ala Ala Arg Met Leu Ala
570 575 580

aat ggt caa tgg agt gcg gaa ttt gat gtc cgc gca aac ggc ccc caa 1891
Asn Gly Gln Trp Ser Ala Glu Phe Asp Val Arg Ala Asn Gly Pro Gln
585 590 595

gat ttt gat cgc cag cat ttc ctg cag gca tat caa tcc ggt gtg ttt 1939
Asp Phe Asp Pro Gln His Phe Leu Gln Ala Tyr Gln Ser Gly Val Phe
600 605 610

tcc gag gtt ccc att cca gca ctt ggg ata aca gcc aca ttt tgg cac 1987
Ser Glu Val Pro Ile Pro Ala Leu Gly Ile Thr Ala Thr Phe Trp His
615 620 625

ggg aac act tta gaa gtg cgc act gag ctt cgc aca gga gct att ttt 2035
Gly Asn Thr Leu Glu Val Arg Thr Glu Leu Arg Thr Gly Ala Ile Phe
630 635 640 645

gcc ctg ctc aga aca ttg ccc gat gcc ctc tgg atc aac gct gtg acc 2083
Ala Leu Leu Arg Thr Leu Pro Asp Ala Leu Trp Ile Asn Ala Val Thr
650 655 660

cgc ggt gcg acc ctg att atc cag gca gca ctg aag ccc ggc ttc gat 2131
Arg Gly Ala Thr Leu Ile Ile Gln Ala Ala Leu Lys Pro Gly Phe Asp
665 670 675

cga gca acg gtg gaa cgc tcc gta gtc agg tgg ttg gca ggt agc 2176
Arg Ala Thr Val Glu Arg Ser Val Val Arg Ser Leu Ala Gly Ser
680 685 690

tgacgtgacc tgacggggg caa 2199

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20 25 30
Thr Gly Ser Leu Ala Arg Ser Glu Leu Thr Pro Tyr Ser Asp Leu Asp

35	40	45
Leu Ile Leu Ile His Pro Pro Gly Ala Thr Pro Asp Gly Val Glu Asp 50 55 60		
Leu Trp Tyr Pro Ile Trp Asp Ala Lys Lys Arg Leu Asp Tyr Ser Val 65 70 75 80		
Arg Thr Pro Asp Glu Cys Val Ala Met Ile Ser Ala Asp Ser Thr Ala 85 90 95		
Ala Leu Ala Met Leu Asp Leu Arg Phe Val Ala Gly Asp Glu Asp Leu 100 105 110		
Cys Ala Lys Thr Arg Arg Arg Ile Val Glu Lys Trp Arg Gln Glu Leu 115 120 125		
Asn Lys Asn Phe Asp Ala Val Val Asp Thr Ala Ile Ala Arg Trp Arg 130 135 140		
Arg Ser Gly Pro Val Val Ala Met Thr Arg Pro Asp Leu Lys His Gly 145 150 155 160		
Arg Gly Gly Leu Arg Asp Phe Glu Leu Ile Lys Ala Leu Ala Leu Gly 165 170 175		
His Leu Cys Asn Leu Pro Gln Leu Asp Ala Gln His Gln Leu Leu Leu 180 185 190		
Asp Ala Arg Thr Leu Leu His Val His Ala Arg Arg Ser Arg Asp Val 195 200 205		
Leu Asp Pro Glu Phe Ala Val Asp Val Ala Met Asp Leu Gly Phe Val 210 215 220		
Asp Arg Tyr His Leu Gly Arg Glu Ile Ala Asp Ala Ala Arg Ala Ile 225 230 235 240		
Asp Asp Gly Leu Thr Thr Ala Leu Ala Thr Ala Arg Gly Ile Leu Pro 245 250 255		
Arg Arg Thr Gly Phe Ala Phe Arg Asn Ala Ser Arg Arg Pro Leu Asp 260 265 270		
Leu Asp Val Val Asp Ala Asn Gly Thr Ile Glu Leu Ser Lys Lys Pro 275 280 285		
Asp Leu Asn Asp Pro Ala Leu Pro Leu Arg Val Ala Ala Ala Ala 290 295 300		
Thr Thr Gly Leu Pro Val Ala Glu Ser Thr Trp Val Arg Leu Asn Glu 305 310 315 320		
Cys Pro Pro Leu Pro Glu Pro Trp Pro Ala Asn Ala Ala Gly Asp Phe 325 330 335		
Phe Arg Ile Leu Ser Ser Pro Lys Asn Ser Arg Arg Val Val Lys Asn 340 345 350		
Met Asp Arg His Gly Leu Trp Ser Arg Phe Val Pro Glu Trp Asp Arg 355 360 365		

Leu Ala Gly Ser
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<210> 75
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<212> DNA
<213> Corynebacterium glutamicum

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<223> RXA02210

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Val Ser Val Ala Ala
1 5
ggc gac aaa cca aca aat agc cgt caa gaa atc ctc gaa ggt gcc cga 163
Gly Asp Lys Pro Thr Asn Ser Arg Gln Glu Ile Leu Glu Gly Ala Arg
10 15 20
cgg tgc ttc gct gag cac ggc tat gaa ggc gca acc gta cgc cga ctg 211
Arg Cys Phe Ala Glu His Gly Tyr Glu Gly Ala Thr Val Arg Arg Leu
25 30 35
gaa gaa gca aca ggt aaa tca cgc gga gcg atc ttt cat cac ttc ggt 259
Glu Glu Ala Thr Gly Lys Ser Arg Gly Ala Ile Phe His His Phe Gly
40 45 50
gac aaa gaa aac ctg ttc cta gcc ctc gcg cgg gaa gat gca gcc cgc 307
Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg Glu Asp Ala Ala Arg
55 60 65
atg gcg gag gtg gtg tct gaa aat ggc ctc gtt gaa gtg atg cga gga 355
Met Ala Glu Val Val Ser Glu Asn Gly Leu Val Glu Val Met Arg Gly
70 75 80 85
atg ctg gaa gat cct gaa cga tat gac tgg atg tca gta cgc ctg gag 403
Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met Ser Val Arg Leu Glu
90 95 100
atc tcc aag cag ctg cgc acc gac ccg gta ttc cgc gca aaa tgg att 451
Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe Arg Ala Lys Trp Ile
105 110 115
gat cac caa agt gtt cta gac gaa gct gtc cgc gtg cgt ttg tcc cgc 499
Asp His Gln Ser Val Leu Asp Glu Ala Val Arg Val Arg Leu Ser Arg
120 125 130
aac gtg gat aag gga caa atg cgc act gac gtc ccg atc gaa gtg ctg 547
Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val Pro Ile Glu Val Leu
135 140 145
cac acc ttc tta gag act gtt ctc gac ggt ttc atc tcc cgt ctt gct 595
His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe Ile Ser Arg Leu Ala
150 155 160 165

acc ggc gca tcc aca gaa gga ctg tcc gaa gta ttg gat ctg gtc gag 643
 Thr Gly Ala Ser Thr Glu Gly Leu Ser Glu Val Leu Asp Leu Val Glu
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gga act gtc cgt aaa cgc gac taaacgaccc ctgattcaca ctt 687
 Gly Thr Val Arg Lys Arg Asp
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<210> 76

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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Thr Val Arg Arg Leu Glu Glu Ala Thr Gly Lys Ser Arg Gly Ala Ile
 35 40 45

Phe His His Phe Gly Asp Lys Glu Asn Leu Phe Leu Ala Leu Ala Arg
 50 55 60

Glu Asp Ala Ala Arg Met Ala Glu Val Val Ser Glu Asn Gly Leu Val
 65 70 75 80

Glu Val Met Arg Gly Met Leu Glu Asp Pro Glu Arg Tyr Asp Trp Met
 85 90 95

Ser Val Arg Leu Glu Ile Ser Lys Gln Leu Arg Thr Asp Pro Val Phe
 100 105 110

Arg Ala Lys Trp Ile Asp His Gln Ser Val Leu Asp Glu Ala Val Arg
 115 120 125

Val Arg Leu Ser Arg Asn Val Asp Lys Gly Gln Met Arg Thr Asp Val
 130 135 140

Pro Ile Glu Val Leu His Thr Phe Leu Glu Thr Val Leu Asp Gly Phe
 145 150 155 160

Ile Ser Arg Leu Ala Thr Gly Ala Ser Thr Glu Gly Leu Ser Glu Val
 165 170 175

Leu Asp Leu Val Glu Gly Thr Val Arg Lys Arg Asp
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<210> 77

<211> 342

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 Met Leu Ala Gly Met
 1 5

cct aat tta aac gct gag gag cta gca gtc cgc gtg cga ccc gcg ctg 163
 Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg Val Arg Pro Ala Leu
 10 15 20

aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc 211
 Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu
 25 30 35

tcg ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca 259
 Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro
 40 45 50

tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc 307
 Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr
 55 60 65

gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt 355
 Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg
 70 75 80 85

atc cgc gac acc aaa gac cgc cga gcc gtg cag gtt cag ctc act gat 403
 Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp
 90 95 100

cat gga cgc gaa gag ctt gag cgc gtg aac aat gaa cga aac gca gag 451
 His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala Glu
 105 110 115

atg gct cga ctc ctt gaa atg ctc acc cca gag cag ctg gaa cgt acc 499
 Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu Gln Leu Glu Arg Thr
 120 125 130

gaa gac ctg gtg gat atc att act gag ctt gca gag gtg tac ggt agc 547
 Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala Glu Val Tyr Gly Ser
 135 140 145

tgg aaa gag acc gac agc ggt tct taacagtttt ctccatctca act 594
 Trp Lys Glu Thr Asp Ser Gly Ser
 150 155

<210> 80

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 80

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 20 25 30

Val Asn Ser Asp Leu Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu

35	40	45
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Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu 65 70 75 80		
Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln 85 90 95		
Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn 100 105 110		
Glu Arg Asn Ala Glu Met Ala Arg Leu Leu Glu Met Leu Thr Pro Glu 115 120 125		
Gln Leu Glu Arg Thr Glu Asp Leu Val Asp Ile Ile Thr Glu Leu Ala 130 135 140		
Glu Val Tyr Gly Ser Trp Lys Glu Thr Asp Ser Gly Ser 145 150 155		

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 Met Leu Ala Gly Met
 1 5
 cct aat tta aac gct gag gag cta gca gtc cgc gtg cga ccc gcg ctg 163
 Pro Asn Leu Asn Ala Glu Glu Leu Ala Val Arg Val Arg Pro Ala Leu
 10 15 20
 aca aaa ctc tac gtt ctc tat ttc cgc cgc tct gtg aat tct gac ctc 211
 Thr Lys Leu Tyr Val Leu Tyr Phe Arg Arg Ser Val Asn Ser Asp Leu
 25 30 35
 tgc ggt cca cag ctc act att ttg agt cgc ctg gaa gaa aac ggc cca 259
 Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu Glu Glu Asn Gly Pro
 40 45 50
 tcc cga att agt cgc atc gcg gaa ctt gaa gat att cgt atg cca acc 307
 Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp Ile Arg Met Pro Thr
 55 60 65
 gct tcg aat gct ctg cat cag ctg gag caa ctc aac ctg gtt gag cgt 355
 Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu Asn Leu Val Glu Arg
 70 75 80 85

atc cgc gac acc aaa gac cgc cga ggc gtg cag gtt cag ctc act gat 403
Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln Val Gln Leu Thr Asp
90 95 100

cat gga cgc gaa gag ctt gag cgc gtg aac aat gaa cga aac gca 448
His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn Glu Arg Asn Ala
105 110 115

<210> 82

<211> 116

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 82

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20 25 30

Val Asn Ser Asp Leu Ser Gly Pro Gln Leu Thr Ile Leu Ser Arg Leu
35 40 45

Glu Glu Asn Gly Pro Ser Arg Ile Ser Arg Ile Ala Glu Leu Glu Asp
50 55 60

Ile Arg Met Pro Thr Ala Ser Asn Ala Leu His Gln Leu Glu Gln Leu
65 70 75 80

Asn Leu Val Glu Arg Ile Arg Asp Thr Lys Asp Arg Arg Gly Val Gln
85 90 95

Val Gln Leu Thr Asp His Gly Arg Glu Glu Leu Glu Arg Val Asn Asn
100 105 110

Glu Arg Asn Ala
115

<210> 83

<211> 588

<212> DNA

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<222> (101) .. (565)

<223> RXA01763

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agatcgaaac tatttttcag ccagttcaca tggagccact atg acc acc agc aac 115
Met Thr Thr Ser Asn
1 5

ccc acc gcc gag atc att ggc gga cca gaa cga ttc ctc gag gcc gaa 163
Pro Thr Ala Glu Ile Ile Gly Gly Pro Glu Arg Phe Leu Glu Ala Glu
10 15 20

ttg tcc cag cag att caa ttc ctc act gcc cgc gca cga gcc aag gga 211
 Leu Ser Gln Gln Ile Gln Phe Leu Thr Ala Arg Ala Arg Ala Lys Gly
 25 30 35

tcc gcc aaa gga aac gaa gcc tta gtc gac ctc gga ctt aaa gtt cgc 259
 Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu Gly Leu Lys Val Arg
 40 45 50

caa tac tcc aca ctg tcc cta gcg gcc agc gga tta aaa cca acc caa 307
 Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly Leu Lys Pro Thr Gln
 55 60 65

cga gaa ttg gga gca ttt ctc gac cta gac cca agt cag att gtt gcc 355
 Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro Ser Gln Ile Val Ala
 70 75 80 85

ttg gtc gat ttc cta gaa aag cgc gga tta gtg gcc cgg gaa gtt gac 403
 Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val Ala Arg Glu Val Asp
 90 95 100

ccc cgg gat agg cgc tgg aag atc atc atc gcc acc gaa aaa ggt ctg 451
 Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala Thr Glu Lys Gly Leu
 105 110 115

gaa att cac gac gaa gcc acc aaa cgc ctc ctc atc gcc gag ggt gaa 499
 Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu Ile Ala Glu Gly Glu
 120 125 130

tct cta aaa aac ctc acc tcc gac gag caa gaa caa cta agg gaa ctg 547
 Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu Gln Leu Arg Glu Leu
 135 140 145

ctg ctc aaa atc gcc ttt taagtctctt aaccacgccg gcc 588
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<210> 84

<211> 155

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

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Phe Leu Glu Ala Glu Leu Ser Gln Gln Ile Gln Phe Leu Thr Ala Arg
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Ala Arg Ala Lys Gly Ser Ala Lys Gly Asn Glu Ala Leu Val Asp Leu
 35 40 45

Gly Leu Lys Val Arg Gln Tyr Ser Thr Leu Ser Leu Ala Ala Ser Gly
 50 55 60

Leu Lys Pro Thr Gln Arg Glu Leu Gly Ala Phe Leu Asp Leu Asp Pro
 65 70 75 80

Ser Gln Ile Val Ala Leu Val Asp Phe Leu Glu Lys Arg Gly Leu Val
 85 90 95

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Ala Arg Glu Val Asp Pro Arg Asp Arg Arg Ser Lys Ile Ile Ile Ala
100 105 110

Thr Glu Lys Gly Leu Glu Ile His Asp Glu Ala Thr Lys Arg Leu Leu
115 120 125

Ile Ala Glu Gly Glu Ser Leu Lys Asn Leu Thr Ser Asp Glu Gln Glu
130 135 140

Gln Leu Arg Glu Leu Leu Leu Lys Ile Ala Phe
145 150 155

<210> 85

<211> 717

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(694)

<223> RXA02667

<400> 85

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ggttctagca aaaatggaac cgccattaga aggagtggga atg gaa ttc aag gtc 115
Met Glu Phe Lys Val
1 5

gga gat acc gtc gtt tac cgc cac cac gga gct gca att att tca gcc 163
Gly Asp Thr Val Val Tyr Pro His His Gly Ala Ala Ile Ile Ser Ala
10 15 20

ctg gag cag cgt gaa atg aat ggt gag acg gtg gac tac ctg gtt ctc 211
Leu Glu Gln Arg Glu Met Asn Gly Glu Thr Val Asp Tyr Leu Val Leu
25 30 35

cag atc aat cat tcc gat ctc gtc gtt cgc gtt cca gca aag aac gct 259
Gln Ile Asn His Ser Asp Leu Val Val Arg Val Pro Ala Lys Asn Ala
40 45 50

gaa ctc gtt ggc gtg cgt gac gtt gtc ggc gag gag ggc ctg cag aag 307
Glu Leu Val Gly Val Arg Asp Val Val Gly Glu Glu Gly Leu Gln Lys
55 60 65

gtt ttc tct gtt ctt cgt gaa att gac gtc gaa gaa gcc ggc aac tgg 355
Val Phe Ser Val Leu Arg Glu Ile Asp Val Glu Glu Ala Gly Asn Trp
70 75 80 85

tcc cgc cgt tac aag gct aac cag gag cgt ttg gct tcc ggt gac gtg 403
Ser Arg Arg Tyr Lys Ala Asn Gln Glu Arg Leu Ala Ser Gly Asp Val
90 95 100

aac aag gtc gct gag gtt gtc cgt gac ctg tgg cgt cgt gat cag gat 451
Asn Lys Val Ala Glu Val Val Arg Asp Leu Trp Arg Arg Asp Gln Asp
105 110 115

cgt ggc ctt tcc gct ggt gag aag cgc atg ctc tcc aag gcg cgt cag 499
Arg Gly Leu Ser Ala Gly Glu Lys Arg Met Leu Ser Lys Ala Arg Gln
120 125 130

gtt	ctt	ggt	ggt	gag	ctc	gcg	ctc	gcc	gaa	acc	gtg	gac	gat	gag	aag	547
Val	Leu	Val	Gly	Glu	Leu	Ala	Leu	Ala	Glu	Thr	Val	Asp	Asp	Glu	Lys	
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gag	gat	gct	ttc	ctc	agc	cag	gtc	gat	gag	acc	att	gct	cgc	cac	cgc	595
Ala	Asp	Ala	Phe	Leu	Ser	Gln	Val	Asp	Glu	Thr	Ile	Ala	Arg	His	Arg	
150																
gct	gac	ctg	ctc	ggc	gac	gag	gaa	gag	aag	aag	gac	gca	ttc	gac	gac	643
Ala	Asp	Leu	Leu	Gly	Asp	Glu	Glu	Glu	Lys	Lys	Asp	Ala	Phe	Asp	Asp	
170																
ttc	gac	gat	toc	gac	gtg	gat	ctt	gac	gat	ctg	agc	ttc	gac	gac	gaa	691
Phe	Asp	Asp	Ser	Asp	Val	Asp	Leu	Asp	Asp	Leu	Ser	Phe	Asp	Asp	Glu	
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190																
195																
717																

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<212> PRT
<213> Corynebacterium glutamicum
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Ala	Ile	Ile	Ser	Ala	Leu	Glu	Gln	Arg	Glu	Met	Asn	Gly	Glu	Thr	Val
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Asp	Tyr	Leu	Val	Leu	Gln	Ile	Asn	His	Ser	Asp	Leu	Val	Val	Arg	Val
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Pro	Ala	Lys	Asn	Ala	Glu	Leu	Val	Gly	Val	Arg	Asp	Val	Val	Gly	Glu
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Ser	Lys	Ala	Arg	Gln	Val	Leu	Val	Gly	Glu	Leu	Ala	Leu	Ala	Glu	Thr
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Ile	Ala	Arg	His	Arg	Ala	Asp	Leu	Leu	Gly	Asp	Glu	Glu	Glu	Lys	Lys
				165				170						175	

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Ser Phe Asp Asp Glu Asp
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<210> 87

<211> 479

<212> DNA

<213> Corynebacterium glutamicum

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<222> (1) . . (456)

<223> RXA00348

<400> 87

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gtc agg ggt gcc atg gaa gtc ttt atc gaa gcg gga atc gat ccc ggc 96
Val Arg Gly Ala Met Glu Val Phe Ile Glu Ala Gly Ile Asp Pro Gly
20 25 30

acc gtg ccg atc atg gaa tgc tgg atc aac aac cgc caa cac aac ttc 144
Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
35 40 45

gaa gtg gcc aaa gaa ctt cta gaa aca cac cca gac ctc acc gca gta 192
Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
50 55 60

ctc tgt acc gtc gat gca ctg gca ttc ggc gtt ctg gaa tac ctt aaa 240
Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys
65 70 75 80

agc gta ggt aaa tca gcg cct gca gat cta tcc ctc act ggt ttc gat 288
Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp
85 90 95

ggc acc cac atg gca ctc gca cgg gat ctc acc acc gtc atc caa ccc 336
Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro
100 105 110

aac aaa ctc aaa ggg ttc aaa gcc ggc gaa aca ctg ttg aaa atg att 384
Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile
115 120 125

gac aaa gaa tac gtg gaa cca gaa gtg gaa ttg gaa act tcc ttc cac 432
Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His
130 135 140

cca ggt tcc acg gtt gcg cca atc taggcttgtg gcacttttcg tgc 479
Pro Gly Ser Thr Val Ala Pro Ile
145 150

<210> 88

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 88

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20 25 30

Thr Val Pro Ile Met Glu Cys Trp Ile Asn Asn Arg Gln His Asn Phe
35 40 45

Glu Val Ala Lys Glu Leu Leu Glu Thr His Pro Asp Leu Thr Ala Val
50 55 60

Leu Cys Thr Val Asp Ala Leu Ala Phe Gly Val Leu Glu Tyr Leu Lys
65 70 75 80

Ser Val Gly Lys Ser Ala Pro Ala Asp Leu Ser Leu Thr Gly Phe Asp
85 90 95

Gly Thr His Met Ala Leu Ala Arg Asp Leu Thr Thr Val Ile Gln Pro
100 105 110

Asn Lys Leu Lys Gly Phe Lys Ala Gly Glu Thr Leu Leu Lys Met Ile
115 120 125

Asp Lys Glu Tyr Val Glu Pro Glu Val Glu Leu Glu Thr Ser Phe His
130 135 140

Pro Gly Ser Thr Val Ala Pro Ile
145 150

<210> 89

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101) .. (544)

<223> RXA01500

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tgtttcgcga agtcccattg ttggagttag gcttataccc atg gct acg cat cca 115
Met Ala Thr His Pro
1 5

gat att ccc aca gag ttg ctt gaa tct ccg agc tat caa ctt gaa cga 163
Asp Ile Pro Thr Glu Leu Leu Glu Ser Pro Ser Tyr Gln Leu Glu Arg
10 15 20

ctt cga cga cgc act cgt gac cat gtt gag gcc gaa ttg gcc aag cat 211
Leu Arg Arg Arg Thr Arg Asp His Val Glu Ala Glu Leu Ala Lys His

 25 30 35

gag acc acg atg agg gaa ttc tgg acg ctt aca tgt ctg gtt cat tcc 259

Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr Cys Leu Val His Ser
 40 45 50

gac gct gca agc cag tca gtt ctg tgt gag ctg ctg gcc att gat gca 307
 Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu Ala Ile Asp Ala
 55 60 65

tcg gat atg gtc aga ctc gtt gac tca ctt gag gta cgc gcc tgg gcg 355
 Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu Val Arg Gly Trp Ala
 70 75 80 85

aaa agg gaa cgt gat ccc aaa gac cgt cgt cgc caa att gtt gcg tca 403
 Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Gln Ile Val Ala Ser
 90 95 100

acg aag aag gga aaa aac gcc cag gcg gat ctg cac aaa gtt gtg ctt 451
 Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu His Lys Val Val Leu
 105 110 115

gag gca gag gat gct gcg ttg gat gag tct acg tcc aag cag ttg aag 499
 Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr Ser Lys Gln Leu Lys
 120 125 130

cac ctt cgt aaa ttg gcc gca gca att atc tcc acc gaa gag gac 544
 His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser Thr Glu Glu Asp
 135 140 145

taaatataac gtggcattga gca 567

<210> 90
 <211> 148
 <212> PRT
 <213> Corynebacterium glutamicum

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 20 25 30

Glu Leu Ala Lys His Glu Thr Thr Met Arg Glu Phe Trp Thr Leu Thr
 35 40 45

Cys Leu Val His Ser Asp Ala Ala Ser Gln Ser Val Leu Cys Glu Leu
 50 55 60

Leu Ala Ile Asp Ala Ser Asp Met Val Arg Leu Val Asp Ser Leu Glu
 65 70 75 80

Val Arg Gly Trp Ala Lys Arg Glu Arg Asp Pro Lys Asp Arg Arg Arg
 85 90 95

Gln Ile Val Ala Ser Thr Lys Lys Gly Lys Asn Ala Gln Ala Asp Leu
 100 105 110

His Lys Val Val Leu Glu Ala Glu Asp Ala Ala Leu Asp Glu Ser Thr
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Ser Lys Gln Leu Lys His Leu Arg Lys Leu Ala Ala Ala Ile Ile Ser

140

Tyr Asp Ala Ser Leu His Asn

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70

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<212> DNA
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<223> RXN00822
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Val Glu Gly Val Gln
1 5

gag atc ctg tcg cgc gcc gga att ttt caa ggc gtt gac cca acg gca 163
Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala
10 15 20

gtc aat aac ctc atc cag gat atg gag acc gtt cgc ttc cca cgc gga 211
Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly
25 30 35

gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc 259
Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile
40 45 50

acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa 307
Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu
55 60 65

aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctc tcc 355
Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser
70 75 80 85

atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa 403
Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu
90 95 100

ggt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct 451
Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala
105 110 115

gac cac cca gct atc gct gag cag ctc ctg cgc gtt ctg gct cgt cgt 499
Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg
120 125 130

ctg cgt cgc acc aac gct tcc ctg gct gac ctc atc ttc acc gac gtc 547
Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val
135 140 145

cca ggc cgc gtt gct aag acc ctt ctg cag ctg gct aac cgc ttc ggc 595
Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu Ala Asn Arg Phe Gly
150 155 160 165

acc caa gaa gct qgc gcg ctg cgc gtg aac cac gac ctc act cag gaa 643

Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His Asp Leu Thr Gln Glu
 170 175 180
 gaa atc gca cag ctc gtc ggt gct tcc cgt gaa act gtg aat aag gct 691
 Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu Thr Val Asn Lys Ala
 185 190 195
 ctt gca acg ttc gca cac cgt ggc tgg atc cgc ctc gag ggc aag tcc 739
 Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg Leu Glu Gly Lys Ser
 200 205 210
 gtc ctc att gtg gac acc gag cat ttg gca cgt cgc gct cga 781
 Val Leu Ile Val Asp Thr Glu His Leu Ala Arg Arg Ala Arg
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 <213> Corynebacterium glutamicum

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 35 40 45
 Arg Leu Tyr Ile Ile Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala
 50 55 60
 Pro Asp Gly Arg Glu Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met
 65 70 75 80
 Phe Gly Glu Leu Ser Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala
 85 90 95
 Val Cys Val Thr Glu Val His Ala Ala Thr Met Asn Ser Asp Met Leu
 100 105 110
 Arg Asn Trp Val Ala Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg
 115 120 125
 Val Leu Ala Arg Arg Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu
 130 135 140
 Ile Phe Thr Asp Val Pro Gly Arg Val Ala Lys Thr Leu Leu Gln Leu
 145 150 155 160
 Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His
 165 170 175
 Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu
 180 185 190
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195 200 205

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Arg Ala Arg
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 Val Glu Gly Val Gln
 1 5

gag atc ctg tgg cgc gcc gga att ttt caa ggc gtt gac cca acg gca 163
 Glu Ile Leu Ser Arg Ala Gly Ile Phe Gln Gly Val Asp Pro Thr Ala
 10 15 20

gtc aat aac ctc atc cag gat atg gag acc gtt cgc ttc cca cgc gga 211
 Val Asn Asn Leu Ile Gln Asp Met Glu Thr Val Arg Phe Pro Arg Gly
 25 30 35

gca acc atc ttc gac gag ggc gag cca ggt gac cgc ctt tac atc atc 259
 Ala Thr Ile Phe Asp Glu Gly Glu Pro Gly Asp Arg Leu Tyr Ile Ile
 40 45 50

acc tcc ggc aaa gtg aag ctt gcg cgc cac gca ccg gac ggc cgc gaa 307
 Thr Ser Gly Lys Val Lys Leu Ala Arg His Ala Pro Asp Gly Arg Glu
 55 60 65

aac ctg ctg acc atc atg ggt cct tcc gac atg ttc ggt gag ctc tcc 355
 Asn Leu Leu Thr Ile Met Gly Pro Ser Asp Met Phe Gly Glu Leu Ser
 70 75 80 85

atc ttc gac cca ggc cca cgc acc tcc tct gca gtg tgt gtc acc gaa 403
 Ile Phe Asp Pro Gly Pro Arg Thr Ser Ser Ala Val Cys Val Thr Glu
 90 95 100

gtt cat gca gca acc atg aac tct gac atg ctg cgc aac tgg gta gct 451
 Val His Ala Ala Thr Met Asn Ser Asp Met Leu Arg Asn Trp Val Ala
 105 110 115

gac cac cca gct atc gct gag cag ctc ctg cgc gtt ctg gct cgt cgt 499
 Asp His Pro Ala Ile Ala Glu Gln Leu Leu Arg Val Leu Ala Arg Arg
 120 125 130

ctg cgt cgc acc aac gct tcc ctg gct gac ctc atc ttc acc gac gtc 547
 Leu Arg Arg Thr Asn Ala Ser Leu Ala Asp Leu Ile Phe Thr Asp Val
 135 140 145

Ala Asn Arg Phe Gly Thr Gln Glu Ala Gly Ala Leu Arg Val Asn His

	165	170	175
Asp Leu Thr Gln Glu Glu Ile Ala Gln Leu Val Gly Ala Ser Arg Glu			
	180	185	190
Thr Val Asn Lys Ala Leu Ala Thr Phe Ala His Arg Gly Trp Ile Arg			
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Leu Glu Gly Lys Ser Val Leu Ile Val Asp Thr Glu His Leu Ala Arg			
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Arg Ala Arg			
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act	gggaaca	aatt	tttaggg
aa	gggaggt	ga	acctaacg
atg	gtt	act	tat
aca			
	115		
Met	Val	Thr	Tyr
Thr			
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acc	ctt	cta	gac
aag	ccg	att	tca
gaa	tct	gcc	cca
cgg	aaa	gct	cca
	163		
Thr	Leu	Leu	Asp
Lys	Pro	Ile	Ser
Glu	Ser	Ala	Pro
Arg	Lys	Ala	Pro
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gag	cca	ctt	ctc
cgc	gaa	gct	ctg
ggt	gca	gct	ctt
cgt	tct	ttc	cgt
	211		
Glu	Pro	Leu	Leu
Arg	Glu	Ala	Leu
Gly	Ala	Ala	Leu
Arg	Ser	Phe	Arg
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gct	gac	aag	ggc
gtt	act	ttg	cgt
gag	ctg	gcg	gaa
gct	tca	cgt	gtg
	259		
Ala	Asp	Lys	Gly
Val	Thr	Leu	Arg
Glu	Glu	Leu	Ala
Glu	Ala	Ser	Arg
Val			
	40		45
tca	cct	ggt	tat
ctt	tca	gaa	ttg
gaa	cgc	ggc	cgc
aaa	gag	gtg	tcc
	307		
Ser	Pro	Gly	Tyr
Leu	Ser	Glu	Leu
Glu	Arg	Gly	Arg
Lys	Glu	Val	Ser
	55		60
tct	gag	ctt	ctt
gcc	tcc	gtg	tgc
cac	gct	ttg	ggg
gcc	agc	gtt	gcg
	355		
Ser	Glu	Leu	Leu
Ala	Ser	Val	Cys
His	Ala	Leu	Gly
Ala	Ser	Val	Ala
	70		75
gat	gtg	ttg	atc
gaa	gct	gca	ggt
tcc	atg	gcg	ctg
caa	gca	gcg	cag
	403		
Asp	Val	Leu	Ile
Glu	Ala	Ala	Gly
Ser	Met	Ala	Leu
Gln	Ala	Ala	Gln
	90		95
gaa	gac	ctc	gct
cgc	gtc	taag	cgcatg
ggt	gggcgc	gaa	
	444		
Glu	Asp	Leu	Ala
Arg	Val		
	105		

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gcaaaagcttt cgctgctga ttgaccatat tgagtgcag tgactcaagt ttccaggtaa 60
actgggaaca aattttaggg aaaggggagt gaacctaacg atg gtt act tat aca 115
Met Val Thr Tyr Thr
1 5
acc ctt cta gac aag ccg att tca gaa tct gcc cca cgg aaa gct cca 163
Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala Pro Arg Lys Ala Pro
10 15 20
gag cca ctt ctc cgc gaa gct ctg ggt gca gct ctt cgt tct ttc cgt 211
Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala Leu Arg Ser Phe Arg
25 30 35
gct gac aag ggc gtt act ttg cgt gag ctg gcg gaa gct tca cgt gtg 259
Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala Glu Ala Ser Arg Val
40 45 50
tca cct ggt tat ctt tca gaa ttg gaa cgc gcc cgc aaa gag gtg tcc 307
Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly Arg Lys Glu Val Ser
55 60 65

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tct gag ctt ctt gcc tcc gtg tgc cac gct ttg ggg gcc agc gtt gcg 355
 Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu Gly Ala Ser Val Ala
 70 75 80 85

gat gtg ttg atc gaa gct gca ggt tcc atg gcg ctg caa gca gcg cag 403
 Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala Leu Gln Ala Ala Gln
 90 95 100

gaa gac ctc gct cgc gtc taagcgcatg ggtggcgctc gaa 444
 Glu Asp Leu Ala Arg Val
 105

<210> 100

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

Met Val Thr Tyr Thr Thr Leu Leu Asp Lys Pro Ile Ser Glu Ser Ala
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Pro Arg Lys Ala Pro Glu Pro Leu Leu Arg Glu Ala Leu Gly Ala Ala
 20 25 30

Leu Arg Ser Phe Arg Ala Asp Lys Gly Val Thr Leu Arg Glu Leu Ala
 35 40 45

Glu Ala Ser Arg Val Ser Pro Gly Tyr Leu Ser Glu Leu Glu Arg Gly
 50 55 60

Arg Lys Glu Val Ser Ser Glu Leu Leu Ala Ser Val Cys His Ala Leu
 65 70 75 80

Gly Ala Ser Val Ala Asp Val Leu Ile Glu Ala Ala Gly Ser Met Ala
 85 90 95

Leu Gln Ala Ala Gln Glu Asp Leu Ala Arg Val
 100 105

<210> 101

<211> 492

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(469)

<223> RXA02698

<400> 101

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aagattctcc attagagctc gaaccagcta aattaagact gtg agt tcc aac aat 115
 Val Ser Ser Asn Asn
 1 5

gaa tct tcc ttc gcc ctg ccc gac aat gaa cca ttg ctg acc ctt ccg 163
 Glu Ser Ser Phe Ala Leu Pro Asp Asn Glu Pro Leu Leu Thr Leu Pro
 10 15 20

gag aca gcc gag cgc ctc ggc gtt gtt gtc acc aag gtg atg gat ctg 211
 Glu Thr Ala Glu Arg Leu Gly Val Val Thr Lys Val Met Asp Leu
 25 30 35

gtc aat gaa cac aaa ttg atc gtg gtc cgg cgc gac ggt att cgc tac 259
 Val Asn Glu His Lys Leu Ile Val Val Arg Arg Asp Gly Ile Arg Tyr
 40 45 50

att cca gaa gct ttc ctg agc acc aag aag gaa aac acc aac cgt ttc 307
 Ile Pro Glu Ala Phe Leu Ser Thr Lys Lys Glu Asn Thr Asn Arg Phe
 55 60 65

atc cct gga gtt att gcc ttg ctt gcc gac ggt ggc ttc agc gac gag 355
 Ile Pro Gly Val Ile Ala Leu Leu Ala Asp Gly Gly Phe Ser Asp Glu
 70 75 80 85

gaa atc ctc gcg ttc ctg ttt acc gaa gac gag acc ctt cct ggt cgc 403
 Glu Ile Leu Ala Phe Leu Phe Thr Glu Asp Glu Thr Leu Pro Gly Arg
 90 95 100

ccc atc gat gca ctt cat ggc cag ttg gct cgt gaa gtt atg cga cgc 451
 Pro Ile Asp Ala Leu His Gly Gln Leu Ala Arg Glu Val Met Arg Arg
 105 110 115

gct caa gca atg gcg ttc taagcgcttt ctaaaagatc taa 492
 Ala Gln Ala Met Ala Phe
 120

<210> 102
 <211> 123
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 102
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 1 5 10 15

Leu Leu Thr Leu Pro Glu Thr Ala Glu Arg Leu Gly Val Val Val Thr
 20 25 30

Lys Val Met Asp Leu Val Asn Glu His Lys Leu Ile Val Val Arg Arg
 35 40 45

Asp Gly Ile Arg Tyr Ile Pro Glu Ala Phe Leu Ser Thr Lys Lys Glu
 50 55 60

Asn Thr Asn Arg Phe Ile Pro Gly Val Ile Ala Leu Leu Ala Asp Gly
 65 70 75 80

Gly Phe Ser Asp Glu Glu Ile Leu Ala Phe Leu Phe Thr Glu Asp Glu
 85 90 95

Thr Leu Pro Gly Arg Pro Ile Asp Ala Leu His Gly Gln Leu Ala Arg
 100 105 110

Glu Val Met Arg Arg Ala Gln Ala Met Ala Phe
 115 120

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<221> CDS  
<222> (101)..(427)  
<223> BXA00350
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Leu Pro Ala Lys Ile
1 5

acg gac act cgt ccc acc cca gaa tcc ctt cac gct gtt gaa gag gaa 163
Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His Ala Val Glu Glu Glu
10 15 20

acc gca gcc ggt gcc cgc agg att gtt gcc acc tat tct aag gac ttc 211
Thr Ala Ala Gly Ala Arg Arg Ile Val Ala Thr Tyr Ser Lys Asp Phe
25 30 35

ttc gac ggc gtc act ttg atg tgc atg ctc ggc gtt gaa cct cag ggc 259
Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly Val Glu Pro Gln Gly
40 45 50

ctg cgt tac acc aag gtc gct tct gaa cac gag gaa gct cag cca aag 307
Leu Arg Tyr Thr Lys Val Ala Ser Glu His Glu Glu Ala Gln Pro Lys
55 60 65

aag gct aca aag cgg act cgt aag gca cca gct aag aag gct gct gct 355
 Lys Ala Thr Lys Arg Thr Arg Lys Ala Pro Ala Lys Lys Ala Ala Ala
 70 75 80 85

aag aaa acg acc aag aag acc act aag aaa act act aaa aag acc acc 403
Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr Lys Lys Thr Thr
90 95 100

gca aag aag acc aca aag aag tct taagccggat cttatatgga tga 450
Ala Lys Lys Thr Thr Lys Lys Ser
105

<210> 104
<211> 109
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 104
Leu Pro Ala Lys Ile Thr Asp Thr Arg Pro Thr Pro Glu Ser Leu His
1 5 10 15

Ala Val Glu Glu Glu Thr Ala Ala Gly Ala Arg Arg Ile Val Ala Thr
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Tyr Ser Lys Asp Phe Phe Asp Gly Val Thr Leu Met Cys Met Leu Gly
35 40 45

Thr Lys Lys Thr Thr Ala Lys Lys Thr Thr Lys Lys Ser
100 105

<223> RXA02830

cgc gcc tgc att ttc cgg tct ttc ttg cag cgc cgc ttg gat gcc aac 480

Arg Ala Cys Ile Phe Arg Ser Phe Leu Gln Arg Arg Leu Asp Ala Asn
145 150 155 160

agc atc tat tgg caa
Ser Ile Tyr Trp Gln
165

495

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<210> 106
<211> 165
<212> PRT
<213> Corynebacterium glutamicum
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<400> 106
Leu Glu Asp Ser Leu Gly Val Ser Leu Phe Glu Arg Ala Gly Arg Gly
1 5 10 15

Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala Arg Arg
20 25 30

Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala Gly Ala
35 40 45

Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile Tyr Pro
50 55 60

Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro Arg Val
65 70 75 80

Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu Gln Phe
85 90 95

Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu Leu Gly
100 105 110

Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val Gly Ala
115 120 125

Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala Phe Glu
130 135 140

Arg Ala Cys Ile Phe Arg Ser Phe Leu Gln Arg Arg Leu Asp Ala Asn
145 150 155 160

Ser Ile Tyr Trp Gln
165

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<210> 107
<211> 459
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(436)
<223> RXA00947
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taaattcaat actgttttac gagatcattt ggaggggtgc atg gcc cgc aaa ttg 115
Met Ala Arg Lys Leu
1 5

gaa cat cca tct ttg gcc gag atg aat tta aat gcc atc atg ttt gcg 163
Glu His Pro Ser Leu Ala Glu Met Asn Leu Asn Ala Ile Met Phe Ala
10 15 20

ctg tcg gat cct att agg cga caa atc ctg tcg cag ctg tcg tgc gga 211
Leu Ser Asp Pro Ile Arg Arg Gln Ile Leu Ser Gln Leu Ser Cys Gly
25 30 35

cat aat gat cag gca tgt gtt gcc ttc gag ctt cca gta tct aaa tcc 259
His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu Pro Val Ser Lys Ser
40 45 50

acc tca acg cac cac ttc cgc gta ctc cgt gag gcg ggt ctg att act 307
Thr Ser Thr His His Phe Arg Val Leu Arg Glu Ala Gly Leu Ile Thr
55 60 65

cag cgc tat gaa gga act gcc att cta agt gcg ctg cgc agc gaa gat 355
Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala Leu Arg Ser Glu Asp
70 75 80 85

atg gaa gcg cgt ttt cgc gga ctg ctg act tct gtc atg cga gcg gaa 403
Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser Val Met Arg Ala Glu
90 95 100

gtg gaa gag cgc aac gca gct gac ttg ccc gtt taggacgggt agcaagtatt 456
Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val
105 110

atc 459

<210> 108

<211> 112

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Met Ala Arg Lys Leu Glu His Pro Ser Leu Ala Glu Met Asn Leu Asn
1 5 10 15

Ala Ile Met Phe Ala Leu Ser Asp Pro Ile Arg Arg Gln Ile Leu Ser
20 25 30

Gln Leu Ser Cys Gly His Asn Asp Gln Ala Cys Val Ala Phe Glu Leu
35 40 45

Pro Val Ser Lys Ser Thr Ser Thr His His Phe Arg Val Leu Arg Glu
50 55 60

Ala Gly Leu Ile Thr Gln Arg Tyr Glu Gly Thr Ala Ile Leu Ser Ala
65 70 75 80

Leu Arg Ser Glu Asp Met Glu Ala Arg Phe Pro Gly Leu Leu Thr Ser
85 90 95

Val Met Arg Ala Glu Val Glu Glu Arg Asn Ala Ala Asp Leu Pro Val
100 105 110

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<210> 109

<211> 828

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101) .. (805)

<223> RXA01836

<400> 109

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cttcaccacg tctcattggg tgaaatgcta aattcaaggt atg gga cag caa gaa 115
Met Gly Gln Gln Glu
1 5

att atc gag gac tcc acc gag agc ggt att aag gtt tta gac cgc act 163
Ile Ile Glu Asp Ser Thr Glu Ser Gly Ile Lys Val Leu Asp Arg Thr
10 15 20

gta tta atc ctc aat gtc atc gca gaa cag cct cga tgc ttg gca gag 211
Val Leu Ile Leu Asn Val Ile Ala Glu Gln Pro Arg Ser Leu Ala Glu
25 30 35

ctc gca gct gcc acc gat ctg ccc agg gct aca gcc cac cgc ctc gcc 259
Leu Ala Ala Thr Asp Leu Pro Arg Ala Thr Ala His Arg Leu Ala
40 45 50

tca gcg ctt gag gta cac ggc atg ttg gca cgc tcc cgc gat aat aga 307
Ser Ala Leu Glu Val His Gly Met Leu Ala Arg Ser Arg Asp Asn Arg
55 60 65

tgg acc atc ggc gca cgg ctt gcc tca ttg ggt gca cgc ggc gct gac 355
 Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly Ala Arg Gly Ala Asp
 70 75 80 85

acc ctc atc gat acg gcc gta cca att atg gcc gac ctt atg gag cgc 403
Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala Asp Leu Met Glu Arg
90 95 100

acc ggc gaa tcc gtt cag ctt tat cgc ctc acc ggc acc acc cgc acg 451
Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr Gly Thr Thr Arg Thr
105 110 115

tgt gtg gcc agc caa gag ccc agc tcc ggg cta aaa aac gtg gtt ccc 499
Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu Lys Asn Val Val Pro
120 125 130

gtg ggc act cgc atg cct tta aat gca ggg tca gca gcg cgc gtt ttt 547
Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser Ala Ala Arg Val Phe
135 140 145

gcc gcc tac ctc ccc atc ccc tct gcc agc gtc ttt tcc cgc gag gag 595
Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val Phe Ser Arg Glu Glu
150 155 160 165

ctt gac cag gtg cgc gcc agc ggc tta gcg gag tcc gtg ggc gag cgt 643
 Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu Ser Val Gly Glu Arg
 170 175 180

gag ctc ggc ctt gct agc ctc tcc tcc cct gtt ttt gat tcc aac gga 691
 Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val Phe Asp Ser Asn Gly
 185 190 195

tcc atg atc gcg gca ctg tcc atc tcc ggc gtg gcc gag cgc ctc aag 739
 Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val Ala Glu Arg Leu Lys
 200 205 210

ccc cac ccc gcc gcc atg tgg ggc acc gag ctt atc gac gcc gcc gag 787
 Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu Ile Asp Ala Ala Glu
 215 220 225

cgc cta ggc gct ttg ctt taagagcttt togacgcaca acc 828
 Arg Leu Gly Ala Leu Leu
 230 235

<210> 110

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Gly Gln Gln Glu Ile Ile Glu Asp Ser Thr Glu Ser Gly Ile Lys
 1 5 10 15

Val Leu Asp Arg Thr Val Leu Ile Leu Asn Val Ile Ala Glu Gln Pro
 20 25 30

Arg Ser Leu Ala Glu Leu Ala Ala Thr Asp Leu Pro Arg Ala Thr
 35 40 45

Ala His Arg Leu Ala Ser Ala Leu Glu Val His Gly Met Leu Ala Arg
 50 55 60

Ser Arg Asp Asn Arg Trp Thr Ile Gly Ala Arg Leu Ala Ser Leu Gly
 65 70 75 80

Ala Arg Gly Ala Asp Thr Leu Ile Asp Thr Ala Val Pro Ile Met Ala
 85 90 95

Asp Leu Met Glu Arg Thr Gly Glu Ser Val Gln Leu Tyr Arg Leu Thr
 100 105 110

Gly Thr Thr Arg Thr Cys Val Ala Ser Gln Glu Pro Ser Ser Gly Leu
 115 120 125

Lys Asn Val Val Pro Val Gly Thr Arg Met Pro Leu Asn Ala Gly Ser
 130 135 140

Ala Ala Arg Val Phe Ala Ala Tyr Leu Pro Ile Pro Ser Ala Ser Val
 145 150 155 160

Phe Ser Arg Glu Glu Leu Asp Gln Val Arg Ala Ser Gly Leu Ala Glu
 165 170 175

Ser Val Gly Glu Arg Glu Leu Gly Leu Ala Ser Leu Ser Ser Pro Val
180 185 190

Phe Asp Ser Ser Asn Gly Ser Met Ile Ala Ala Leu Ser Ile Ser Gly Val
195 200 205

Ala Glu Arg Leu Lys Pro His Pro Ala Ala Met Trp Gly Thr Glu Leu
210 215 220

Ile Asp Ala Ala Glu Arg Leu Gly Ala Leu Leu
225 230 235

<210> 111

<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(754)

<223> RXA00292

<400> 111

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gcgctgtatt tggagtgaac ctaccgggag taatggagta atg gat caa aca ctt 115
Met Asp Gln Thr Leu
1 5

aaa gtt tta gta att gat gat gat ttc cgc gtc gcc ggc att cac gcc 163
Lys Val Leu Val Ile Asp Asp Asp Phe Arg Val Ala Gly Ile His Ala
10 15 20

tcc atc gtt gat gcg tcc cct gga ttt tgc gtg gtc ggt acc gcg cgt 211
Ser Ile Val Asp Ala Ser Pro Gly Phe Ser Val Val Gly Thr Ala Arg
25 30 35

acc ctc gca gag gca aaa acc ctg atc gcc aca ttt tcc ccg gat ctc 259
Thr Leu Ala Glu Ala Lys Thr Leu Ile Ala Thr Phe Ser Pro Asp Leu
40 45 50

cta ctt gtt gat gtc tac ctc ccc gac ggc gat ggc att gac ctc gtg 307
Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp Gly Ile Asp Leu Val
55 60 65

ggc acc tcc aat att gat gcg ttt gtg ctc agc gca gcc gat gac atc 355
Gly Thr Ser Asn Ile Asp Ala Phe Val Leu Ser Ala Ala Asp Asp Ile
70 75 80 85

aaa aca gtt cga cgc gcc atg cgt gcc ggg gca ctc gga tat ctg ctc 403
Lys Thr Val Arg Arg Ala Met Arg Ala Gly Ala Leu Gly Tyr Leu Leu
90 95 100

aaa cca ttt ccc caa aaa cgt ctc gtg gaa cgc ctt gac cgt tac gtc 451
Lys Pro Phe Pro Gln Lys Arg Leu Val Glu Arg Leu Asp Arg Tyr Val
105 110 115

cgc tac cgc cat gtc tta tcc gcc acc caa gga ctt tcc caa gac aaa 499
Arg Tyr Arg His Val Leu Ser Gly Thr Gln Gly Leu Ser Gln Asp Lys
120 125 130

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att gac cag gca acc gca atc ctc aac ggc acc caa gcg ccg gtc acc 547
 ile asp gln ala thr ala ile leu asn gly thr gln ala pro val thr
 135 140 145

gtc tct aga tcc gcc aca gag caa tta ctt ctc gac gcc ctg gaa ggc 595
 val ser arg ser ala thr glu gln leu leu leu asp ala leu glu gly
 150 155 160 165

caa gaa ctc tcc gca aca gaa gct tcc gaa gct gcc gga gtt tca cgt 643
 gln glu leu ser ala thr glu ala ser glu ala ala gly val ser arg
 170 175 180

gcc aca gca cag cgc agg ctg gca gcg atg gct agc caa ggt gtg atc 691
 ala thr ala gln arg arg leu ala ala met ala ser gln gly val ile
 185 190 195

cag gtt cgc ctt cgg tac gga cag tcc ggg cga cca gaa cat cta tat 739
 gln val arg leu arg tyr gly gln ser gly arg pro glu his leu tyr
 200 205 210

tca aag cca ctg ctc tagtaacctt tgtggatgtc cac 777
 ser lys pro leu leu
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<210> 112
 <211> 218
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 112
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 20 25 30
 Val Gly Thr Ala Arg Thr Leu Ala Glu Ala Lys Thr Leu Ile Ala Thr
 35 40 45
 Phe Ser Pro Asp Leu Leu Val Asp Val Tyr Leu Pro Asp Gly Asp
 50 55 60
 Gly Ile Asp Leu Val Gly Thr Ser Asn Ile Asp Ala Phe Val Leu Ser
 65 70 75 80
 Ala Ala Asp Asp Ile Lys Thr Val Arg Arg Ala Met Arg Ala Gly Ala
 85 90 95
 Leu Gly Tyr Leu Leu Lys Pro Phe Pro Gln Lys Arg Leu Val Glu Arg
 100 105 110
 Leu Asp Arg Tyr Val Arg Tyr Arg His Val Leu Ser Gly Thr Gln Gly
 115 120 125
 Leu Ser Gln Asp Lys Ile Asp Gln Ala Thr Ala Ile Leu Asn Gly Thr
 130 135 140
 Gln Ala Pro Val Thr Val Ser Arg Ser Ala Thr Glu Gln Leu Leu Leu
 145 150 155 160

002250-4282056

tat caa ggc ctg gcg cgt ttt gtg cag gcc ggc cgc gtc acg ctt cgc 499
Tyr Gln Gly Leu Ala Arg Phe Val Gln Ala Gly Arg Val Thr Leu Arg

120	125	130	
acg gtg atg atg gat aat gcc tgg tgg ccc cag tgg caa cta tct gcc Thr Val Met Met Asp Asn Ala Trp Trp Pro Gln Trp Gln Leu Ser Ala 135 140 145			547
agc ctg tcg gag cgt ggg tgg ctc gcg gaa atg aac cat gcc gcg ccg Ser Leu Ser Glu Arg Gly Trp Leu Ala Glu Met Asn His Ala Ala Pro 150 155 160 165			595
ggc att ttg cgg att aat ggt ggc cga gat ttg gcc gga agc atg tcc Gly Ile Leu Arg Ile Asn Gly Gly Arg Asp Leu Ala Gly Ser Met Ser 170 175 180			643
aat gag ctt ccg cac tgg atc gcc aac gcc att ttg cgt gat tac cgc Asn Glu Leu Pro His Trp Ile Ala Asn Ala Ile Leu Arg Asp Tyr Arg 185 190 195			691
gat gaa acc atg ccg tat gcg cgc cat gag ttt gtt gag gcg ttg ctg Asp Glu Thr Met Pro Tyr Ala Arg His Glu Phe Val Glu Ala Leu Leu 200 205 210			739
ttt aac cat tcg ctg cgc aag ggc tcg acc atg ctc acc cat gcg ctg Phe Asn His Ser Leu Arg Lys Gly Ser Thr Met Leu Thr His Ala Leu 215 220 225			787
aat cag tgg aaa aac acc att aca tct gcg tct ttg cag ctg gtg att Asn Gln Trp Lys Asn Thr Ile Thr Ser Ala Ser Leu Gln Leu Val Ile 230 235 240 245			835
ttg gtg gag gag ccc oct gcg gaa tcg gat tat gaa gat ccg atg gat Leu Val Glu Glu Pro Pro Ala Glu Ser Asp Tyr Glu Asp Pro Met Asp 250 255 260			883
tcc gtg tgg ccg gtg cgt ttg atg gtg cgc acg ggc gtg gat gcg ccg Ser Val Trp Pro Val Arg Leu Met Val Arg Thr Gly Val Asp Ala Pro 265 270 275			931
cag gcg att caa aaa gga tcg atc gat agc ggg gga atg gag caa ctg Gln Ala Ile Gln Lys Gly Ser Ile Asp Ser Gly Gly Met Glu Gln Leu 280 285 290			979
gcg tcc caa tac gaa acc gca aaa acc acc tcc atg ctg ctg gat cct Arg Ser Gln Tyr Glu Thr Ala Lys Thr Thr Ser Met Leu Leu Asp Pro 295 300 305			1027
gcg cgc gaa gac gcg atg ctg ggg cat atg gtg gac atc gcc caa aac Ala Arg Glu Asp Ala Met Leu Gly His Met Val Asp Ile Ala Gln Asn 310 315 320 325			1075
ggc gac tgg gat att ttc acc acc gag gag atc gtc aac ttt atc Gly Asp Trp Asp Ile Phe Leu Thr Thr Glu Glu Ile Val Asn Phe Ile 330 335 340			1123
tcc cac gat gta gcc aag ctg cgc aaa gcc ggc att ccc gtc atg ctg Ser His Asp Val Ala Lys Leu Arg Lys Ala Gly Ile Pro Val Met Leu 345 350 355			1171
ccc aaa gcc tgg agc acc tat gaa acc cgc gcg cag gtg gaa gcg cgc Pro Lys Ala Trp Ser Thr Tyr Glu Thr Arg Ala Gln Val Glu Ala Arg 360 365 370			1219

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 Thr Pro Asn Asp Ala Ala Asp Ser Ser Thr Lys Ala Ile Ile Gly Leu
 375 380 385

gac cag ctc gtg gaa tac aac tgg cgc atc agc gtc ggc gat att cag 1315
 Asp Gln Leu Val Glu Tyr Asn Trp Arg Ile Ser Val Gly Asp Ile Gln
 390 395 400 405

ctg tcc gac gaa gag atg cgc gaa ctc atc gat tcc aaa aca ggc ctc 1363
 Leu Ser Asp Glu Glu Met Arg Glu Leu Ile Asp Ser Lys Thr Gly Leu
 410 415 420

atc cgc ctg cgc ggc gat tgg gtc atg gcg gac caa gac gcg ttg cga 1411
 Ile Arg Leu Arg Gly Asp Trp Val Met Ala Asp Gln Asp Ala Leu Arg
 425 430 435

cgc atc acc agc tac atg gag gaa cta tca aag tcc tcc gaa aaa cgc 1459
 Arg Ile Thr Ser Tyr Met Glu Glu Leu Ser Lys Ser Ser Glu Lys Arg
 440 445 450

gcg cgc acc gaa atg gaa aaa gtg gcc atg cag gcc aaa ctc gcc gaa 1507
 Ala Arg Thr Glu Met Glu Lys Val Ala Met Gln Ala Lys Leu Ala Glu
 455 460 465

gca aac ggc gaa gaa ggt tgg caa ctc ctg gct gcc aag gct gaa act 1555
 Ala Asn Gly Glu Glu Gly Trp Gln Leu Leu Ala Ala Lys Ala Glu Thr
 470 475 480 485

ctc cgc aag gaa ttc aat gag aaa ttc agt gcc gat gga caa ggc gaa 1603
 Leu Arg Lys Glu Phe Asn Glu Lys Phe Ser Gly Asp Gly Gln Gly Glu
 490 495 500

gta acc ctt gct gaa ctg cgc gaa atc gca ctg aaa gcc gcc gaa aac 1651
 Val Thr Leu Ala Glu Leu Arg Glu Ile Ala Leu Lys Ala Ala Glu Asn
 505 510 515

gaa cca gtg gaa ttc acc ggc tgg caa tgg ttc aac tcc ttg ctc ggc 1699
 Glu Pro Val Glu Phe Thr Gly Ser Gln Trp Phe Asn Ser Leu Leu Gly
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 Gln Asp Ala Leu Arg Arg Ile Thr Ser Tyr Met Glu Glu Leu Ser Lys
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Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys Lys Pro Gln Val Ala	250	255	260	
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Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile Leu Thr Gly Ala Phe	265	270	275	
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Arg Arg Gly Lys Thr Leu Arg Asp Gly Asp Val Val Cys Ile Gly Glu
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Val Cys Ala Gln Val Ser Thr Gly Asp Ala Ala Asp Asp Asp Tyr Phe
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Asp Glu Ala Thr Ala Asn Asp Asp Phe Asp Pro Glu Lys Trp Arg Asn
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Met

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170 175 180

Figure 1. The effect of the concentration of the inhibitor on the rate of polymerization of α -methylstyrene in the presence of SnCl_4 at 25°C .

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 200 205 210

acc gtc cgc ggt gtt ggc tac aaa act ggc cac aac gat taagtgttttc 788
 Thr Val Arg Gly Val Gly Tyr Lys Thr Gly His Asn Asp
 215 220 225

atttaaaaaa ggg 801

<210> 120

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Met Ser Gln Lys Ile Leu Val Val Asp Asp Asp Pro Ala Ile Ser Glu
 1 5 10 15

Met Leu Thr Ile Val Leu Ser Ala Glu Gly Phe Asp Thr Val Ala Val
 20 25 30

Thr Asp Gly Ala Leu Ala Val Glu Thr Ala Ser Arg Glu Gln Pro Asp
 35 40 45

Leu Ile Leu Leu Asp Leu Met Leu Pro Gly Met Asn Gly Ile Asp Ile
 50 55 60

Cys Arg Leu Ile Arg Gln Glu Ser Ser Val Pro Ile Ile Met Leu Thr
 65 70 75 80

Ala Lys Thr Asp Thr Val Asp Val Val Leu Gly Leu Glu Ser Gly Ala
 85 90 95

Asp Asp Tyr Val Asn Lys Pro Phe Lys Ala Lys Glu Leu Val Ala Arg
 100 105 110

Ile Arg Ala Arg Leu Arg Ala Thr Val Asp Glu Pro Ser Glu Ile Ile
 115 120 125

Glu Val Gly Asp Leu Ser Ile Asp Val Pro Ala His Thr Val Lys Arg
 130 135 140

Asn Gly Ala Glu Ile Ser Leu Thr Pro Leu Glu Phe Asp Leu Leu Leu
 145 150 155 160

Glu Leu Ala Arg Lys Pro Gln Gln Val Phe Thr Arg Glu Glu Leu Leu
 165 170 175

Gly Lys Val Trp Gly Tyr Arg His Ala Ser Asp Thr Arg Leu Val Asn
 180 185 190

Val His Val Gln Arg Leu Arg Ala Lys Ile Glu Lys Asp Pro Glu Asn
 195 200 205

Pro Gln Ile Val Leu Thr Val Arg Gly Val Gly Tyr Lys Thr Gly His
 210 215 220

Asn Asp
 225

<210> 121
 <211> 1149
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1126)
 <223> RXA00885

<400> 121
 caacctggcg gtgaccgatg cgggacgttt gcttgccgac ggcatcatcg ccgacatttt 60
 gcttagtgaa gaagactaaa tatttagtag ggttacagac atg gtg agt gca aca 115
 Met Val Ser Ala Thr
 1 5
 gag aaa cgt aga tac gaa gtg ttg cgg gcc atc gtc gct gat tac att 163
 Glu Lys Arg Arg Tyr Glu Val Leu Arg Ala Ile Val Ala Asp Tyr Ile
 10 15 20
 gcg tct cag gaa cct gtc gga tcg aag tca ctc ctc gag cgc cat aag 211
 Ala Ser Gln Glu Pro Val Gly Ser Lys Ser Leu Leu Glu Arg His Lys
 25 30 35
 ctc aac gtg agt tct gcg acg atc cgc aac gat atg tcg gtg ctg gaa 259
 Leu Asn Val Ser Ser Ala Thr Ile Arg Asn Asp Met Ser Val Leu Glu
 40 45 50
 tcc gat ggc ttt atc gtc cag gag cat gca agt tct ggc cgg gta cca 307
 Ser Asp Gly Phe Ile Val Gln Glu His Ala Ser Ser Gly Arg Val Pro
 55 60 65
 acc gaa agg ggt tac cgc ctt ttt gtt gat tcc atc cat gac atc aaa 355
 Thr Glu Arg Gly Tyr Arg Leu Phe Val Asp Ser Ile His Asp Ile Lys
 70 75 80 85
 ccg ctg tcg ctg gcg gaa cgg cgc gct att ttg ggc ttc ctt gaa ggg 403
 Pro Leu Ser Leu Ala Glu Arg Arg Ala Ile Leu Gly Phe Leu Glu Gly
 90 95 100
 gga gtg gac tta gag gac gtg ctg cgc aga tct gtg cag ctg ttg tct 451
 Gly Val Asp Leu Glu Asp Val Leu Arg Arg Ser Val Gln Leu Leu Ser
 105 110 115
 cag ctc acc cat cag gct gcc gtg gtg cag ctg ccc acc ctg aaa aca 499
 Gln Leu Thr His Gln Ala Ala Val Val Gln Leu Pro Thr Leu Lys Thr
 120 125 130
 gcg cgc gtg aag cac tgc gag gtg gtg ccg ctg tcg ccg atg cgc ttg 547
 Ala Arg Val Lys His Cys Glu Val Val Pro Leu Ser Pro Met Arg Leu
 135 140 145
 ctg ctg gtg ctc att acc gat act ggc cgt gta gat cag cgc aac gtg 595

Leu Leu Val Leu Ile Thr Asp Thr Gly Arg Val Asp Gln Arg Asn Val
 150 155 160 165
 gaa ctt gag gaa cgc ctg gcg gcg gaa gaa gtt aat gtg ctg cgc gat 643
 Glu Leu Glu Glu Pro Leu Ala Ala Glu Glu Val Asn Val Leu Arg Asp
 170 175 180
 ctg ctc aac ggc gcg cta ggg gag aaa acg ctg acg gct gca tca gat 691
 Leu Leu Asn Gly Ala Leu Gly Glu Lys Thr Leu Thr Ala Ala Ser Asp
 185 190 195
 gcg ctg gaa gag ttg gct cag caa gcc cca acc gat att cgt gat gcc 739
 Ala Leu Glu Glu Leu Ala Gln Gln Ala Pro Thr Asp Ile Arg Asp Ala
 200 205 210
 atg cgc cgc tgc tgc gat gtg ctg gtg aac acg ctt gtc gat caa ccc 787
 Met Arg Arg Cys Cys Asp Val Leu Val Asn Thr Leu Val Asp Gln Pro
 215 220 225
 tct gac cgc ctg atc ctc gcc ggc acc tca aac ctc acc cgc tta agc 835
 Ser Asp Arg Leu Ile Leu Ala Gly Thr Ser Asn Leu Thr Arg Leu Ser
 230 235 240 245
 cgc gaa acc tcc ggc agc ctg ccc atg gtt tta gaa gcc ttg gaa gag 883
 Arg Glu Thr Ser Ala Ser Leu Pro Met Val Leu Glu Ala Leu Glu Glu
 250 255 260
 cag gtg gtc atg ttg aaa ctg ctg tcc aat gtc act gat ctt gac caa 931
 Gln Val Val Met Leu Lys Leu Leu Ser Asn Val Thr Asp Leu Asp Gln
 265 270 275
 gtg cgc gtg cat att ggc ggc gaa aat gaa gac att gag ctg cgc agc 979
 Val Arg Val His Ile Gly Gly Glu Asn Glu Asp Ile Glu Leu Arg Ser
 280 285 290
 gca acg gtg att acc acc ggt tac ggc tcc cag ggc agc gca ctg ggc 1027
 Ala Thr Val Ile Thr Thr Gly Tyr Gly Ser Gln Gly Ser Ala Leu Gly
 295 300 305
 gga ttg ggg gtg gtt ggc ccc acc tat atg gac tac tcg gga aca att 1075
 Gly Leu Gly Val Val Gly Pro Thr Tyr Met Asp Tyr Ser Gly Thr Ile
 310 315 320 325
 tct aag gtg tcc gcc gtt gct aag tat gtt ggt cgt gtg ctc gct ggc 1123
 Ser Lys Val Ser Ala Val Ala Lys Tyr Val Gly Arg Val Leu Ala Gly
 330 335 340
 gaa tagctgcggg tatagttgcc cat 1149
 Glu
 <210> 122
 <211> 342
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 122
 Met Val Ser Ala Thr Glu Lys Arg Arg Tyr Glu Val Leu Arg Ala Ile
 1 5 10 15

000000-123CP-153

Val Ala Asp Tyr Ile Ala Ser Gln Glu Pro Val Gly Ser Lys Ser Leu
 20 25 30

Leu Glu Arg His Lys Leu Asn Val Ser Ser Ala Thr Ile Arg Asn Asp
 35 40 45

Met Ser Val Leu Glu Ser Asp Gly Phe Ile Val Gln Glu His Ala Ser
 50 55 60

Ser Gly Arg Val Pro Thr Glu Arg Gly Tyr Arg Leu Phe Val Asp Ser
 65 70 75 80

Ile His Asp Ile Lys Pro Leu Ser Leu Ala Glu Arg Arg Ala Ile Leu
 85 90 95

Gly Phe Leu Glu Gly Gly Val Asp Leu Glu Asp Val Leu Arg Arg Ser
 100 105 110

Val Gln Leu Leu Ser Gln Leu Thr His Gln Ala Ala Val Val Gln Leu
 115 120 125

Pro Thr Leu Lys Thr Ala Arg Val Lys His Cys Glu Val Val Pro Leu
 130 135 140

Ser Pro Met Arg Leu Leu Leu Val Leu Ile Thr Asp Thr Gly Arg Val
 145 150 155 160

Asp Gln Arg Asn Val Glu Leu Glu Glu Pro Leu Ala Ala Glu Glu Val
 165 170 175

Asn Val Leu Arg Asp Leu Leu Asn Gly Ala Leu Gly Glu Lys Thr Leu
 180 185 190

Thr Ala Ala Ser Asp Ala Leu Glu Glu Leu Ala Gln Gln Ala Pro Thr
 195 200 205

Asp Ile Arg Asp Ala Met Arg Arg Cys Cys Asp Val Leu Val Asn Thr
 210 215 220

Leu Val Asp Gln Pro Ser Asp Arg Leu Ile Leu Ala Gly Thr Ser Asn
 225 230 235 240

Leu Thr Arg Leu Ser Arg Glu Thr Ser Ala Ser Leu Pro Met Val Leu
 245 250 255

Glu Ala Leu Glu Glu Gln Val Val Met Leu Lys Leu Ser Asn Val
 260 265 270

Thr Asp Leu Asp Gln Val Arg Val His Ile Gly Gly Glu Asn Glu Asp
 275 280 285

Ile Glu Leu Arg Ser Ala Thr Val Ile Thr Thr Gly Tyr Gly Ser Gln
 290 295 300

Gly Ser Ala Leu Gly Gly Leu Gly Val Val Gly Pro Thr Tyr Met Asp
 305 310 315 320

Tyr Ser Gly Thr Ile Ser Lys Val Ser Ala Val Ala Lys Tyr Val Gly
 325 330 335

Arg Val Leu Ala Gly Glu

340

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<210> 123
<211> 369
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(346)
<223> RXA01418
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400> 123	aacactcaaa tgatcatttg actattagcg aaagaaatta tcaatggagc atcaacctca	60
tctcctgaag ctgcgcgatg agtgggcgcc aacattcaaa	atg ctc ggc gat cgc	115
	Met Leu Gly Asp Arg	
	1 5	
acg cgc ctc cgc ctc ctc atc gcg ctg cat tat cac ggc ccc ggt gaa		163
Thr Arg Leu Arg Leu Leu Ile Ala Leu His Tyr His Gly Pro Gly Glu		
	10 15 20	
gcc acc gtc tca gaa ctc gcg gac atc gtc ggc gtc acc ctg ccc acg		211
Ala Thr Val Ser Glu Leu Ala Asp Ile Val Gly Val Thr Leu Pro Thr		
	25 30 35	
gcc tcc gca gcg ctc caa ctg ctc gca gat aac gga gtg gtc gag tcc		259
Ala Ser Ala Ala Leu Gln Leu Leu Ala Asp Asn Gly Val Val Glu Ser		
	40 45 50	
ttc aag gag ggg cgg gtg aca aga tat aag ctt gtc gac gcc acg acc		307
Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu Val Asp Ala Thr Thr		
	55 60 65	
cac acc ttg ctt cac cac ctc ggg ggc acc cac cga cat taaaggaac		356
His Thr Leu Leu His His Leu Gly Gly Thr His Arg His		
	70 75 80	
caaatagcgt tcg		369

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<210> 124
<211> 82
<212> PRT
<213> Corynebacterium glutamicum
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400> 124
Met Leu Gly Asp Arg Thr Arg Leu Arg Leu Ile Ala Leu His Tyr
1 5 10 15
His Gly Pro Gly Glu Ala Thr Val Ser Glu Leu Ala Asp Ile Val Gly
20 25 30
Val Thr Leu Pro Thr Ala Ser Ala Ala Leu Gln Leu Leu Ala Asp Asn
35 40 45
Gly Val Val Glu Ser Phe Lys Glu Gly Arg Val Thr Arg Tyr Lys Leu
50 55 60

Ile Pro Ala Val Lys Pro Leu Pro His Phe Glu His Arg Ile Ile Asp
 150 155 160 165
 tcc gaa cca gtc gtt atc gtc gaa tcc acc cag gac agc acc gac ccc 643
 Ser Glu Pro Val Val Ile Val Glu Ser Thr Gln Asp Ser Thr Asp Pro
 170 175 180
 ata gaa ctt cgc gag act cag cac gaa cgg ttc att ctg gta ccc gac 691
 Ile Glu Leu Arg Glu Thr Gln His Glu Pro Phe Ile Leu Val Pro Asp
 185 190 195
 aca tgc ggt tta acc act ttc acc aat caa ctg ttt gaa aca aat gac 739
 Thr Cys Gly Leu Thr Thr Phe Thr Asn Gln Leu Phe Glu Thr Asn Asp
 200 205 210
 ctg gca tta aac gcc tat tcc ggc gaa gca gcc agc tac caa gta ctc 787
 Leu Ala Leu Asn Ala Tyr Ser Gly Glu Ala Ala Ser Tyr Gln Val Leu
 215 220 225
 gaa cag tgg gcc aca ctt gga ctc gga tct gca atg ctt cca ctt tct 835
 Glu Gln Trp Ala Thr Leu Gly Leu Gly Ser Ala Met Leu Pro Leu Ser
 230 235 240 245
 aaa ctc agc tcc cct aca gca ccc cat tgaccactcc gcgaacaagg 882
 Lys Leu Ser Ser Pro Thr Ala Pro His
 250
 cct 885

 <210> 126
 <211> 254
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 126
 Met Thr Lys Arg Leu Ser Leu Glu Gly Leu Arg Tyr Ala Gln Ala Val
 1 5 10 15
 Ala Glu Thr His Ser Phe Ser Ala Ala Ala Arg Glu Tyr Gly Val Thr
 20 25 30
 Gln Pro Ala Leu Ser Asn Gly Ile Ala Lys Leu Glu Asp Arg Leu Gly
 35 40 45
 Glu Gln Leu Phe Asp Arg Ser Thr Gln Gly Val Thr Pro Thr Ser Phe
 50 55 60
 Gly Leu His Ile Leu Pro Leu Ile Gln Arg Ala Leu Thr Glu Ile Asp
 65 70 75 80
 Ala Ile Thr Ala Glu Ala His Arg Leu Ile Asn Ser Glu Ala Arg Ser
 85 90 95
 Ile Arg Val Gly Ile Ser Pro Leu Ile Asn Pro Gln Leu Val Ala Arg
 100 105 110
 Thr Tyr Thr Ala Val Arg Glu Leu Pro Thr Ala His Asp Leu Val Leu
 115 120 125
 Arg Glu Ala Asn Met Lys Glu Leu His Glu Gly Leu Leu Ala Gly Glu

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130 135 140

Leu Asn Val Ile Leu Ile Pro Ala Val Lys Pro Leu Pro His Phe Glu
145 150 155 160

His Arg Ile Ile Asp Ser Glu Pro Val Val Ile Val Glu Ser Thr Gln
165 170 175

Asp Ser Thr Asp Pro Ile Glu Leu Arg Glu Thr Gln His Glu Pro Phe
180 185 190

Ile Leu Val Pro Asp Thr Cys Gly Leu Thr Thr Phe Thr Asn Gln Leu
195 200 205

Phe Glu Thr Asn Asp Leu Ala Leu Asn Ala Tyr Ser Gly Glu Ala Ala
210 215 220

Ser Tyr Gln Val Leu Glu Gln Trp Ala Thr Leu Gly Leu Gly Ser Ala
225 230 235 240

Met Leu Pro Leu Ser Lys Leu Ser Ser Pro Thr Ala Pro His
245 250

<210> 127
<211> 843
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(820)
<223> RXN00363

<400> 127
tgaatttgat ggtgtgagtc atggtgggctc cttttgtgaa attcgatcca agcgggcttt 60

gagtaacatg ttaccgggta ctgtggtgaa ttgtgcgata atg tca gac atg cca 115
Met Ser Asp Met Pro
1 5

aca aaa agg gtt gcc ccc goa cgc tca ctc acc gac caa gtc atg gat 163
Thr Lys Arg Val Ala Pro Ala Arg Ser Leu Thr Asp Gln Val Met Asp
10 15 20

ttc gtc cgc gaa tcc acc ctt gat aaa aca atg gtc acc gga gag tgg 211
Phe Val Arg Glu Ser Thr Leu Asp Lys Thr Met Val Thr Gly Glu Trp
25 30 35

tac agc gtt tac cag gtc agc gac caa tta ggc att tcc cgc tcc ccc 259
Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly Ile Ser Arg Ser Pro
40 45 50

gtc aga gac gcg ctg ctc cgc ctg gaa gaa gca ggg ctc atc cgc ttc 307
Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala Gly Leu Ile Arg Phe
55 60 65

acc agg aac cgc gga ttc caa att gtc gaa acc aaa ccc tct gat gtc 355
Thr Arg Asn Arg Gly Phe Gln Ile Val Glu Thr Lys Pro Ser Asp Val
70 75 80 85

gcc gaa att ttt gcc ctt cgt cta gcc att gaa ccc gcc gca gca tac 403
 Ala Glu Ile Phe Ala Leu Arg Leu Gly Ile Glu Pro Ala Ala Ala Tyr
 90 95 100

cgg gca gca cag cta cgc acc gaa gaa cag ctc cac gaa gca gat gac 451
 Arg Ala Ala Gln Leu Arg Thr Glu Glu Gln Leu His Glu Ala Asp Asp
 105 110 115

atc att gca ctc atg cgc caa gcc gag gcc gac aat gac gaa gaa gca 499
 Ile Ile Ala Leu Met Ala Gln Ala Glu Ala Asp Asn Asp Glu Glu Ala
 120 125 130

ttt ttc acc cat gac cgg cag ttt cac cga caa att atg acc atg gga 547
 Phe Phe Thr His Asp Arg Gln Phe His Arg Gln Ile Met Thr Met Gly
 135 140 145

cac tcc caa cgc ggg gct gac ctg gta gaa aaa cta cgc gca cac acc 595
 His Ser Gln Arg Gly Ala Asp Leu Val Glu Lys Leu Arg Ala His Thr
 150 155 160 165

cgt atc ctc ggt gct tct act gcc ggg aac aaa cgc acc ctt ggc gat 643
 Arg Ile Leu Gly Ala Ser Thr Ala Gly Asn Lys Arg Thr Leu Gly Asp
 170 175 180

att ttg gaa gaa cac gaa cca atc ttg gat gcc atc aaa cga caa tca 691
 Ile Leu Glu Glu His Glu Pro Ile Leu Asp Ala Ile Lys Arg Gln Ser
 185 190 195

gca gaa atg gca cga gcc acc atg cgg gag cat atc caa gtc acc gga 739
 Ala Glu Met Ala Arg Ala Thr Met Arg Glu His Ile Gln Val Thr Gly
 200 205 210

aag cta cta cta gaa caa gca gtg gaa aaa tcc gcc gaa gga gct gct 787
 Lys Leu Leu Leu Glu Gln Ala Val Glu Lys Ser Gly Glu Gly Ala Ala
 215 220 225

cag aag att tgg gat cag tac acg cgc gga gtt taggcatatt tacctaata 840
 Gln Lys Ile Trp Asp Gln Tyr Thr Ala Gly Val
 230 235 240

att 843

<210> 128

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Met Ser Asp Met Pro Thr Lys Arg Val Ala Pro Ala Arg Ser Leu Thr
 1 5 10 15

Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu Asp Lys Thr Met
 20 25 30

Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser Asp Gln Leu Gly
 35 40 45

Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg Leu Glu Glu Ala
 50 55 60


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>400> 130
Arg Ser Leu Thr Asp Gln Val Met Asp Phe Val Arg Glu Ser Thr Leu
      1          5          10          15
Asp Lys Thr Met Val Thr Gly Glu Trp Tyr Ser Val Tyr Gln Val Ser
      20          25          30
Asp Gln Leu Gly Ile Ser Arg Ser Pro Val Arg Asp Ala Leu Leu Arg

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[illegible]

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<210> 131
<211> 843
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(820)  
<223> RXA00516
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c400> 131
aagcaaaaaa ttgcttgtag acgtctcccc caacctagca tccactttct gcaaccagtt 60
gtcacaaaaa gtctaaattt cgggtgtacta aggtgtgttc atg gtc caa aaa gat 115
                                         Met Val Gln Lys Asp
                                         1           5
gcc cag gcc tcc cct gct acg aga aaa gca gat cag gta tac aca cag 163
Ala Gln Ala Ser Pro Ala Thr Arg Lys Ala Asp Gln Val Tyr Thr Gln
                        10                15                20
att cgt cgt gaa atc gaa gat gga acc tta aat cct ggg caa cga atg 211

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[illegible]

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<210> 132
<211> 240
<212> PRT
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<223> RXA01537

[illegible]

<400> 133
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aagtgcctag gtgtgtcccc agtcctttaa gatcagtcac atg acg cag gca ata 115
 Met Thr Gln Ala Ile
 1 5

gca gca tcc ctt gat tta gcg gct cga atc acc gcc aaa att gat caa 163
 Ala Ala Ser Leu Asp Leu Ala Ala Arg Ile Thr Ala Lys Ile Asp Gln
 10 15 20

gga gtg ctc act cca ggt act cga cta ccc gag gtt gct ttg gca gaa 211
 Gly Val Leu Thr Pro Gly Thr Arg Leu Pro Glu Val Ala Leu Ala Glu
 25 30 35

gaa ctt ggc gtt tca cgg aac acg ctg cgt gaa gct ttt cgg gta ctc 259
 Glu Leu Gly Val Ser Arg Asn Thr Leu Arg Glu Ala Phe Arg Val Leu
 40 45 50

atg caa gac gga ctg gtg gat cat att ccc aac cgt ggg gtt ttc gtg 307
 Met Gln Asp Gly Leu Val Asp His Ile Pro Asn Arg Gly Val Phe Val
 55 60 65

cac acg ttc acc aag tcg gat gtg gaa gat atc tat gct tac cgc aca 355
 His Thr Phe Thr Lys Ser Asp Val Glu Asp Ile Tyr Ala Tyr Arg Thr
 70 75 80 85

ttt atc gag gtt gct gcg att agg tcg gcg cgg aaa aat cct cag ttg 403
 Phe Ile Glu Val Ala Ala Ile Arg Ser Ala Arg Lys Asn Pro Gln Leu
 90 95 100

ctg gag cag tct ttg ggg gta atg cga gag gcc tac gaa agg ggt gct 451
 Leu Glu Gln Ser Leu Gly Val Met Arg Glu Ala Tyr Glu Arg Gly Ala
 105 110 115

gca gcc aat gcc gtg ggt gat tgg caa act gtc ggt tct gcc aac agt 499
 Ala Ala Asn Ala Val Gly Asp Trp Gln Thr Val Gly Ser Ala Asn Ser
 120 125 130

gct ttt cac ttg gcg att gtg gac cta gca gga gtg gct agg ttg tca 547
 Ala Phe His Leu Ala Ile Val Asp Leu Ala Gly Val Ala Arg Leu Ser
 135 140 145

gca gac gct cga aaa gtg ttg gcg ctg gct cgc atc gga ttc atg gcc 595
 Ala Asp Ala Arg Lys Val Leu Ala Leu Ala Arg Ile Gly Phe Met Ala
 150 155 160 165

acc tac aac gtg gag aca ttc cat agc att tac gtg gaa aag aac cat 643
 Thr Tyr Asn Val Glu Thr Phe His Ser Ile Tyr Val Glu Lys Asn His
 170 175 180

caa atc ttg aag tat ttg gct gcc ggt gaa ttc gaa gag gcg gaa caa 691
 Gln Ile Leu Lys Tyr Leu Ala Ala Gly Glu Phe Glu Glu Ala Glu Gln
 185 190 195

tac ctc cag aaa tac ttc gaa gat tcg cgc gat gat ttg tct gcg cac 739
 Tyr Leu Gln Lys Tyr Phe Glu Asp Ser Arg Asp Asp Leu Ser Ala His
 200 205 210

cta ccg gaa ttt tgaaattgcy atagcataga tga 774

Leu Pro Glu Phe
215

<210> 134
<211> 217
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 134
Met Thr Gln Ala Ile Ala Ala Ser Leu Asp Leu Ala Ala Arg Ile Thr
1 5 10 15
Ala Lys Ile Asp Gln Gly Val Leu Thr Pro Gly Thr Arg Leu Pro Glu
20 25 30
Val Ala Leu Ala Glu Glu Leu Gly Val Ser Arg Asn Thr Leu Arg Glu
35 40 45
Ala Phe Arg Val Leu Met Gln Asp Gly Leu Val Asp His Ile Pro Asn
50 55 60
Arg Gly Val Phe Val His Thr Phe Thr Lys Ser Asp Val Glu Asp Ile
65 70 75 80
Tyr Ala Tyr Arg Thr Phe Ile Glu Val Ala Ala Ile Arg Ser Ala Arg
85 90 95
Lys Asn Pro Gln Leu Leu Glu Gln Ser Leu Gly Val Met Arg Glu Ala
100 105 110
Tyr Glu Arg Gly Ala Ala Ala Asn Ala Val Gly Asp Trp Gln Thr Val
115 120 125
Gly Ser Ala Asn Ser Ala Phe His Leu Ala Ile Val Asp Leu Ala Gly
130 135 140
Val Ala Arg Leu Ser Ala Asp Ala Arg Lys Val Leu Ala Leu Ala Arg
145 150 155 160
Ile Gly Phe Met Ala Thr Tyr Asn Val Glu Thr Phe His Ser Ile Tyr
165 170 175
Val Glu Lys Asn His Gln Ile Leu Lys Tyr Leu Ala Ala Gly Glu Phe
180 185 190
Glu Glu Ala Glu Gln Tyr Leu Gln Lys Tyr Phe Glu Asp Ser Arg Asp
195 200 205
Asp Leu Ser Ala His Leu Pro Glu Phe
210 215

<210> 135
<211> 819
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(796)

<223> RXA02494

<400> 135

cagagtcctcaa ggaaccggca ggaatctaagc agggacctag ttggattca cctattcgta 60

cgactgcgtc caaagcatct gggcgccgaa aggaaaaatc atg acg aga atc ctg 115
 Met Thr Arg Ile Leu
 1 5

atc gtt gaa gat gag gaa tcg tta gca gat cct ttg gcc ttt ctt ctt 163
 Ile Val Glu Asp Glu Glu Ser Leu Ala Asp Pro Leu Ala Phe Leu Leu
 10 15 20

cgc aaa gaa ggt ttt gac acc atc atc gcc ggt gat ggc cca acc gca 211
 Arg Lys Glu Gly Phe Asp Thr Ile Ile Ala Gly Asp Gly Pro Thr Ala
 25 30 35

ctt gtg gag ttc agt cgc aac gaa atc gac atc gtc ctc tta gac ctc 259
 Leu Val Glu Phe Ser Arg Asn Glu Ile Asp Ile Val Leu Leu Asp Leu
 40 45 50

atg ctc cca ggc atg tct ggc acc gac gta tgc aaa gaa ctc cgc agc 307
 Met Leu Pro Gly Met Ser Gly Thr Asp Val Cys Lys Glu Leu Arg Ser
 55 60 65

gta tcc act gtt ccc gtc atc atg gtc acc gcc cgc gac tcc gag atc 355
 Val Ser Thr Val Pro Val Ile Met Val Thr Ala Arg Asp Ser Glu Ile
 70 75 80 85

gac aaa gtt gtt ggc ctc gaa ctc ggc gcc gat gat tat gta acc aag 403
 Asp Lys Val Val Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys
 90 95 100

cca tat tct tcc cgc gaa ctc atc gcc cgc atc cgc gct gtc ctg cgc 451
 Pro Tyr Ser Ser Arg Glu Leu Ile Ala Arg Ile Arg Ala Val Leu Arg
 105 110 115

cga cgc gga gtt act gaa acc gaa gcc gaa gaa tta cca ctt gac gat 499
 Arg Arg Gly Val Thr Glu Thr Glu Ala Glu Glu Leu Pro Leu Asp Asp
 120 125 130

caa atc ctc gaa ggc ggc cgc gtc cgc atg gac gtc gat tcc cac acc 547
 Gln Ile Leu Glu Gly Gly Arg Val Arg Met Asp Val Asp Ser His Thr
 135 140 145

gtc acc gtc ggt ggc gaa cca gtg agc atg cca ctg aag gaa ttc gac 595
 Val Thr Val Gly Gly Glu Pro Val Ser Met Pro Leu Lys Glu Phe Asp
 150 155 160 165

ctt ctg gag tac ctc ctc cga aac gcc gcc cga gtc ctc acc cgc gga 643
 Leu Leu Glu Tyr Leu Leu Arg Asn Ala Gly Arg Val Leu Thr Arg Gly
 170 175 180

cag ctc atc gac cga att tgg ggc gca gat tac gtc ggc gac acc aaa 691
 Gln Leu Ile Asp Arg Ile Trp Gly Ala Asp Tyr Val Gly Asp Thr Lys
 185 190 195

acc ctc gac gtt cat gtc aaa agg ttg cgt tcc aag atc gaa gaa gag 739
 Thr Leu Asp Val His Val Lys Arg Leu Arg Ser Lys Ile Glu Glu Glu
 200 205 210

CCDS:123CP

cca tct cgc cct cgt tac ctc gtg acc gtg cgt gga ttg ggc tac aaa 787
Pro Ser Arg Pro Arg Tyr Leu Val Thr Val Arg Gly Leu Gly Tyr Lys
215 220 225

ttc gag ctg tagggctctg ttaggccctg ttg 819
Phe Glu Leu
230

<210> 136

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met Thr Arg Ile Leu Ile Val Glu Asp Glu Glu Ser Leu Ala Asp Pro
1 5 10 15

Leu Ala Phe Leu Leu Arg Lys Glu Gly Phe Asp Thr Ile Ile Ala Gly
20 25 30

Asp Gly Pro Thr Ala Leu Val Glu Phe Ser Arg Asn Glu Ile Asp Ile
35 40 45

Val Leu Leu Asp Leu Met Leu Pro Gly Met Ser Gly Thr Asp Val Cys
50 55 60

Lys Glu Leu Arg Ser Val Ser Thr Val Pro Val Ile Met Val Thr Ala
65 70 75 80

Arg Asp Ser Glu Ile Asp Lys Val Val Gly Leu Glu Leu Gly Ala Asp
85 90 95

Asp Tyr Val Thr Lys Pro Tyr Ser Ser Arg Glu Leu Ile Ala Arg Ile
100 105 110

Arg Ala Val Leu Arg Arg Arg Gly Val Thr Glu Thr Glu Ala Glu Glu
115 120 125

Leu Pro Leu Asp Asp Gln Ile Leu Glu Gly Gly Arg Val Arg Met Asp
130 135 140

Val	Asp	Ser	His	Thr	Val	Thr	Val	Gly	Gly	Glu	Pro	Val	Ser	Met	Pro
145					150					155					160

Leu Lys Glu Phe Asp Leu Leu Glu Tyr Leu Leu Arg Asn Ala Gly Arg
165 170 175

Val Leu Thr Arg Gly Gln Leu Ile Asp Arg Ile Trp Gly Ala Asp Tyr
180 185 190

Val Gly Asp Thr Lys Thr Leu Asp Val His Val Lys Arg Leu Arg Ser
195 200 205

Lys Ile Glu Glu Glu Pro Ser Arg Pro Arg Tyr Leu Val Thr Val Arg
210 215 220

Gly Leu Gly Tyr Lys Phe Glu Leu
225 230

<210> 137
 <211> 660
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(637)
 <223> RXA00029

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<400> 137
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ttgcogtgcg ccaggtgagg accgagagggc caaacgcatt ttg gcc cag gcc acc 115
                Leu Ala Gln Ala Thr
                1                    5

gcc caa cta atc gct gat gat gaa gca gta att ttc gac aac ggc acc 163
Ala Gln Leu Ile Ala Asp Asp Glu Ala Val Ile Phe Asp Asn Gly Thr
                10                    15                    20

acc tgc cag gca gtg gcc caa gag ttg gcg ggg cgt ccc atc acg gca 211
Thr Cys Gln Ala Val Ala Gln Glu Leu Ala Gly Arg Pro Ile Thr Ala
                25                    30                    35

ttg tgt ctg tct cta cat tcg gcg gtc gcc ctg gga agc cga gct ggc 259
Leu Cys Leu Ser Leu His Ser Ala Val Ala Leu Gly Ser Arg Ala Gly
                40                    45                    50

acc aac gtt ttc atc ccc ggc ggc ccc gtg gaa aac gac tca ctc gcc 307
Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu Asn Asp Ser Leu Ala
                55                    60                    65

tta tct ggc ccg gct gtg atc acc gcg tta cga gat ttc tcc gcc gat 355
Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg Asp Phe Ser Ala Asp
                70                    75                    80                    85

gtc gtg atc ctc ggt tcc tgc tct aca tca ctg gag cac ggg ttg gcc 403
Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu Glu His Gly Leu Ala
                90                    95                    100

acc act acc tac gac gat gcg gaa aac aag cgc gca gcc atc cat gct 451
Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg Ala Ala Ile His Ala
                105                    110                    115

gcc acc cga cga atc ctt gtg gtg tcc gcc cgt aaa ctc aac cac gtt 499
Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg Lys Leu Asn His Val
                120                    125                    130

tcc act ttc cgt ttc gca gac gtc gcg gac tta cac cag ctg gtc aca 547
Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu His Gln Leu Val Thr
                135                    140                    145

acc tcc gat gcg cca cgg gag att ctc gcc gag atc cgg gat ctc ggc 595
Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu Ile Arg Asp Leu Gly
                150                    155                    160                    165

gtg cag gtt att act gtt ccc gcc cct gac gag caa cga agt 637
Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu Gln Arg Ser
                170                    175

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002250 12320000

taactcttca tggttgctga gca

660

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<210> 138
<211> 179
<212> PRT
<213> Corynebacterium glutamicum
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4A00> 138
Leu Ala Gln Ala Thr Ala Gln Leu Ile Ala Asp Asp Glu Ala Val Ile
  1              5              10              15
Phe Asp Asn Gly Thr Thr Cys Gln Ala Val Ala Gln Glu Leu Ala Gly
              20              25              30
Arg Pro Ile Thr Ala Leu Cys Leu Ser Leu His Ser Ala Val Ala Leu
              35              40              45
Gly Ser Arg Ala Gly Thr Asn Val Phe Ile Pro Gly Gly Pro Val Glu
  50              55              60
Asn Asp Ser Leu Ala Leu Ser Gly Pro Ala Val Ile Thr Ala Leu Arg
  65              70              75              80
Asp Phe Ser Ala Asp Val Val Ile Leu Gly Ser Cys Ser Thr Ser Leu
              85              90              95
Glu His Gly Leu Ala Thr Thr Thr Tyr Asp Asp Ala Glu Asn Lys Arg
              100              105              110
Ala Ala Ile His Ala Ala Thr Arg Arg Ile Leu Val Val Ser Ala Arg
              115              120              125
Lys Leu Asn His Val Ser Thr Phe Arg Phe Ala Asp Val Ala Asp Leu
              130              135              140
His Gln Leu Val Thr Thr Ser Asp Ala Pro Arg Glu Ile Leu Ala Glu
              145              150              155              160
Ile Arg Asp Leu Gly Val Gln Val Ile Thr Val Pro Ala Pro Asp Glu
              165              170              175
Gln Arg Ser

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<210> 139
<211> 762
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(739)
<223> RXA00655
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ttgcctgtgg attaaaacta tacgaacogg ttgtgtctata ttggtgttag acagttcgtc 60
gtatcttgaa acagaccaac ccgaagagac gtggccgaac gta gct gct agc gct 115
Val Ala Ala Ser Ala

1

5

tca ggc aag agt aaa aca agt gcc ggg gca aac cgt cgt cgc aat cga 163
 Ser Gly Lys Ser Lys Thr Ser Ala Gly Ala Asn Arg Arg Arg Asn Arg
 10 15 20

cca agc ccc cga cag cgt ctc ctc gat agc gca acc aac ctt ttc acc 211
 Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala Thr Asn Leu Phe Thr
 25 30 35

aca gaa ggt att cgc gtc atc ggt att gat cgt atc ctc cgt gaa gct 259
 Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg Ile Leu Arg Glu Ala
 40 45 50

gac gtg gcg aag gcg agc ctc tat tcc ctt ttc gga tgc aag gac gcc 307
 Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe Gly Ser Lys Asp Ala
 55 60 65

ttg gtt att gca tac ctg gag aac ctc gat cag ctg tgg cgt gaa gcg 355
 Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln Leu Trp Arg Glu Ala
 70 75 80 85

tgg cgt gag cgc acc gtc ggt atg aag gat ccg gaa gat aaa atc atc 403
 Trp Arg Glu Arg Thr Val Gly Met Lys Asp Pro Glu Asp Lys Ile Ile
 90 95 100

gcg ttc ttt gat cag tgc att gag gaa gaa cca gaa aaa gat ttc cgc 451
 Ala Phe Phe Asp Gln Cys Ile Glu Glu Glu Pro Glu Lys Asp Phe Arg
 105 110 115

ggc tgc cac ttt cag aat gcg gct agt gag tac cct cgc ccc gaa act 499
 Gly Ser His Phe Gln Asn Ala Ala Ser Glu Tyr Pro Arg Pro Glu Thr
 120 125 130

gat agc gaa aag ggc att gtt gca gca gtg tta gag cac cgc gag tgg 547
 Asp Ser Glu Lys Gly Ile Val Ala Ala Val Leu Glu His Arg Glu Trp
 135 140 145

tgt cat aag act ctg act gat ttg ctc act gag aag aac ggc tac cca 595
 Cys His Lys Thr Leu Thr Asp Leu Leu Thr Glu Lys Asn Gly Tyr Pro
 150 155 160 165

ggc acc acc cag gcg aat cag ctg ttg gtg ttc ctt gat ggt gga ctt 643
 Gly Thr Thr Gln Ala Asn Gln Leu Leu Val Phe Leu Asp Gly Gly Leu
 170 175 180

gct gga tct cga ttg gtc cac aac atc agt cct ctt gag acg gct cgc 691
 Ala Gly Ser Arg Leu Val His Asn Ile Ser Pro Leu Glu Thr Ala Arg
 185 190 195

gat ttg gct cgg cag ttg ttg tgc gct cca cct gcg gac tac tca att 739
 Asp Leu Ala Arg Gln Leu Leu Ser Ala Pro Pro Ala Asp Tyr Ser Ile
 200 205 210

tagttttcttc attttccgaa ggg 762

<210> 140

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

0505074-050300

4000> 140
Val Ala Ala Ser Ala Ser Gly Lys Ser Lys Thr Ser Ala Gly Ala Asn
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Arg Arg Arg Asn Arg Pro Ser Pro Arg Gln Arg Leu Leu Asp Ser Ala
20 25 30
Thr Asn Leu Phe Thr Thr Glu Gly Ile Arg Val Ile Gly Ile Asp Arg
35 40 45
Ile Leu Arg Glu Ala Asp Val Ala Lys Ala Ser Leu Tyr Ser Leu Phe
50 55 60
Gly Ser Lys Asp Ala Leu Val Ile Ala Tyr Leu Glu Asn Leu Asp Gln
65 70 75 80
Leu Trp Arg Glu Ala Trp Arg Glu Arg Thr Val Gly Met Lys Asp Pro
85 90 95
Glu Asp Lys Ile Ile Ala Phe Phe Asp Gln Cys Ile Glu Glu Glu Pro
100 105 110
Glu Lys Asp Phe Arg Gly Ser His Phe Gln Asn Ala Ala Ser Glu Tyr
115 120 125
Pro Arg Pro Glu Thr Asp Ser Glu Lys Gly Ile Val Ala Ala Val Leu
130 135 140
Glu His Arg Glu Trp Cys His Lys Thr Leu Thr Asp Leu Leu Thr Glu
145 150 155 160
Lys Asn Gly Tyr Pro Gly Thr Thr Gln Ala Asn Gln Leu Leu Val Phe
165 170 175
Leu Asp Gly Gly Leu Ala Gly Ser Arg Leu Val His Asn Ile Ser Pro
180 185 190
Leu Glu Thr Ala Arg Asp Leu Ala Arg Gln Leu Leu Ser Ala Pro Pro
195 200 205
Ala Asp Tyr Ser Ile
210

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<210> 141
<211> 2538
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(2515)
<223> BXN03136
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taaaaatccc cgaaactcc ttggacacat cgcccacaaa ttg ggt gcg cac tcc 115
                Leu Gly Ala His Ser
                1             5

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gcc aac tcc atc cgt ggt gtg atc gac cgt ctc gat gcc tcc acc gtg 163
 Ala Asn Ser Ile Arg Gly Val Ile Asp Arg Leu Asp Ala Ser Thr Val
 10 15 20

gtg atc gtt gcc gat gtc cac tgg gcc gac gtg gaa tcc atg caa aaa 211
 Val Ile Val Ala Asp Val His Trp Ala Asp Val Glu Ser Met Gln Lys
 25 30 35

ctc atc gaa tat tcc atg cgc atg gtt tct ggc cgt ttc gca ctc atc 259
 Leu Ile Glu Tyr Ser Met Arg Met Val Ser Gly Arg Phe Ala Leu Ile
 40 45 50

atg att ggc ctt gat gaa gag aac tta gtg ttc cac gat gag gtg gtc 307
 Met Ile Gly Leu Asp Glu Asn Leu Val Phe His Asp Glu Val Val
 55 60 65

tcg ctc ccc tcc atc gca gac tcc acc tac gta ttg ccg ccg atg agt 355
 Ser Leu Pro Ser Ile Ala Asp Ser Thr Tyr Val Leu Pro Pro Met Ser
 70 75 80 85

att gaa gaa atc cgc cag ctt ccg ctt acc gat gtc cgc ggc cgc atc 403
 Ile Glu Glu Ile Arg Gln Leu Ala Leu Thr Asp Val Arg Gly Arg Ile
 90 95 100

agc acc acc acc gcc aca gac atc cag cgc atc acc ggc ggc atc tac 451
 Ser Thr Thr Thr Ala Thr Asp Ile Gln Arg Ile Thr Gly Gly Ile Tyr
 105 110 115

ggg cga gtc aaa gaa gtc ctc cac tcg gaa tcc ccc gat cac tgg cga 499
 Gly Arg Val Lys Glu Val Leu His Ser Glu Ser Pro Asp His Trp Arg
 120 125 130

atg ccc aac cca aat att ccc atc cca caa agc tgg cat gcc aac ctg 547
 Met Pro Asn Pro Asn Ile Pro Ile Pro Gln Ser Trp His Ala Asn Leu
 135 140 145

ttg aga cgc atc acc aac gaa gaa gtc tgg cat gta cta ctc gcc gtc 595
 Leu Arg Arg Ile Thr Asn Glu Glu Val Trp His Val Leu Leu Ala Val
 150 155 160 165

gct gtc ctt ccc tcc gga ggc ccc att gac ctg gta aaa ctc ata ggc 643
 Ala Val Leu Pro Ser Gly Gly Pro Ile Asp Leu Val Lys Leu Ile Gly
 170 175 180

aac gac ccc acg ggc atg ctt tgc gac gac gcc gtc cgc tca ggc ctg 691
 Asn Asp Pro Thr Gly Met Leu Cys Asp Asp Ala Val Arg Ser Gly Leu
 185 190 195

ctc cgc gtg ctg ccg tct gac ggc caa cca caa gtg gat ttg gtc ctg 739
 Leu Arg Val Leu Pro Ser Asp Gly Gln Pro Gln Val Asp Leu Val Leu
 200 205 210

ccg atc gac cgc gcc gta ctg caa tca cgc act ccg ctc aac att ctg 787
 Pro Ile Asp Arg Ala Val Leu Gln Ser Arg Thr Pro Leu Asn Ile Leu
 215 220 225

gcg cag ttg cac cac aag gca gcc gaa tat tac gcc aag tgg aat caa 835
 Ala Gln Leu His His Lys Ala Ala Glu Tyr Tyr Gly Lys Trp Asn Gln
 230 235 240 245

aaa gat gcc caa ctg gag cac gaa gca ttt gct gca att gat cca aat 883
 Lys Asp Ala Gln Leu Glu His Glu Ala Phe Ala Ala Ile Asp Pro Asn
 250 255 260

gat cca gca gtg cga gcc cta gcg cag cgc gga tat gcg ttg ggt agg 931
 Asp Pro Ala Val Arg Ala Leu Ala Gln Arg Gly Tyr Ala Leu Gly Arg
 265 270 275

act ggc cac tgg atg gaa tcg gca cac gcc cta tct ctt gcc gcg aac 979
 Thr Gly His Trp Met Glu Ser Ala His Ala Leu Ser Leu Ala Ala Asn
 280 285 290

cgc act gca cac caa gaa gaa tca aat aag tac ttg ctg gag tcc atc 1027
 Arg Thr Ala His Gln Glu Ser Asn Lys Tyr Leu Leu Glu Ser Ile
 295 300 305

gat tca ctg atc gcc gcc gcc gat ctc ccc caa gct cga tcc aga gca 1075
 Asp Ser Leu Ile Ala Ala Ala Asp Leu Pro Gln Ala Arg Ser Arg Ala
 310 315 320 325

tcc acc ctt gat ctt gga gaa acc ggc att caa caa gac tca atg ctg 1123
 Ser Thr Leu Asp Leu Gly Glu Thr Gly Ile Gln Gln Asp Ser Met Leu
 330 335 340

ggc tac ctg gca atc cac gaa ggc cgg cgc ctc gaa gca cgc aat ctc 1171
 Gly Tyr Leu Ala Ile His Glu Gly Arg Arg Leu Glu Ala Arg Asn Leu
 345 350 355

ctt cat cgt gct tct gaa gaa ttg ctg gcg cag cac cgg att gat cgg 1219
 Leu His Arg Ala Ser Glu Glu Leu Leu Ala Gln His Pro Ile Asp Pro
 360 365 370

atc cac ggc ccc cgc atg gct cag cgc aaa gta ctg tta aac tta gtg 1267
 Ile His Gly Pro Arg Met Ala Gln Arg Lys Val Leu Leu Asn Leu Val
 375 380 385

gac tgg aat cca gaa gaa ctc ctg gtg tgg gct gat aga gca gtc gca 1315
 Asp Trp Asn Pro Glu Glu Leu Leu Val Trp Ala Asp Arg Ala Val Ala
 390 395 400 405

tgg act gaa gag gat gct ggc gaa aag gtt gag gcc caa gct att tcc 1363
 Trp Thr Glu Glu Asp Ala Gly Glu Lys Val Glu Ala Gln Ala Ile Ser
 410 415 420

ctc att gga caa tcc atc ctc gat ggc tgc ctc ccc gaa gat aaa ccc 1411
 Leu Ile Gly Gln Ser Ile Leu Asp Gly Cys Leu Pro Glu Asp Lys Pro
 425 430 435

atc ccc ggt gaa acc acc ctt cac gca caa cgc cgc cac atg gca atg 1459
 Ile Pro Gly Glu Thr Thr Leu His Ala Gln Arg Arg His Met Ala Met
 440 445 450

ggc tgg ctt tcc atg gtt cac gat gat cca gta act gca cgt caa aag 1507
 Gly Trp Leu Ser Met Val His Asp Asp Pro Val Thr Ala Arg Gln Lys
 455 460 465

ctt gaa cgt cgc aca tcc atc aat ggt tca gaa cgc atc agt ttg tgg 1555
 Leu Glu Arg Arg Thr Ser Ile Asn Gly Ser Glu Arg Ile Ser Leu Trp
 470 475 480 485

caa gac gga tgg ctg gct cgg tcc cta ctg ctg ctc ggc gaa tgg gag 1603

Gln Asp Gly Trp Leu Ala Arg Ser Leu Leu Leu Leu Gly Glu Trp Glu
 490 495 500

tcc gca gca cgc acc gta gaa atc ggt ctg gcc cgc gcc gaa cag ttt 1651
 Ser Ala Ala Arg Thr Val Glu Ile Gly Leu Ala Arg Ala Glu Gln Phe
 505 510 515

ggc atc cgc ttc ctc gaa cca ctg tta ctg tgg tgc ggc gcc aca att 1699
 Gly Ile Arg Phe Leu Glu Pro Leu Leu Leu Trp Ser Gly Ala Thr Ile
 520 525 530

gca aca gcc cgc gga aac tct gac ttg gca cga aat tac atg agc aga 1747
 Ala Thr Ala Arg Gly Asn Ser Asp Leu Ala Arg Asn Tyr Met Ser Arg
 535 540 545

ctg tcc acc gat caa gac tcc ttc atc gtc caa tct atg cca tct gcg 1795
 Leu Ser Thr Asp Gln Asp Ser Phe Ile Val Gln Ser Met Pro Ser Ala
 550 555 560 565

atg tgt cgc atg tgg gtc cac cgc cat aga aat gaa atc ccc ggt gcg 1843
 Met Cys Arg Met Trp Val His Arg His Arg Asn Glu Ile Pro Gly Ala
 570 575 580

atc gtg gcc gga gaa caa ttg gaa aaa atc gcc gca cac aaa cac gtc 1891
 Ile Val Ala Gly Glu Gln Leu Glu Lys Ile Ala Ala His Lys His Val
 585 590 595

aac gca cct gga ttc tgg cca tgg caa gac gtc cac gca acg cat ctc 1939
 Asn Ala Pro Gly Phe Trp Pro Trp Gln Asp Val His Ala Thr His Leu
 600 605 610

atc cgc atc ggc gaa act gag cgc gcc cag gag tta gtg aac tcc acg 1987
 Ile Arg Ile Gly Glu Thr Glu Arg Ala Gln Glu Val Asn Ser Thr
 615 620 625

ctt gag gag ctc aga ggc tcc gat atc atg tct gcc cac gca aaa att 2035
 Leu Glu Glu Leu Arg Gly Ser Asp Ile Met Ser Ala His Ala Lys Ile
 630 635 640 645

gcc gtt ccc gac gcc atg ttg atg atc cac cac gga gat gtg aaa aag 2083
 Ala Val Pro Asp Ala Met Leu Met Ile His His Gly Asp Val Lys Lys
 650 655 660

gga ttt aag cgt ttc gac gac gcc ctc gat atg atc gat ccc ctc acc 2131
 Gly Phe Lys Arg Phe Asp Asp Ala Leu Asp Met Ile Asp Pro Leu Thr
 665 670 675

ctc ccc tac tat cgg gca cgc atc tgc ttt gaa tac ggc cag gcc ctg 2179
 Leu Pro Tyr Trp Arg Ala Arg Ile Cys Phe Glu Tyr Gly Gln Ala Leu
 680 685 690

aga cgc cag ggg caa cgt cga cgt gct gat gaa caa ttt gcc cgt gca 2227
 Arg Arg Gln Gly Gln Arg Arg Arg Ala Asp Glu Gln Phe Ala Arg Ala
 695 700 705

gct tcc cta ttc caa gac atg ggc gcc gac gcg atg gtc acc cta gcc 2275
 Ala Ser Leu Phe Gln Asp Met Gly Ala Asp Ala Met Val Thr Leu Ala
 710 715 720 725

aac cga gaa cgc cgg gtg ggt gcc ctt ggt caa cga tcc gag caa gcc 2323
 Asn Arg Glu Arg Arg Val Gly Gly Leu Gly Gln Arg Ser Glu Gln Ala

00602874-052300

730										735					740					
ggt	ggg	ctc	acc	cct	cag	gaa	tat	gaa	att	gcc	cga	tta	gtg	tca	tct	2371				
Gly	Gly	Leu	Thr	Pro	Gln	Glu	Tyr	Glu	Ile	Ala	Arg	Leu	Val	Ser	Ser					
745																				
ggg	cat	gcc	aac	cga	gag	gtc	gca	cag	gag	ctt	ttc	ctc	tcg	cct	aag	2419				
Gly	His	Ala	Asn	Arg	Glu	Val	Ala	Gln	Glu	Leu	Phe	Leu	Ser	Pro	Lys					
760																				
acc	gtg	gaa	tac	cat	ctc	acc	cgg	gtg	tac	aaa	aag	ctc	gga	ata	cgc	2467				
Thr	Val	Glu	Tyr	His	Leu	Thr	Arg	Val	Tyr	Lys	Lys	Leu	Gly	Ile	Arg					
775																				
aat	cgg	atg	gaa	ctt	gcc	gag	gct	ttg	aag	aag	tac	tca	cac	gac	gcc	2515				
Asn	Arg	Met	Glu	Leu	Ala	Glu	Ala	Leu	Lys	Lys	Tyr	Ser	His	Asp	Ala					
790																				
tagcagcggga tatgttttgcg gac																				
2538																				

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<210> 142
<211> 805
<212> PRT
<213> Corynebacterium glutamicum
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Asp	Ala	Ser	Thr	Val	Val	Ile	Val	Ala	Asp	Val	His	Trp	Ala	Asp	Val	
			20					25					30			
Glu	Ser	Met	Gln	Lys	Leu	Ile	Glu	Tyr	Ser	Met	Arg	Met	Val	Ser	Gly	
		35					40					45				
Arg	Phe	Ala	Leu	Ile	Met	Ile	Gly	Leu	Asp	Glu	Glu	Asn	Leu	Val	Phe	
	50					55					60					
His	Asp	Glu	Val	Val	Ser	Leu	Pro	Ser	Ile	Ala	Asp	Ser	Thr	Tyr	Val	
	65				70					75					80	
Leu	Pro	Pro	Met	Ser	Ile	Glu	Glu	Ile	Arg	Gln	Leu	Ala	Leu	Thr	Asp	
			85						90					95		
Val	Arg	Gly	Arg	Ile	Ser	Thr	Thr	Thr	Ala	Thr	Asp	Ile	Gln	Arg	Ile	
			100						105				110			
Thr	Gly	Gly	Ile	Tyr	Gly	Arg	Val	Lys	Glu	Val	Leu	His	Ser	Glu	Ser	
		115					120					125				
Pro	Asp	His	Trp	Arg	Met	Pro	Asn	Pro	Asn	Ile	Pro	Ile	Pro	Gln	Ser	
	130					135					140					
Trp	His	Ala	Asn	Leu	Leu	Arg	Arg	Ile	Thr	Asn	Glu	Glu	Val	Trp	His	
					150					155					160	
Val	Leu	Leu	Ala	Val	Ala	Val	Leu	Pro	Ser	Gly	Gly	Pro	Ile	Asp	Leu	
			165					170					175			
Val	Lys	Leu	Ile	Gly	Asn	Asp	Pro	Thr	Gly	Met	Leu	Cys	Asp	Asp	Ala	

180										185					190				
Val	Arg	Ser	Gly	Leu	Leu	Arg	Val	Leu	Pro	Ser	Asp	Gly	Gln	Pro	Gln				
			195						200					205					
Val	Asp	Leu	Val	Leu	Pro	Ile	Asp	Arg	Ala	Val	Leu	Gln	Ser	Arg	Thr				
		210					215					220							
Pro	Leu	Asn	Ile	Leu	Ala	Gln	Leu	His	His	Lys	Ala	Ala	Glu	Tyr	Tyr				
		225				230					235				240				
Gly	Lys	Trp	Asn	Gln	Lys	Asp	Ala	Gln	Leu	Glu	His	Glu	Ala	Phe	Ala				
			245						250					255					
Ala	Ile	Asp	Pro	Asn	Asp	Pro	Ala	Val	Arg	Ala	Leu	Ala	Gln	Arg	Gly				
			260					265						270					
Tyr	Ala	Leu	Gly	Arg	Thr	Gly	His	Trp	Met	Glu	Ser	Ala	His	Ala	Leu				
		275					280						285						
Ser	Leu	Ala	Ala	Asn	Arg	Thr	Ala	His	Gln	Glu	Glu	Ser	Asn	Lys	Tyr				
		290				295						300							
Leu	Leu	Glu	Ser	Ile	Asp	Ser	Leu	Ile	Ala	Ala	Ala	Asp	Leu	Pro	Gln				
		305				310					315				320				
Ala	Arg	Ser	Arg	Ala	Ser	Thr	Leu	Asp	Leu	Gly	Glu	Thr	Gly	Ile	Gln				
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Gln	Asp	Ser	Met	Leu	Gly	Tyr	Leu	Ala	Ile	His	Glu	Gly	Arg	Arg	Leu				
			340				345						350						
Glu	Ala	Arg	Asn	Leu	Leu	His	Arg	Ala	Ser	Glu	Glu	Leu	Leu	Ala	Gln				
			355				360						365						
His	Pro	Ile	Asp	Pro	Ile	His	Gly	Pro	Arg	Met	Ala	Gln	Arg	Lys	Val				
		370				375					380								
Leu	Leu	Asn	Leu	Val	Asp	Trp	Asn	Pro	Glu	Glu	Leu	Leu	Val	Trp	Ala				
		385				390				395				400					
Asp	Arg	Ala	Val	Ala	Trp	Thr	Glu	Glu	Asp	Ala	Gly	Glu	Lys	Val	Glu				
			405						410					415					
Ala	Gln	Ala	Ile	Ser	Leu	Ile	Gly	Gln	Ser	Ile	Leu	Asp	Gly	Cys	Leu				
			420					425					430						
Pro	Glu	Asp	Lys	Pro	Ile	Pro	Gly	Glu	Thr	Thr	Leu	His	Ala	Gln	Arg				
		435					440					445							
Arg	His	Met	Ala	Met	Gly	Trp	Leu	Ser	Met	Val	His	Asp	Asp	Pro	Val				
		450				455						460							
Thr	Ala	Arg	Gln	Lys	Leu	Glu	Arg	Arg	Thr	Ser	Ile	Asn	Gly	Ser	Glu				
		465				470				475				480					
Arg	Ile	Ser	Leu	Trp	Gln	Asp	Gly	Trp	Leu	Ala	Arg	Ser	Leu	Leu	Leu				
			485					490						495					
Leu	Gly	Glu	Trp	Glu	Ser	Ala	Ala	Arg	Thr	Val	Glu	Ile	Gly	Leu	Ala				
			500					505					510						

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Val Ile Val Ala Asp Val His Trp Ala Asp Val Glu Ser Met Gln Lys
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aac gac ccc acg ggc atg ctt tgc gac gac gcc gtc cgc tca ggc ctg 691
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1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Figure 1**
 10. **Figure 2**
 11. **Figure 3**
 12. **Figure 4**
 13. **Figure 5**
 14. **Figure 6**
 15. **Figure 7**
 16. **Figure 8**
 17. **Figure 9**
 18. **Figure 10**
 19. **Figure 11**
 20. **Figure 12**
 21. **Figure 13**
 22. **Figure 14**
 23. **Figure 15**
 24. **Figure 16**
 25. **Figure 17**
 26. **Figure 18**
 27. **Figure 19**
 28. **Figure 20**
 29. **Figure 21**
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 31. **Figure 23**
 32. **Figure 24**
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 10 15 20
 gag atg act ttg gat gat ctg ttc gga gcg gtt gag caa gaa tgg cag 211
 Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val Glu Gln Glu Trp Gln
 25 30 35
 gag cag gcg ctg tgt gcg caa act gat cct gaa gca ttc ttt cca gaa 259
 Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu Ala Phe Phe Pro Glu
 40 45 50
 aaa ggt ggc tca act cgc gaa gcc aag cgg atc tgc cag ggc tgc ccg 307
 Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile Cys Gln Gly Cys Pro
 55 60 65
 gtt cgg gat gaa tgc cta gag ttt gct ctt gag cat gat gaa cgc ttt 355
 Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu His Asp Glu Arg Phe
 70 75 80 85
 gga att tgg ggt ggt ctc tct gaa cgt gag cgc cgc cgc ctg aaa cgc 403
 Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg Arg Arg Leu Lys Arg
 90 95 100
 gaa att tcg taaaactta agaccagtaa gcg 435
 Glu Ile Ser

<210> 152
 <211> 104
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 152
 Met Glu Asp Ser Ala Gly Asp Val Ser Ala Lys Leu Lys Ala Gly Gln
 1 5 10 15
 Thr Arg Thr Ala Leu Glu Met Thr Leu Asp Asp Leu Phe Gly Ala Val
 20 25 30
 Glu Gln Glu Trp Gln Glu Gln Ala Leu Cys Ala Gln Thr Asp Pro Glu
 35 40 45

Ala Phe Phe Pro Glu Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile
50 55 60

Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe Ala Leu Glu
65 70 75 80

His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu Arg Glu Arg
85 90 95

Arg Arg Leu Lys Arg Glu Ile Ser
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<210> 153

<211> 152

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(129)

<223> FRXA01368

<400> 153

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Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe
1 5 10 15

gct ctt gag cat gat gaa cgc ttt gga att tgg ggt ggt ctc tct gaa 96
Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu
20 25 30

cgt gag cgc cgc cgc ctg aaa cgc gaa att tcg taaaacttca agaccagtaa 149
Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser
35 40

gcg 152

<210> 154

<211> 43

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Lys Arg Ile Cys Gln Gly Cys Pro Val Arg Asp Glu Cys Leu Glu Phe
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Ala Leu Glu His Asp Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu
20 25 30

Arg Glu Arg Arg Arg Leu Lys Arg Glu Ile Ser
35 40

<210> 155

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

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Gln Leu Ala Gln Gln Arg Gly Val Pro Ile Val Glu Ile Ser Pro Thr			
215	220	225	
cgc acc gaa ctt agc cgg atc gca gac ttc acc tgg atg tcc acc gca			835
Arg Thr Glu Leu Ser Arg Ile Ala Asp Phe Thr Trp Met Ser Thr Ala			
230	235	240	245
gcc caa gcg cta cca gcg ttg atg cga ggt ttg agc gcc taacatgact			884
Ala Gln Ala Leu Pro Ala Leu Met Arg Gly Leu Ser Ala			
250	255		
gaagatgact tag			897
<210> 156			
<211> 258			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 156			
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Ala Arg Glu Ala Arg Asn Ile Glu Val Phe Thr Gly Ala Gly Met Ser			
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Ala Asp Ser Gly Leu Glu Thr Tyr Arg Asp Asp Lys Thr Gly Leu Trp			
35	40	45	
Ser Asn Val Asp Pro Gln Ala Met Ala Ser Ile Asp Ala Trp Arg Lys			
50	55	60	
Asp Pro Glu Pro Met Trp Ala Trp Tyr Arg Trp Arg Ala Gly Val Ala			
65	70	75	80
Ala Arg Ala Glu Pro Asn Ala Gly His Gln Ala Ile Ser Tyr Trp Glu			
85	90	95	
Gly Ser Asp Thr Val Glu His Val His Ile Thr Thr Gln Asn Ile Asp			
100	105	110	
Asn Leu His Glu Arg Ala Gly Ser Ser Asp Val Thr His Leu His Gly			
115	120	125	
Ser Leu Phe Glu Tyr Arg Cys Ser Asp Cys Ala Thr Pro Trp Glu Asp			
130	135	140	
Asp Lys Asn Tyr Pro Gln Glu Pro Ile Ala Arg Leu Ala Pro Pro Gln			
145	150	155	160
Cys Glu Lys Cys Gly Gly Leu Ile Arg Pro Gly Val Val Trp Phe Gly			
165	170	175	
Glu Asn Leu Pro Val Glu Glu Trp Asp Ile Ala Glu Gln Arg Ile Ala			
180	185	190	
Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly Ile Val His Pro			
195	200	205	

00502874.083300

Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly Val Pro Ile Val
210 215 220

Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile Ala Asp Phe Thr
225 230 235 240

Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu Met Arg Gly Leu
245 250 255

Ser Ala

<210> 157

<211> 355

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (75)..(332)

<223> FRXA00464

<400> 157

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ttagaccagg tgtggtg tgg ttt ggt gag aac ctg ccc gta gaa gag tgg 110
Val Trp Phe Gly Glu Asn Leu Pro Val Glu Glu Trp
1 5 10

gat att gca gag caa cgc atc gca gaa gcc gat ctc atg atc att gtg 158
Asp Ile Ala Glu Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val
15 20 25

ggt acc tcc ggg att gtt cat cct gca gca gca ctc ccg caa tta gcc 206
Gly Thr Ser Gly Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala
30 35 40

caa caa cgc ggc gtt ccc atc gtg gag atc tcc cca acg cgc acc gaa 254
Gln Gln Arg Gly Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu
45 50 55 60

ctt agc cgg atc gca gac ttc acc tgg atg tcc acc gca gcc caa gcg 302
Leu Ser Arg Ile Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala
65 70 75

cta cca cgc ttg atg cga ggt ttg agc gcc taacatgact gaagatgact 352
Leu Pro Ala Leu Met Arg Gly Leu Ser Ala
80 85

tag 355

<210> 158

<211> 86

<212> PRT

<213> Corynebacterium glutamicum

<400> 158

Val Trp Phe Gly Glu Asn Leu Pro Val Glu Glu Trp Asp Ile Ala Glu

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Gln Arg Ile Ala Glu Ala Asp Leu Met Ile Ile Val Gly Thr Ser Gly			
20		25	30
Ile Val His Pro Ala Ala Ala Leu Pro Gln Leu Ala Gln Gln Arg Gly			
35	40		45
Val Pro Ile Val Glu Ile Ser Pro Thr Arg Thr Glu Leu Ser Arg Ile			
50	55		60
Ala Asp Phe Thr Trp Met Ser Thr Ala Ala Gln Ala Leu Pro Ala Leu			
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Met Arg Gly Leu Ser Ala			
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<210> 159

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1459)

<223> RXA01655

<400> 159

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gtcacttgca ttagaccact tttttgagga cgatgaagcc atg ctt gcc gac ctt 115
 Met Leu Ala Asp Leu
 1 5

ccc atc gcc tta aac cca cac gaa cca aca tcc atc ccc acg cag ctc 163
 Pro Ile Ala Leu Asn Pro His Glu Pro Thr Ser Ile Pro Thr Gln Leu
 10 15 20

aca gaa cag atc cgt cgt ctc gtg gcg agg gga att ctc acc cca gga 211
 Thr Glu Gln Ile Arg Arg Leu Val Ala Arg Gly Ile Leu Thr Pro Gly
 25 30 35

gac cgg ctt ccc agc agt cgc tca cta tcc acc caa ttg ggg gta tcc 259
 Asp Pro Leu Pro Ser Ser Arg Ser Leu Ser Thr Gln Leu Gly Val Ser
 40 45 50

cgc gcc agt gtg gtg acc gct tat gac caa ttg gcc ggt gaa ggc tac 307
 Arg Gly Ser Val Val Thr Ala Tyr Asp Gln Leu Ala Gly Glu Gly Tyr
 55 60 65

ctc agc acc gcc cgc ggt tcc ggt aca acg atc aac cca gat ctg cat 355
 Leu Ser Thr Ala Arg Gly Ser Gly Thr Thr Ile Asn Pro Asp Leu His
 70 75 80 85

ttg ttg aag cct gtg gaa att gag aag aag gag acg tgg aga agc gtc 403
 Leu Leu Lys Pro Val Glu Ile Glu Lys Lys Glu Thr Ser Arg Ser Val
 90 95 100

ccg ccc ccg ctg ctc aac ctg agc ccc gcc gtg ccc gat acc gcg acg 451
 Pro Pro Pro Leu Leu Asn Leu Ser Pro Gly Val Pro Asp Thr Ala Thr

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105	110	115	
ctc gcc gat tcc gca tgg cgc gct gcg tgg cgc gaa gcc tgc gcc aag Leu Ala Asp Ser Ala Trp Arg Ala Ala Trp Arg Glu Ala Cys Ala Lys 120 125 130			499
cca ccc acg cac tcc cct gag cag gga ctt ttg agg ctg cgg atc gag Pro Pro Thr His Ser Pro Glu Gln Gly Leu Leu Arg Leu Arg Ile Glu 135 140 145			547
atc gcc gac cac ctg cgc cag atg cgt gcc ctc atg gtc gag cgg gag Ile Ala Asp His Leu Arg Gln Met Arg Gly Leu Met Val Glu Pro Glu 150 155 160 165			595
cag atc atc gtc acc gcc ggc gcg cgc gag ggg ctg agt ctg ctg ctg Gln Ile Ile Val Thr Ala Gly Ala Arg Glu Gly Leu Ser Leu Leu Leu 170 175 180			643
cgc acc atg gat gcg cct gcc cgc atc gcc gtc gaa tgg ccc gcc tac Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val Glu Ser Pro Gly Tyr 185 190 195			691
ccc agc ctg cgc cgc atc ccg cag gtg ctt gcc cat gag acg atc gat Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly His Glu Thr Ile Asp 200 205 210			739
gtg cgg acc gac gaa tcc gcc ctc gta ccc cgc gcg ctg ccc cac gac Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg Ala Leu Pro His Asp 215 220 225			787
ctt aac gcg cta ctg gta acc cct agc cat caa tat ccc tac gcc gcc Leu Asn Ala Leu Leu Val Thr Pro Ser His Gln Tyr Pro Tyr Gly Gly 230 235 240 245			835
tgg ctg ccc gcc gat cgc cgc acc gcg cta gtc gcg tgg gct gag gca Ser Leu Pro Ala Asp Arg Arg Thr Ala Leu Val Ala Trp Ala Glu Ala 250 255 260			883
aac gat gcg ttg ctt att gaa gac gac ttc gat tct gag ctg cgc tac Asn Asp Ala Leu Leu Ile Glu Asp Asp Phe Asp Ser Glu Leu Arg Tyr 265 270 275			931
gtc ggt atg ccg ctt ccg ccg ctg cgt gcg ctg gcg ccc gat cgc acg Val Gly Met Pro Leu Pro Pro Leu Arg Ala Leu Ala Pro Asp Arg Thr 280 285 290			979
att ctg ctc gcc acg ttt tcc tcc gtg atc aca cca caa gtc gcc tgc Ile Leu Leu Gly Thr Phe Ser Ser Val Ile Thr Pro Gln Val Ala Cys 295 300 305			1027
gga tac ctc atc gcg ccg acg ccc cag gcg cgc gtg ctc gcc acg ctt Gly Tyr Leu Ile Ala Pro Thr Pro Gln Ala Arg Val Leu Ala Thr Leu 310 315 320 325			1075
cgc ggg att ctc gcc cag cca gtc gcc gcc atc acc caa cac gcg ctc Arg Gly Ile Leu Gly Gln Pro Val Gly Ala Ile Thr Gln His Ala Leu 330 335 340			1123
gcg tcc tac ctc gcc tca gcc gct tta cga cgc cgc acc caa cgt ttg Ala Ser Tyr Leu Ala Ser Gly Ala Leu Arg Arg Arg Thr Gln Arg Leu 345 350 355			1171

cgg cgc ctt tac cga cac cgc cgc tcc atc gtc caa gac acc ctc ggt 1219
 Arg Arg Leu Tyr Arg His Arg Arg Ser Ile Val Gln Asp Thr Leu Gly
 360 365 370

gac ctc ccg aat acg cag ctt cgc ccc atc aac ggt ggc ctc cac gca 1267
 Asp Leu Pro Asn Thr Gln Leu Arg Pro Ile Asn Gly Gly Leu His Ala
 375 380 385

gtt ctc ctt tgc gac aaa ccc caa gac ctc gtt gtc acc aca ctc gcc 1315
 Val Leu Leu Cys Asp Lys Pro Gln Asp Leu Val Thr Thr Leu Ala
 390 395 400 405

tcc cga ggc ctt aac gtc acc gcg ctt tcc cac tac tgg ggc ggc acc 1363
 Ser Arg Gly Leu Asn Val Thr Ala Leu Ser His Tyr Trp Gly Gly Thr
 410 415 420

ggc gca gac aac ggc atc gtc ttc ggc ttc ggc tcc cac gac gaa gac 1411
 Gly Ala Asp Asn Gly Ile Val Phe Gly Phe Gly Ser His Asp Glu Asp
 425 430 435

acc ctc aga tgg gtg ctt gct gag atc agc gat gcg gtg tct cta gcc 1459
 Thr Leu Arg Trp Val Leu Ala Glu Ile Ser Asp Ala Val Ser Leu Gly
 440 445 450

taaagaaaaa acagcccag agg 1482

<210> 160
 <211> 453
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 160
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Ile Pro Thr Gln Leu Thr Glu Gln Ile Arg Arg Leu Val Ala Arg Gly
 20 25 30

Ile Leu Thr Pro Gly Asp Pro Leu Pro Ser Ser Arg Ser Leu Ser Thr
 35 40 45

Gln Leu Gly Val Ser Arg Gly Ser Val Val Thr Ala Tyr Asp Gln Leu
 50 55 60

Ala Gly Glu Gly Tyr Leu Ser Thr Ala Arg Gly Ser Gly Thr Thr Ile
 65 70 75 80

Asn Pro Asp Leu His Leu Leu Lys Pro Val Glu Ile Glu Lys Lys Leu
 85 90 95

Thr Ser Arg Ser Val Pro Pro Pro Leu Leu Asn Leu Ser Pro Gly Val
 100 105 110

Pro Asp Thr Ala Thr Leu Ala Asp Ser Ala Trp Arg Ala Ala Trp Arg
 115 120 125

Glu Ala Cys Ala Lys Pro Pro Thr His Ser Pro Glu Gln Gly Leu Leu
 130 135 140

Arg Leu Arg Ile Glu Ile Ala Asp His Leu Arg Gln Met Arg Gly Leu
 145 150 155 160
 Met Val Glu Pro Glu Gln Ile Ile Val Thr Ala Gly Ala Arg Glu Gly
 165 170 175
 Leu Ser Leu Leu Leu Arg Thr Met Asp Ala Pro Ala Arg Ile Gly Val
 180 185 190
 Glu Ser Pro Gly Tyr Pro Ser Leu Arg Arg Ile Pro Gln Val Leu Gly
 195 200 205
 His Glu Thr Ile Asp Val Pro Thr Asp Glu Ser Gly Leu Val Pro Arg
 210 215 220
 Ala Leu Pro His Asp Leu Asn Ala Leu Leu Val Thr Pro Ser His Gln
 225 230 235 240
 Tyr Pro Tyr Gly Gly Ser Leu Pro Ala Asp Arg Arg Thr Ala Leu Val
 245 250 255
 Ala Trp Ala Glu Ala Asn Asp Ala Leu Leu Ile Glu Asp Asp Phe Asp
 260 265 270
 Ser Glu Leu Arg Tyr Val Gly Met Pro Leu Pro Pro Leu Arg Ala Leu
 275 280 285
 Ala Pro Asp Arg Thr Ile Leu Leu Gly Thr Phe Ser Ser Val Ile Thr
 290 295 300
 Pro Gln Val Ala Cys Gly Tyr Leu Ile Ala Pro Thr Pro Gln Ala Arg
 305 310 315 320
 Val Leu Ala Thr Leu Arg Gly Ile Leu Gly Gln Pro Val Gly Ala Ile
 325 330 335
 Thr Gln His Ala Leu Ala Ser Tyr Leu Ala Ser Gly Ala Leu Arg Arg
 340 345 350
 Arg Thr Gln Arg Leu Arg Arg Leu Tyr Arg His Arg Arg Ser Ile Val
 355 360 365
 Gln Asp Thr Leu Gly Asp Leu Pro Asn Thr Gln Leu Arg Pro Ile Asn
 370 375 380
 Gly Gly Leu His Ala Val Leu Leu Cys Asp Lys Pro Gln Asp Leu Val
 385 390 395 400
 Val Thr Thr Leu Ala Ser Arg Gly Leu Asn Val Thr Ala Leu Ser His
 405 410 415
 Tyr Trp Gly Gly Thr Gly Ala Asp Asn Gly Ile Val Phe Gly Phe Gly
 420 425 430
 Ser His Asp Glu Asp Thr Leu Arg Trp Val Leu Ala Glu Ile Ser Asp
 435 440 445
 Ala Val Ser Leu Gly
 450

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<210> 161
 <211> 786
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(763)
 <223> RXA00126

<400> 161
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 acatcaatgc ggtgaccaca attggggagga gaagtagcac gtg act aca cct gct 115
 Val Thr Thr Pro Ala
 1 5

gag aac aac acc ctt agc ccc gag acc aaa gta agc atc act ggt cga 163
 Glu Asn Asn Thr Leu Ser Pro Glu Thr Lys Val Ser Ile Thr Gly Arg
 10 15 20

aac gtt gag gtt cct gat cac ttt gca gaa cga gta aat acc aaa ctc 211
 Asn Val Glu Val Pro Asp His Phe Ala Glu Arg Val Asn Thr Lys Leu
 25 30 35

gca aag att gag cgc ctc gac cca acg ctg acc ttc ttc cac gtt gag 259
 Ala Lys Ile Glu Arg Leu Asp Pro Thr Leu Thr Phe Phe His Val Glu
 40 45 50

cta cag cac gag cca aac cca cgt cgt gct gac gaa agt gat cgc att 307
 Leu Gln His Glu Pro Asn Pro Arg Arg Ala Asp Glu Ser Asp Arg Ile
 55 60 65

cag atc acc gcc acc ggc aag gga cac atc gcc cga gca gaa gca aag 355
 Gln Ile Thr Ala Thr Gly Lys Gly His Ile Ala Arg Ala Glu Ala Lys
 70 75 80 85

gaa gac agc ttc tac gcg gca ctg gaa act gca cta gcc aag atg gag 403
 Glu Asp Ser Phe Tyr Ala Ala Leu Glu Thr Ala Leu Ala Lys Met Glu
 90 95 100

cgc tcc ctg cgc aaa gtg aag gca cgt cgc agc att tcc cgc tcc ggt 451
 Arg Ser Leu Arg Lys Val Lys Ala Arg Arg Ser Ile Ser Arg Ser Gly
 105 110 115

cac cgc gca cca cta ggc act ggt gag gtc ggt gca cag ttg gta gcc 499
 His Arg Ala Pro Leu Gly Thr Gly Glu Val Gly Ala Gln Leu Val Ala
 120 125 130

gag tcc caa gag gca cgc ggt gcc gat gaa ctg gcc aaa tac gat gtt 547
 Glu Ser Gln Glu Ala Arg Gly Ala Asp Glu Leu Gly Lys Tyr Asp Val
 135 140 145

gat cct tat gca gat aag gtc gat gac gtc atg cca gcc cag gtt gtt 595
 Asp Pro Tyr Ala Asp Lys Val Asp Asp Val Met Pro Gly Gln Val Val
 150 155 160 165

cgt acc aag gaa cac cca gca acc cca atg agt gtg gat gac gca cta 643
 Arg Thr Lys Glu His Pro Ala Thr Pro Met Ser Val Asp Asp Ala Leu
 170 175 180

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tcc gag atg gaa ttg gtt gga cac gat ttc tac ctc ttc gtc aac gaa 691
 Ser Glu Met Glu Leu Val Gly His Asp Phe Tyr Leu Phe Val Asn Glu
 185 190 195

gag acc aac cag cca tcg gtg gtg tac cgc cga cac gca ttc gac tat 739
 Glu Thr Asn Gln Pro Ser Val Val Tyr Arg Arg His Ala Phe Asp Tyr
 200 205 210

gga tta att tcc ctg tcc gat gca tagcaattag ttgctaagta ccc 786
 Gly Leu Ile Ser Leu Ser Asp Ala
 215 220

<210> 162

<211> 221

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 162

Val Thr Thr Pro Ala Glu Asn Asn Thr Leu Ser Pro Glu Thr Lys Val
 1 5 10 15

Ser Ile Thr Gly Arg Asn Val Glu Val Pro Asp His Phe Ala Glu Arg
 20 25 30

Val Asn Thr Lys Leu Ala Lys Ile Glu Arg Leu Asp Pro Thr Leu Thr
 35 40 45

Phe Phe His Val Glu Leu Gln His Glu Pro Asn Pro Arg Arg Ala Asp
 50 55 60

Glu Ser Asp Arg Ile Gln Ile Thr Ala Thr Gly Lys Gly His Ile Ala
 65 70 75 80

Arg Ala Glu Ala Lys Glu Asp Ser Phe Tyr Ala Ala Leu Glu Thr Ala
 85 90 95

Leu Ala Lys Met Glu Arg Ser Leu Arg Lys Val Lys Ala Arg Arg Ser
 100 105 110

Ile Ser Arg Ser Gly His Arg Ala Pro Leu Gly Thr Gly Glu Val Gly
 115 120 125

Ala Gln Leu Val Ala Glu Ser Gln Glu Ala Arg Gly Ala Asp Glu Leu
 130 135 140

Gly Lys Tyr Asp Val Asp Pro Tyr Ala Asp Lys Val Asp Asp Val Met
 145 150 155 160

Pro Gly Gln Val Val Arg Thr Lys Glu His Pro Ala Thr Pro Met Ser
 165 170 175

Val Asp Asp Ala Leu Ser Glu Met Glu Leu Val Gly His Asp Phe Tyr
 180 185 190

Leu Phe Val Asn Glu Glu Thr Asn Gln Pro Ser Val Val Tyr Arg Arg
 195 200 205

His Ala Phe Asp Tyr Gly Leu Ile Ser Leu Ser Asp Ala
 210 215 220

00502374.052310

actgatcaga gcccgctccct caacaagaag agcaacacca atg aat ctg aaa gat 115
Met Asn Leu Lys Asp
1 5

ctc aag gcc gca gag acc cgt caa agg ttt atc gat gta gcc cac gaa 163
Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile Asp Val Ala His Glu
10 15 20

ctc ttc ttg gag cac ggt tat ggt tcc acc tcc atg aat cag att gct 211
Leu Phe Leu Glu His Gly Tyr Gly Ser Thr Ser Met Asn Gln Ile Ala
25 30 35

cag gca gcg ggt ggt agc cgg gca aac ctt tac ctt cat ttc cgt aac 259
Gln Ala Ala Gly Gly Ser Arg Ala Asn Leu Tyr Leu His Phe Arg Asn
40 45 50

aag ccc gat ctc atg atg gct aaa atg cgg gaa ctt gaa ccc gcg gtc 307
Lys Pro Asp Leu Met Met Ala Lys Met Arg Glu Leu Glu Pro Ala Val
55 60 65

cgc acc cct gtc cta aaa gtt ttt gat ctc cct gaa cac act ttg gag 355
Arg Thr Pro Val Leu Lys Val Phe Asp Leu Pro Glu His Thr Leu Glu
70 75 80 85

tcc att ctt aga tgg ctg gac tcc atg acg gag gtg tgg aaa gcg aat 403
Ser Ile Leu Arg Trp Leu Asp Ser Met Thr Glu Val Trp Lys Ala Asn
90 95 100

gcc aaa gtg ttc ggg gcg atg gaa caa gcg atg gtc gaa gat gct gcg 451
Ala Lys Val Phe Gly Ala Met Glu Gln Ala Met Val Glu Asp Ala Ala
105 110 115

gtg gcc gat gag tgg ctt tca atg atg cag agg ttg agc caa tgg gtg 499
Val Ala Asp Glu Trp Leu Ser Met Met Gln Arg Leu Ser Gln Ser Val
120 125 130

ccc gaa ttg gtt gag aat gaa gag cgt cga gtt cag ttc ctg gct agc 547
Pro Glu Leu Val Glu Asn Glu Glu Arg Arg Val Gln Phe Leu Ala Ser
135 140 145

ttg atg ggc atg gat aga aac ttt tac ttc ctc tat gtc cga ggg caa 595
Leu Met Gly Met Asp Arg Asn Phe Tyr Phe Leu Tyr Val Arg Gly Gln
150 155 160 165

gat gtt gat gag gaa ttg cta aag ttg gct gtg gct cgc caa tgg ttg 643
Asp Val Asp Glu Glu Leu Leu Lys Leu Ala Val Ala Arg Gln Trp Leu
170 175 180

gca gtt ttc caa taggcaatgc gcccaatcc cct 678
Ala Val Phe Gln
185

<210> 166

<211> 185

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

Met Asn Leu Lys Asp Leu Lys Ala Ala Glu Thr Arg Gln Arg Phe Ile

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Leu Lys Ile Gly Asp His Leu Pro Ser Glu Arg Ala Leu Ser Glu Thr
25 30 35

ctc gga gtt tcc cga agc tcc ctg cgc gag gcg ctt cgt gtg ctc gaa 259
 Leu Gly Val Ser Arg Ser Ser Leu Arg Glu Ala Leu Arg Val Leu Glu
 40 50

gcc ctc gcc acc att tcc acc gcc acc gga tcc gcc ccg cgg tct gcc 307
 Ala Leu Gly Thr Ile Ser Thr Ala Thr Gly Ser Gly Pro Arg Ser Gly
 55 65

acc atc atc act gct gcc cct gcc cag gcg ctt tcc ctc tcc gtg acg 355
 Thr Ile Ile Thr Ala Ala Pro Gly Gln Ala Leu Ser Leu Ser Val Thr
 70 85

ctg cag ttg gtc acc aac cag gtc gcc cac cac gat att tat gaa acc 403
 Leu Gln Leu Val Thr Asn Gln Val Gly His His Asp Ile Tyr Glu Thr
 90 100

cgc caa ctc ctt gaa gcc tgg gct gcc ctg cat tcc agc gcc gaa cgt 451
 Arg Gln Leu Leu Glu Gly Trp Ala Ala Leu His Ser Ser Ala Glu Arg
 105 115

gcc gac tgg gac gtg gca gaa gcg ttg ctg gaa aaq atg gac gac ccc 499
 Gly Asp Trp Asp Val Ala Glu Ala Leu Leu Glu Lys Met Asp Asp Pro
 120 125

tgc cta ccg ctc gag gat ttt ttg cgt ttc gac gcc gaa ttc cac gtt 547
 Ser Leu Pro Leu Glu Asp Phe Leu Arg Phe Asp Ala Glu Phe His Val
 135 145

gtt atc tcc aaa gcc gcg gaa aac cct ctg atc agt acg ctc atg gaa 595
 Val Ile Ser Lys Gly Ala Glu Asn Pro Leu Ile Ser Thr Leu Met Glu
 150 155 165

gcc ctc cgt ttg tcc gtg gca gat cac acc gtt gcc agg gcc cgg gcg 643
 Ala Leu Arg Leu Ser Val Ala Asp His Thr Val Ala Arg Ala Arg Ala
 170 175 180

ctc ccc gat tgg cga gcc acc tcg gcg cgt ctg cag aaa gaa cac cgc 691
 Leu Pro Asp Trp Arg Ala Thr Ser Ala Arg Leu Gln Lys Glu His Arg
 185 190 195

gca atc ctc gca gca ctt cgc gca gcc gaa tcc aca gtg gcc gca acc 739
 Ala Ile Leu Ala Ala Leu Arg Ala Gly Glu Ser Thr Val Ala Ala Thr
 200 205 210

ttg atc aaa gaa cac atc gaa gcc tac tac gaa gaa acc gct gcc gcc 787
 Leu Ile Lys Glu His Ile Glu Gly Tyr Tyr Glu Glu Thr Ala Ala Ala
 215 220 225

gag gcc taaatgtccc gcactctgtg gcc 816
 Glu Ala
 230

<210> 168

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Met Ser Val Lys Ala His Glu Ser Val Met Asp Trp Val Thr Glu Glu

1

5

10

15

00502874.062300

tgccctccgg aagtattttc caattccoga ttaggggtca gtg ctg act caa ttg 115
Val Leu Thr Gln Leu
1 5

att gaa tca tgc att ttc gac aac gtt gcg agc agg gag tcc tct gaa 163
 Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser Arg Glu Ser Ser Glu
 10 15 20

ttt ctc ggc cat gct gcc atc gat cta ctt gct ggc ctt gtc tat gaa 211
 Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala Gly Leu Val Tyr Glu
 25 30 35

aaa gcc act ccc tat gct cca gat gaa gca ctt aga gtg gca gtt tat 259
 Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu Arg Val Ala Val Tyr
 40 45 50

ggc tat att cgg gag aac ctt gga tcc tca caa ctt acg gtc gca gct 307
 Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln Leu Thr Val Ala Ala
 55 60 65

gta gcc ggg gcg cat aga atc gcg gtt cgt acg ttg cat cga tta ttt 355
 Val Ala Gly Ala His Arg Ile Ala Val Arg Thr Leu His Arg Leu Phe
 70 75 80 85

gaa gcc gaa gca tac gga gta gcg gaa tta atc cga cac ctc cga tta 403
 Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile Arg His Leu Arg Leu
 90 95 100

gag gca gta tat gaa gac ctt cgg gat cct cgc ctc cag aac ctg acc 451
 Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg Leu Gln Asn Leu Thr
 105 110 115

att ttg gct atc ggc atg cgc cac gcc att tcc agc caa gct cat tta 499
 Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser Ser Gln Ala His Leu
 120 125 130

aca aga ctg ttt cgc gct aaa tat ggg gta ccg ccg gca gag ttt cgc 547
 Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro Pro Ala Glu Phe Arg
 135 140 145

cga ggg tat att aat agc gct gct tgagggcacc gcaagcgtgg cgc 594
 Arg Gly Tyr Ile Asn Ser Ala Ala
 150 155

<210> 170
 <211> 157
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 170
 Val Leu Thr Gln Leu Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser
 1 5 10 15

Arg Glu Ser Ser Glu Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala
 20 25 30

Gly Leu Val Tyr Glu Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu
 35 40 45

Arg Val Ala Val Tyr Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln
 50 55 60

Leu Thr Val Ala Ala Val Ala Gly Ala His Arg Ile Ala Val Arg Thr
 65 70 75 80

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Leu His Arg Leu Phe Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile
85 90 95

Arg His Leu Arg Leu Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg
100 105 110

Leu Gln Asn Leu Thr Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser
115 120 125

Ser Gln Ala His Leu Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro
130 135 140

Pro Ala Glu Phe Arg Arg Gly Tyr Ile Asn Ser Ala Ala
145 150 155

<210> 171

<211> 418

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)...(418)

<223> RXA01001

<400> 171

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atctccggca ccctccgccc cgcctcctg aagggggcta gtg acc gtg tgg tgg 115
Val Thr Val Ser Trp
1 5

cac caa gca act gac gct cca cca agc atc cgc atc acc acg ctt ggc 163
His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg Ile Thr Thr Leu Ala
10 15 20

cca tcg ctg cag cct aat cag cgc aaa gtc gcc gaa gtc atg ctt gtc 211
Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala Glu Val Met Leu Val
25 30 35

gac gcc ccc agc atc gtc gaa ctg acc gct cag ggc ctt gca gat cgc 259
Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln Gly Leu Ala Asp Arg
40 45 50

gtg ggg gtt ggg cgt gcc acc gtc atc cgc acc gcc cag tcc tta ggc 307
Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr Ala Gln Ser Leu Gly
55 60 65

tac gac gga ttc ccg cag ctg cgc gtc gcc ctg gcg cag gaa ctg gca 355
Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu Ala Gln Glu Leu Ala
70 75 80 85

ctg gcg cag gcc gcg tcg aga agc atg gtt gaa gga gcg tta agc tcc 403
Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu Gly Ala Leu Ser Ser
90 95 100

tcg ttg ctt ggt cat
Ser Leu Leu Gly His
105

418

00502074.052300

<210> 172
 <211> 106
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 172
 Val Thr Val Ser Trp His Gln Ala Thr Asp Ala Pro Pro Ser Ile Arg
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Ile Thr Thr Leu Ala Pro Ser Leu Gln Pro Asn Gln Arg Lys Val Ala
 20 25 30

Glu Val Met Leu Val Asp Ala Pro Ser Ile Val Glu Leu Thr Ala Gln
 35 40 45

Gly Leu Ala Asp Arg Val Gly Val Gly Arg Ala Thr Val Ile Arg Thr
 50 55 60

Ala Gln Ser Leu Gly Tyr Asp Gly Phe Pro Gln Leu Arg Val Ala Leu
 65 70 75 80

Ala Gln Glu Leu Ala Leu Ala Gln Gly Ala Ser Arg Ser Met Val Glu
 85 90 95

Gly Ala Leu Ser Ser Ser Leu Leu Gly His
 100 105

<210> 173
 <211> 1578
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1555)
 <223> RXA01375

<400> 173
 caagcagccca atggccgcgt atgaaaaccc ccgctccata aatacagaac acatacagaa 60

cttgaccgac aatctaatta ccgcaagggt ttagcagcac gtg act gaa aag tat 115
 Val Thr Glu Lys Tyr
 1 5

cgt ccc gtc cgt gac att aag cct gct ccg gca gca atg caa tca act 163
 Arg Pro Val Arg Asp Ile Lys Pro Ala Pro Ala Ala Met Gln Ser Thr
 10 15 20

aaa caa gcg ggc cat cct gtg ttc cga agc gtt gtc gct ttt gtt tca 211
 Lys Gln Ala Gly His Pro Val Phe Arg Ser Val Val Ala Phe Val Ser
 25 30 35

gtg ctg gtg ttg gtg gta tcg ggt ttg ggg tat ctt gct gtc gga aaa 259
 Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr Leu Ala Val Gly Lys
 40 45 50

gtg gat ggt gtc gct tct ggc aac ttg aac ctt ggt ggc ggt cgc ggc 307
 Val Asp Gly Val Ala Ser Gly Asn Leu Asn Leu Gly Gly Gly Arg Gly

00502874.052300

gac gaa ggc tgg gag atc atg agc ttt gcc act cag ctg cag aac ctc 1075
 Asp Glu Gly Trp Glu Ile Met Ser Phe Ala Thr Gln Leu Gln Asn Leu
 310 315 320 325

gcg ggc ggc aac gtc aca ttt gcc acc atc ccg gtt acc tct atc gac 1123
 Ala Gly Gly Asn Val Thr Phe Ala Thr Ile Pro Val Thr Ser Ile Asp
 330 335 340

ggc acc ggc gat tac ggc gag tcc gtt gtc acc atc gat gtc aac cag 1171
 Gly Thr Gly Asp Tyr Gly Glu Ser Val Val Thr Ile Asp Val Asn Gln
 345 350 355

gtg cat gca tto ttc caa gaa gca ctc ggc gaa gca gag cca gct cca 1219
 Val His Ala Phe Phe Gln Glu Ala Leu Gly Glu Ala Glu Pro Ala Pro
 360 365 370

gaa gac ggc tcc gac gat caa tct gct gat cag gcc cct gac cta agc 1267
 Glu Asp Gly Ser Asp Asp Gln Ser Ala Asp Gln Ala Pro Asp Leu Ser
 375 380 385

gaa gtc gag gtc cac gtc ctc aac gct tcc tac gtc gaa ggc ctc gcc 1315
 Glu Val Glu Val His Val Leu Asn Ala Ser Tyr Val Glu Gly Leu Ala
 390 395 400 405

aac ggt atc gcc gcg caa ctg cag gaa ttg ggt tac tcc atc gca gag 1363
 Asn Gly Ile Ala Ala Gln Leu Gln Glu Leu Gly Tyr Ser Ile Ala Glu
 410 415 420

acc ggc aac gca gcg gaa ggc ctc tac tac gag tcc cag atc ctc gcc 1411
 Thr Gly Asn Ala Ala Glu Gly Leu Tyr Tyr Glu Ser Gln Ile Leu Ala
 425 430 435

gcc gaa gaa gac agc gcc aag gcc ctc gcg att tcc gaa gcc ctc ggt 1459
 Ala Glu Glu Asp Ser Ala Lys Ala Leu Ala Ile Ser Glu Ala Leu Gly
 440 445 450

ggt etc cca tgg tgg cca act ctt ccc tgg acg aca aca ccg tca tgg 1507
 Gly Leu Pro Ser Trp Pro Thr Leu Pro Ser Thr Thr Thr Pro Ser Ser
 455 460 465

tgg tat ccg ccg gcg att acg ctg gcc cta ccg cgg aag caa acg ccg 1555
 Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro Arg Lys Gln Thr Pro
 470 475 480 485

tgacatccag caccgtcggc cag 1578

<210> 174
 <211> 485
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 174
 Val Thr Glu Lys Tyr Arg Pro Val Arg Asp Ile Lys Pro Ala Pro Ala
 1 5 10 15
 Ala Met Gln Ser Thr Lys Gln Ala Gly His Pro Val Phe Arg Ser Val
 20 25 30
 Val Ala Phe Val Ser Val Leu Val Leu Val Val Ser Gly Leu Gly Tyr

00502874-062300

35										40										45														
Leu	Ala	Val	Gly	Lys	Val	Asp	Gly	Val	Ala	Ser	Gly	Asn	Leu	Asn	Leu	Leu	Ala	Val	Gly	Lys	Val	Asp	Gly	Val	Ala	Ser	Gly	Asn	Leu	Asn	Leu			
50					55					60					65					70					75					80				
Gly	Gly	Gly	Arg	Gly	Ile	Gln	Asp	Gly	Asn	Ala	Ala	Asp	Gly	Ala	Thr	Asp	Ile	Leu	Leu	Val	Gly	Ser	Asp	Ser	Arg	Ser	Asp	Ala	Gln	Gly	Asn			
65					70					75					80					85					90					95				
Thr	Leu	Thr	Glu	Glu	Glu	Leu	Ala	Met	Leu	Arg	Ala	Gly	Asp	Glu	Glu	Thr	Leu	Thr	Glu	Glu	Glu	Leu	Ala	Met	Leu	Arg	Ala	Gly	Asp	Glu	Glu			
100					105					110					115					120					125									
Asn	Asp	Asn	Thr	Asp	Thr	Ile	Met	Val	Ile	Arg	Val	Pro	Asn	Asp	Gly	Asn	Asp	Asn	Thr	Asp	Thr	Ile	Met	Val	Ile	Arg	Val	Pro	Asn	Asp	Gly			
130					135					140					145					150					155									
Ser	Ser	Ala	Thr	Ala	Val	Ala	Ile	Pro	Arg	Asp	Thr	Tyr	Ile	His	Asp	Ser	Ser	Ala	Thr	Ala	Val	Ala	Ile	Pro	Arg	Asp	Thr	Tyr	Ile	His	Asp			
130					135					140					145					150					155									
Asp	Asp	Tyr	Gly	Asn	Met	Lys	Ile	Asn	Gly	Val	Tyr	Gly	Ala	Tyr	Lys	Asp	Asp	Tyr	Gly	Asn	Met	Lys	Ile	Asn	Gly	Val	Tyr	Gly	Ala	Tyr	Lys			
145					150					155					160					165					170									
Asp	Ala	Arg	Arg	Ala	Glu	Leu	Met	Glu	Gln	Gly	Phe	Thr	Asn	Glu	Ser	Asp	Ala	Arg	Arg	Ala	Glu	Leu	Met	Glu	Gln	Gly	Phe	Thr	Asn	Glu	Ser			
165					170					175					180					185					190									
Glu	Leu	Glu	Thr	Arg	Ala	Lys	Asp	Ala	Gly	Arg	Glu	Gly	Leu	Ile	Asp	Glu	Leu	Glu	Thr	Arg	Ala	Lys	Asp	Ala	Gly	Arg	Glu	Gly	Leu	Ile	Asp			
180					185					190					195					200					205									
Ala	Val	Ser	Asp	Leu	Thr	Gly	Ile	Thr	Val	Asp	His	Tyr	Ala	Glu	Val	Ala	Val	Ser	Asp	Leu	Thr	Gly	Ile	Thr	Val	Asp	His	Tyr	Ala	Glu	Val			
195					200					205					210					215					220									
Gly	Leu	Leu	Gly	Phe	Val	Leu	Leu	Thr	Asp	Ala	Val	Gly	Gly	Val	Glu	Gly	Leu	Leu	Gly	Phe	Val	Leu	Leu	Thr	Asp	Ala	Val	Gly	Gly	Val	Glu			
210					215					220					225					230					235									
Val	Cys	Leu	Asn	Asn	Ala	Val	Asp	Glu	Pro	Leu	Ser	Gly	Ala	Asn	Phe	Val	Cys	Leu	Asn	Asn	Ala	Val	Asp	Glu	Pro	Leu	Ser	Gly	Ala	Asn	Phe			
225					230					235					240					245					250									
Pro	Ala	Gly	Arg	Gln	Thr	Leu	Gly	Gly	Ser	Asp	Ala	Leu	Ser	Tyr	Val	Pro	Ala	Gly	Arg	Gln	Thr	Leu	Gly	Gly	Ser	Asp	Ala	Leu	Ser	Tyr	Val			
245					250					255					260					265					270									
Arg	Gln	Arg	His	Asp	Leu	Pro	Arg	Gly	Asp	Leu	Asp	Arg	Ile	Val	Arg	Arg	Gln	Arg	His	Asp	Leu	Pro	Arg	Gly	Asp	Leu	Asp	Arg	Ile	Val	Arg			
260					265					270					275					280					285									
Gln	Gln	Ser	Tyr	Met	Ala	Ser	Leu	Val	Asn	Gln	Val	Leu	Ser	Ser	Gly	Gln	Gln	Ser	Tyr	Met	Ala	Ser	Leu	Val	Asn	Gln	Val	Leu	Ser	Ser	Gly			
275					280					285																								

Ala Glu Pro Ala Pro Glu Asp Gly Ser Asp Asp Gln Ser Ala Asp Gln
370 375 380

Ala Pro Asp Leu Ser Glu Val Glu Val His Val Leu Asn Ala Ser Tyr
385 390 395 400

Val Glu Gly Leu Ala Asn Gly Ile Ala Ala Gln Leu Gln Glu Leu Gly
405 410 415

Tyr Ser Ile Ala Glu Thr Gly Asn Ala Ala Glu Gly Leu Tyr Tyr Glu
420 425 430

Ser Gln Ile Leu Ala Ala Glu Glu Asp Ser Ala Lys Ala Leu Ala Ile
435 440 445

Ser Glu Ala Leu Gly Gly Leu Pro Ser Trp Pro Thr Leu Pro Ser Thr
450 455 460

Thr Thr Pro Ser Ser Tyr Pro Pro Ala Ile Thr Leu Ala Leu Pro
465 470 475 480

Arg Lys Gln Thr Pro
485

<210> 175

<211> 508

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(508)

<223> RXA02831

<400> 175

cgaactggcg cgtgtcttgt ccgacgcagc ctgcccgc tttattgacc cctccggcac 60

gcttcgatag ggctagggaaa accctgtcgg agggagcgccc atg aca cat cgg atc 115
Met Thr His Arg Ile
1 5

aca ccc gaa ctc tcg gcc gaa ttg cgg ggg gtg gcc cac agc ctt gca 163
Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val Ala His Ser Leu Ala
10 15 20

gat gcg gcg cgg ccc gtc acc ttg caa tac ttc cgc aca gca gtc gcg 211
Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe Arg Thr Ala Val Ala
25 30 35

gca gat aac aaa ggc gcg ctg cgc ggg atg gct tac gac ccc gtc acc 259
Ala Asp Asn Lys Gly Ala Leu Arg Gly Met Ala Tyr Asp Pro Val Thr
40 45 50

att gcc gac cgt gca agc gaa cag gcc atg cgt gac att ctg gcc cgt 307
Ile Ala Asp Arg Ala Ser Glu Gln Ala Met Arg Asp Ile Leu Ala Arg
55 60 65

cta cgc ccc gat gat gcg atc ttg ggt gaa gaa ttc ggc ccc aaa gcg 355
Leu Arg Pro Asp Asp Ala Ile Leu Gly Glu Glu Phe Gly Pro Lys Ala

005000041050000

[illegible]

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<210> 176
<211> 136
<212> PRT
<213> Corynebacterium glutamicum
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<400> 176
Met Thr His Arg Ile Thr Pro Glu Leu Ser Ala Glu Leu Arg Gly Val
  1              5              10              15
Ala His Ser Leu Ala Asp Ala Ala Arg Pro Val Thr Leu Gln Tyr Phe
              20              25              30
Arg Thr Ala Val Ala Ala Asp Asn Lys Gly Ala Leu Arg Gly Met Ala
  35              40              45
Tyr Asp Pro Val Thr Ile Ala Asp Arg Ala Ser Glu Gln Ala Met Arg
  50              55              60
Asp Ile Leu Ala Arg Leu Arg Pro Asp Asp Ala Ile Leu Gly Glu Glu
  65              70              75              80
Phe Gly Pro Lys Ala Gly Thr Thr Gly Leu Thr Trp Val Leu Asp Pro
              85              90              95
Ile Asp Gly Thr Arg Ala Tyr Ile Ala Gly Ala Pro Thr Trp Gly Val
  100              105              110
Leu Ile Ala Val Ser Asp Asp Gln Gly Pro Leu Phe Gly Ile Val Asp
  115              120              125
Gln Pro Tyr Ile Gly Glu Arg Phe
  130              135

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<210> 177
<211> 696
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(673)
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<223> RXA01110

<400> 177

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<210> 178

<211> 191
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 178
 Met Leu Ala Ile Val Gln Leu Ser Lys Glu Ser Ile Ile Gly Ala Ala
 1 5 10 15
 Val Ser Ile Leu Ser Glu Phe Gly Leu Ser Asp Met Thr Met Arg Arg
 20 25 30
 Val Ala Lys Gln Leu Asn Val Ala Pro Gly Ala Leu Tyr Trp His Phe
 35 40 45
 Lys Asn Lys Gln Glu Leu Ile Asp Ala Thr Ser Arg Tyr Leu Leu Ala
 50 55 60
 Pro Val Leu Gly Arg Asn Asp Glu Gln Arg Ala Ser Ile Ser Ala Gln
 65 70 75 80
 Glu Thr Cys Ala Glu Met Arg Ser Leu Met Met Gln Thr Lys Asp Gly
 85 90 95
 Ala Glu Val Ile Ser Ala Ala Leu Ser Asn Gln Gln Leu Arg Gln Gln
 100 105 110
 Leu Glu Ser Leu Ile Ser Asp Ser Leu Lys Glu Pro Asn Glu Val Gly
 115 120 125
 Ala Phe Thr Leu Leu His Phe Val Val Gly Ala Val Leu Thr Glu Gln
 130 135 140
 Thr Gln Leu Gln Met His Glu Phe Thr Ala Gly Ala Gly Asp Asp Thr
 145 150 155 160
 Gln Glu Asn Pro Ala Asp Ala Asn Phe Glu Glu Arg Phe Asn Gln Gly
 165 170 175
 Ile Glu Ile Ile Leu Val Gly Leu Asp Ala Leu Gly His Ile Arg
 180 185 190

<210> 179
 <211> 861
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(838)
 <223> RXA00253

<400> 179
 acccatgtta gatgttttat tcagggattt tagttgatat gtccagtatc tcgctgaaaa 60
 cgctgggtgt cttgtagaaa aaggcgtaac gtcataaac atg cct agc gaa act 115
 Met Pro Ser Glu Thr
 1 5
 atg aaa cca gcc gta gcg tca act ctg gcg gcc act tcc acg gga cgt 163
 Met Lys Pro Ala Val Ala Ser Thr Leu Ala Ala Thr Ser Thr Gly Arg

00000-1200000

<210> 180
 <211> 246
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 180
 Met Pro Ser Glu Thr Met Lys Pro Ala Val Ala Ser Thr Leu Ala Ala
 1 5 10 15
 Thr Ser Thr Gly Arg Arg Pro Gly Arg Pro Thr Gln Arg Ile Leu Ser
 20 25 30
 Val Glu Ser Ile Val Glu Arg Thr Leu Asn Ile Ala Gly Arg Glu Gly
 35 40 45
 Phe Ala Ala Val Thr Met Asn Arg Leu Ala Arg Asp Met Gly Val Thr
 50 55 60
 Pro Arg Ala Leu Tyr Asn His Val Leu Asn Arg Gln Glu Ile Ile Asp
 65 70 75 80
 Arg Val Trp Val Arg Ile Ile Asp Asp Ile Lys Val Pro Asp Leu Asp
 85 90 95
 Pro Asp Asn Trp Arg Gln Ser Ile His Thr Leu Trp Ser Ser Leu Arg
 100 105 110
 Asp Gln Phe Arg Glu Thr Pro Arg Val Leu Leu Val Ala Leu Asp Glu
 115 120 125
 Gln Ile Ser Thr Gln Gly Thr Ser Pro Leu Arg Ile Ala Gly Ala Glu
 130 135 140
 Glu Ser Leu Lys Phe Leu Thr Asp Ile Gly Leu Ser Leu Lys Glu Ala
 145 150 155 160
 Thr Ile Ile Arg Glu Met Met Met Ala Asp Val Phe Ser Phe Thr Leu
 165 170 175
 Thr Ser Asp Tyr Thr Phe Asp Asn Arg Pro Glu Gly Glu Lys Pro Asp
 180 185 190
 Val Phe Ala Pro Val Pro Lys Pro Trp Leu Asp Glu Asn Pro Asp Val
 195 200 205
 Glu Ala Pro Leu Thr Arg Lys Ala Val Glu Glu Ser Val Ser Thr Ser
 210 215 220
 Asp Glu Leu Phe Gly Tyr Met Val Glu Ala Arg Ile Ala Tyr Ile Glu
 225 230 235 240
 Lys Leu Leu Ala Ala Lys
 245

<210> 181
 <211> 888
 <212> DNA
 <213> *Corynebacterium glutamicum*

00000000-00000000

Val Asp Gln Glu Leu Glu Pro Gly Leu Arg Ser Leu Ala Ala Pro Ile
195 200 205

Thr Asn Ala Gln Gly Glu Val Val Ala Ser Ile Asn Val Ser Thr Gln
210 215 220

Ser Ala Ser His Ser Val Glu Asp Ile Arg Lys Leu Val Leu Pro Gln
225 230 235 240

Leu Leu Glu Thr Ala Gln Ala Ile Ser Thr Asp Leu Ser Ala Leu
245 250 255

<210> 183

<211> 654

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (1) .. (654)

<223> RXA01840

<400> 183
atc tct gaa gaa gac ggc gcc agc gaa ccc gcc acc ttc gcc gaa cgc 48
Ile Ser Glu Glu Asp Gly Ala Ser Glu Pro Ala Thr Phe Ala Glu Arg
1 5 10 15

tcc caa cgc ctc atc cag cag gaa tgc gtt gca gcc gtg ttt ggt gga 96
Ser Gln Arg Leu Ile Gln Gln Glu Cys Val Ala Ala Val Phe Gly Gly
20 25 30

tgg acc tcc gcc tcc cgc aaa gca atg ctc ccc gtc ttt gag ggc aat 144
 Trp Thr Ser Ala Ser Arg Lys Ala Met Leu Pro Val Phe Glu Gly Asn
 35 40 45

aac tcc ctg ctg ttc tac ccg gtg cag tac gag ggc atg gaa tcc tcg 192
Asn Ser Leu Leu Phe Tyr Pro Val Gln Tyr Glu Gly Met Glu Ser Ser
50 55 60

ccg aat att ttc tac acc gcc gcc acc acc aac cag cag atc atc ccg 240
 Pro Asn Ile Phe Tyr Thr Gly Ala Thr Thr Asn Gln Gln Ile Ile Pro
 65 70 75 80

gct ctt gat tac ctg cgt gaa aac ggc ctg aac cgc ctt ttc ctt gtc 288
Ala Leu Asp Tyr Leu Arg Glu Asn Gly Leu Asn Arg Leu Phe Leu Val
85 90 95

ggt tcc gat tat gtt ttc cca cgc act gca aat tcc atc atc aag gac 336
Gly Ser Asp Tyr Val Phe Pro Arg Thr Ala Asn Ser Ile Ile Lys Asp
100 105 110

tac gcc gaa gcc aat ggt atg gaa atc gtc ggc gaa gac tac gcg cgg 384
Tyr Ala Glu Ala Asn Gly Met Glu Ile Val Gly Glu Asp Tyr Ala Pro
115 120 125

ttg gga tcc acc gac ttc acc acc atc gcc aac cgc atg cgt gac tcc 432
 Leu Gly Ser Thr Asp Phe Thr Thr Ile Ala Asn Arg Met Arg Asp Ser
 130 135 140

aac gca gat gcc gtg ttc aac act ttg aat ggc gat tcc aac gtg gcg 480

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<210> 184
<211> 218
<212> PRT
<213> Corvnebacterium glutamicum
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400> 184
Ile Ser Glu Glu Asp Gly Ala Ser Glu Pro Ala Thr Phe Ala Glu Arg
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Ser Gln Arg Leu Ile Gln Gln Glu Cys Val Ala Ala Val Phe Gly Gly
           20             25             30
Trp Thr Ser Ala Ser Arg Lys Ala Met Leu Pro Val Phe Glu Gly Asn
   35             40             45
Asn Ser Leu Leu Phe Tyr Pro Val Gln Tyr Glu Gly Met Glu Ser Ser
   50             55             60
Pro Asn Ile Phe Tyr Thr Gly Ala Thr Thr Asn Gln Gln Ile Ile Pro
   65             70             75             80
Ala Leu Asp Tyr Leu Arg Glu Asn Gly Leu Asn Arg Leu Phe Leu Val
           85             90             95
Gly Ser Asp Tyr Val Phe Pro Arg Thr Ala Asn Ser Ile Ile Lys Asp
   100            105            110
Tyr Ala Glu Ala Asn Gly Met Glu Ile Val Gly Glu Asp Tyr Ala Pro
   115            120            125
Leu Gly Ser Thr Asp Phe Thr Thr Ile Ala Asn Arg Met Arg Asp Ser
   130            135            140
Asn Ala Asp Ala Val Phe Asn Thr Leu Asn Gly Asp Ser Asn Val Ala
   145            150            155            160
Phe Phe Arg Gln Tyr Asn Ser Leu Gly Phe Asn Ala Asp Thr Leu Pro
           165            170            175
Val Met Ser Val Ser Ile Ala Glu Glu Val Gly Gly Ile Gly Thr
   180            185            190

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Ala Asn Ile Glu Gly Gln Leu Val Ala Trp Asp Tyr Tyr Gln Thr Ile
195 200 205

Asp Thr Pro Glu Asn Glu Thr Phe Val Glu
210 215

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<210> 185
<211> 1002
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(979)  
<223> RXA00400
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<400> 185
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tgaggggcttc cccaccgcga attaattaat tggagttttg ttg ttc act ctt gaa 115
Leu Phe Thr Leu Glu
1 5

cag ttg cgg tgt ttt gtc gcc gtc gcc aat cat ctt cat ttc gga aaa 163
Gln Leu Arg Cys Phe Val Ala Val Ala Asn His Leu His Phe Gly Lys
10 15 20

gct gct gca gag cta tcc atg acg cag ccg ccg ttg agt cgt cag att 211
Ala Ala Ala Glu Leu Ser Met Thr Gln Pro Pro Leu Ser Arg Gln Ile
25 30 35

caa aag ctg gag aag atc gtc ggt gca acc ctg ctt gat cgt gac aac 259
Gln Lys Leu Glu Lys Ile Val Gly Ala Thr Leu Leu Asp Arg Asp Asn
40 45 50

cgc aag gtg gaa ctg acc act gcg ggt ttc gca ttt ttg aag gat gct 307
 Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala Phe Leu Lys Asp Ala
 55 60 65

cgc ctc att ctc aat tcc acc gag aag gcg gct gag cgc gca cga ttg 355
Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala Glu Arg Ala Arg Leu
70 75 80 85

gct agc tct ggc atg tgg gga cag ctc aat att gga tac acc gct gca 403
Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile Gly Tyr Thr Ala Ala
90 95 100

gcg ggt ttt tcc att ctg ggc ccg acg ttg aat cag ttg cat gag aag 451
Ala Gly Phe Ser Ile Leu Gly Pro Thr Leu Asn Gln Leu His Glu Lys
105 110 115

atg ccg ggg gtc agt gtc gat ctt ttt gag atg gtc tcc acc gag cag 499
Met Pro Gly Val Ser Val Asp Leu Phe Glu Met Val Ser Thr Glu Gln
120 125 130

atc gcc gcc ttg gaa tct ggg cta ctg gat ctt ggc att ggc cga ttg 547
Ile Ala Ala Leu Glu Ser Gly Leu Leu Asp Leu Gly Ile Gly Arg Leu
135 145

agc tcg cca gtt gag ggt ctt caa act cga cgt ctc cag gca gat tcc 595
 Ser Ser Pro Val Glu Gly Leu Gln Thr Arg Arg Leu Gln Ala Asp Ser 165
 150 155 160
 ttg gtt ctt gca gct ccg aag ggg cat cca ctt ctt gat cag aat cga 643
 Leu Val Leu Ala Ala Pro Lys Gly His Pro Leu Leu Asp Gln Asn Arg 180
 170 175
 cca ctg ttg cgg aag cat ctg act ggg gtt cct ttt ctg cag cac tct 691
 Pro Leu Leu Arg Lys His Leu Thr Gly Val Pro Phe Leu Gln His Ser 195
 185 190
 ccc acc aag gcg aag tac ctc tac gac atc gtt gtt aga aac ttc acg 739
 Pro Thr Lys Ala Lys Tyr Leu Tyr Asp Ile Val Val Arg Asn Phe Thr 210
 200 205
 atc aat gat gcg cag gtg caa cat acg ctg agc cag atc acc acg atg 787
 Ile Asn Asp Ala Gln Val Gln His Thr Leu Ser Gln Ile Thr Thr Met 225
 215 220
 gtt agt ctg gtg gcc tct gga ctg ggt gtt gcg ctg gtt ccg gag tct 835
 Val Ser Leu Val Ala Ser Gly Leu Gly Val Ala Leu Val Pro Glu Ser 245
 230 235 240
 gcg aaa aaa ctc aat tac agc ggt gtt gag tat cgc cat ttt tat gat 883
 Ala Lys Lys Leu Asn Tyr Ser Gly Val Glu Tyr Arg His Phe Tyr Asp 260
 250 255
 cta cct gtt ggt tta gcg gag ctg cag gct att tat tcc acc tcg aat 931
 Leu Pro Val Gly Leu Ala Glu Leu Gln Ala Ile Tyr Ser Thr Ser Asn 275
 265 270
 gat aat cct gcg gtg cgg aaa ttc atc aaa aac att gac gat acc ttt 979
 Asp Asn Pro Ala Val Arg Lys Phe Ile Lys Asn Ile Asp Asp Thr Phe 290
 280 285
 taagcatttc aacatgccaa act 1002

<210> 186

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

Leu Phe Thr Leu Glu Gln Leu Arg Cys Phe Val Ala Val Ala Asn His
 1 5 10 15

Leu His Phe Gly Lys Ala Ala Ala Glu Leu Ser Met Thr Gln Pro Pro
 20 25 30

Leu Ser Arg Gln Ile Gln Lys Leu Glu Lys Ile Val Gly Ala Thr Leu
 35 40 45

Leu Asp Arg Asp Asn Arg Lys Val Glu Leu Thr Thr Ala Gly Phe Ala
 50 55 60

Phe Leu Lys Asp Ala Arg Leu Ile Leu Asn Ser Thr Glu Lys Ala Ala
 65 70 75 80

Glu Arg Ala Arg Leu Ala Ser Ser Gly Met Trp Gly Gln Leu Asn Ile

00502874-055200

85										90					95				
Gly	Tyr	Thr	Ala	Ala	Ala	Gly	Phe	Ser	Ile	Leu	Gly	Pro	Thr	Leu	Asn				
100					105					110									
Gln	Leu	His	Glu	Lys	Met	Pro	Gly	Val	Ser	Val	Asp	Leu	Phe	Glu	Met				
115					120					125									
Val	Ser	Thr	Glu	Gln	Ile	Ala	Ala	Leu	Glu	Ser	Gly	Leu	Leu	Asp	Leu				
130					135					140									
Gly	Ile	Gly	Arg	Leu	Ser	Ser	Pro	Val	Glu	Gly	Leu	Gln	Thr	Arg	Arg				
145					150					155					160				
Leu	Gln	Ala	Asp	Ser	Leu	Val	Leu	Ala	Ala	Pro	Lys	Gly	His	Pro	Leu				
165					170					175									
Leu	Asp	Gln	Asn	Arg	Pro	Leu	Leu	Arg	Lys	His	Leu	Thr	Gly	Val	Pro				
180					185					190									
Phe	Leu	Gln	His	Ser	Pro	Thr	Lys	Ala	Lys	Tyr	Leu	Tyr	Asp	Ile	Val				
195					200					205									
Val	Arg	Asn	Phe	Thr	Ile	Asn	Asp	Ala	Gln	Val	Gln	His	Thr	Leu	Ser				
210					215					220									
Gln	Ile	Thr	Thr	Met	Val	Ser	Leu	Val	Ala	Ser	Gly	Leu	Gly	Val	Ala				
225					230					235					240				
Leu	Val	Pro	Glu	Ser	Ala	Lys	Lys	Leu	Asn	Tyr	Ser	Gly	Val	Glu	Tyr				
245					250					255									
Arg	His	Phe	Tyr	Asp	Leu	Pro	Val	Gly	Leu	Ala	Glu	Leu	Gln	Ala	Ile				
260					265					270									
Tyr	Ser	Thr	Ser	Asn	Asp	Asn	Pro	Ala	Val	Arg	Lys	Phe	Ile	Lys	Asn				
275					280					285									
Ile	Asp	Asp	Thr	Phe															
290																			

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<210> 187
<211> 1500
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1477)
<223> RXA02787
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<400> 187
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gttgcttggt tgtttcagcc aagcgactaa cctgtgcact atg gcc cag gat tca    115
               Met Ala Gln Asp Ser
                1             5

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ctt ttt gaa acg ccc gaa aca ccg gga tcc gca ggc aac aca agc agc 163
Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala Gly Asn Thr Ser Ser

	10	15	20	
gtg agc aat tcc aaa gcc gcc tcg aag tat ttt cac cca ggc gga cac				211
Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe His Pro Gly Gly His				
	25	30	35	
gca ccc ctt gct gcc cgc atg agg cca agg acg ctt gat gaa gtg gtt				259
Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr Leu Asp Glu Val Val				
	40	45	50	
ggc caa cag cat ttg ctg ggg gag ggc agg cca ctt cgc cgg ctc att				307
Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro Leu Arg Arg Leu Ile				
	55	60	65	
gaa ggt tca ggg gat gcc tcc gtc att ttg tat ggg cct ccc ggc act				355
Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr Gly Pro Pro Gly Thr				
	70	75	80	85
gga aaa aca acc att gcc tca ttg att tct gca gct gca ggc gat cgc				403
Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala Ala Ala Gly Asp Arg				
	90	95	100	
ttt gtg gcg atg tcg gcg ctg tcc tca ggt gtg aaa gaa gtc cgc gcc				451
Phe Val Ala Met Ser Ala Leu Ser Ser Gly Val Lys Glu Val Arg Ala				
	105	110	115	
gtt att gaa cgt gcg agg atg gat ctg caa tta ggg cag cgc acc gtg				499
Val Ile Glu Arg Ala Arg Met Asp Leu Gln Leu Gly Gln Arg Thr Val				
	120	125	130	
ctg ttt att gat gag gtt cat agg ttt tcc aaa act cag cag gac gcg				547
Leu Phe Ile Asp Glu Val His Arg Phe Ser Lys Thr Gln Gln Asp Ala				
	135	140	145	
ttg ctc tct gca gtg gaa aac cgc acc gtg ttg ctc gtt gca gcg acc				595
Leu Leu Ser Ala Val Glu Asn Arg Thr Val Leu Leu Val Ala Ala Thr				
	150	155	160	165
act gag aac ccc tcc ttt tca gtg gtg tct cca ctg ctg tcc agg tcc				643
Thr Glu Asn Pro Ser Phe Ser Val Val Ser Pro Leu Leu Ser Arg Ser				
	170	175	180	
ttg ctg ctc cag ttg gaa tct tta agc gat gag gat att aaa aca gtc				691
Leu Leu Leu Gln Leu Glu Ser Leu Ser Asp Glu Asp Ile Lys Thr Val				
	185	190	195	
ctt aat aaa gcg ctt gaa gat gag cgt gga ctt gcc ggt cga atc acc				739
Leu Asn Lys Ala Leu Glu Asp Glu Arg Gly Leu Ala Gly Arg Ile Thr				
	200	205	210	
gcc acc gat gaa gca gtt gac cag ttg gtt ctt ctt gcc ggt ggc gat				787
Ala Thr Asp Glu Ala Val Asp Gln Leu Val Leu Leu Ala Gly Gly Asp				
	215	220	225	
gcc cgc cga ggc ctg acc tac att gaa gcc gct gca gaa gcc gta gaa				835
Ala Arg Arg Gly Leu Thr Tyr Ile Glu Ala Ala Ala Glu Ala Val Glu				
	230	235	240	245
gat ggc ggc gtt tta gat att gac acc gtc atg gcc aac gtg aac cgc				883
Asp Gly Gly Val Leu Asp Ile Asp Thr Val Met Ala Asn Val Asn Arg				
	250	255	260	

000250-1280950

gca gtg gtc cgc tat gac cgc gat ggc gat cag cac tat gac gtg gtc 931
Ala Val Val Arg Tyr Asp Arg Asp Gly Asp Gln His Tyr Asp Val Val
265 270 275

agt gcc tgg atc aaa tca att aga ggc tcc gat gta gac gca gcc ttg 979
Ser Ala Trp Ile Lys Ser Ile Arg Gly Ser Asp Val Asp Ala Ala Leu
280 285 290

cac tac ttg gcg cgc atg att gat gcc ggt gaa gac cca cgg ttt att 1027
His Tyr Leu Ala Arg Met Ile Asp Ala Gly Glu Asp Pro Arg Phe Ile
295 300 305

gcc cgc cgg ttg gtg gtt cac tca agt gaa gac atc ggt atg gct gat 1075
Ala Arg Arg Leu Val Val His Ser Ser Glu Asp Ile Gly Met Ala Asp
310 315 320 325

cct tcg gcc atg caa gtg gcc att gct gca gct caa gct gtc caa tta 1123
Pro Ser Ala Met Gln Val Ala Ile Ala Ala Ala Gln Ala Val Gln Leu
330 335 340

atc ggt atg cca gag gcg cgg atc aat ttg gcg caa cgc acc att cat 1171
Ile Gly Met Pro Glu Ala Arg Ile Asn Leu Ala Gln Ala Thr Ile His
345 350 355

ttg gct ctt gct ccc aaa tcc aat gct gtc atc atg gcc atg gat gct 1219
Leu Ala Leu Ala Pro Lys Ser Asn Ala Val Ile Met Ala Met Asp Ala
360 365 370

gct ttg act gat gtt cag caa ggc cac atc ggt acc gtt cct gcg cat 1267
Ala Leu Thr Asp Val Gln Gln Gly His Ile Gly Thr Val Pro Ala His
375 380 385

ctt cgc gat ggt cac tat gaa ggc gcc aaa aag ctc gga aat gca gtg 1315
Leu Arg Asp Gly His Tyr Glu Gly Ala Lys Lys Leu Gly Asn Ala Val
390 395 400 405

gga tat tcc tat cct cac gat gat ccc agg gga gtg gtc cgg caa gaa 1363
Gly Tyr Ser Tyr Pro His Asp Asp Pro Arg Gly Val Val Arg Gln Glu
410 415 420

tat tta ccg gag aac ctg cgc gat cgg gtc tat tac gag ccc acc aca 1411
Tyr Leu Pro Glu Asn Leu Arg Asp Arg Val Tyr Tyr Glu Pro Thr Thr
425 430 435

cac ggt gga gag aag cgg att gcc gag tac att ggc agg ctt cgt cgt 1459
His Gly Gly Glu Lys Arg Ile Ala Glu Tyr Ile Gly Arg Leu Arg Arg
440 445 450

ata atc cgt gga acc aag tagcccggt tgctcaacac cta 1500
Ile Ile Arg Gly Thr Lys
455

<210> 188

<211> 459

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Ala Gln Asp Ser Leu Phe Glu Thr Pro Glu Thr Pro Gly Ser Ala

09602874.052370

1 5 10 15
 Gly Asn Thr Ser Ser Val Ser Asn Ser Lys Ala Ala Ser Lys Tyr Phe
 20 25 30
 His Pro Gly Gly His Ala Pro Leu Ala Ala Arg Met Arg Pro Arg Thr
 35 40 45
 Leu Asp Glu Val Val Gly Gln Gln His Leu Leu Gly Glu Gly Arg Pro
 50 55 60
 Leu Arg Arg Leu Ile Glu Gly Ser Gly Asp Ala Ser Val Ile Leu Tyr
 65 70 75 80
 Gly Pro Pro Gly Thr Gly Lys Thr Thr Ile Ala Ser Leu Ile Ser Ala
 85 90 95
 Ala Ala Gly Asp Arg Phe Val Ala Met Ser Ala Leu Ser Ser Gly Val
 100 105 110
 Lys Glu Val Arg Ala Val Ile Glu Arg Ala Arg Met Asp Leu Gln Leu
 115 120 125
 Gly Gln Arg Thr Val Leu Phe Ile Asp Glu Val His Arg Phe Ser Lys
 130 135 140
 Thr Gln Gln Asp Ala Leu Leu Ser Ala Val Glu Asn Arg Thr Val Leu
 145 150 155 160
 Leu Val Ala Ala Thr Thr Glu Asn Pro Ser Phe Ser Val Val Ser Pro
 165 170 175
 Leu Leu Ser Arg Ser Leu Leu Leu Glu Leu Ser Leu Ser Asp Glu
 180 185 190
 Asp Ile Lys Thr Val Leu Asn Lys Ala Leu Glu Asp Glu Arg Gly Leu
 195 200 205
 Ala Gly Arg Ile Thr Ala Thr Asp Glu Ala Val Asp Gln Leu Val Leu
 210 215 220
 Leu Ala Gly Gly Asp Ala Arg Arg Gly Leu Thr Tyr Ile Glu Ala Ala
 225 230 235 240
 Ala Glu Ala Val Glu Asp Gly Gly Val Leu Asp Ile Asp Thr Val Met
 245 250 255
 Ala Asn Val Asn Arg Ala Val Val Arg Tyr Asp Arg Asp Gly Asp Gln
 260 265 270
 His Tyr Asp Val Val Ser Ala Trp Ile Lys Ser Ile Arg Gly Ser Asp
 275 280 285
 Val Asp Ala Ala Leu His Tyr Leu Ala Arg Met Ile Asp Ala Gly Glu
 290 295 300
 Asp Pro Arg Phe Ile Ala Arg Arg Leu Val Val His Ser Ser Glu Asp
 305 310 315 320
 Ile Gly Met Ala Asp Pro Ser Ala Met Gln Val Ala Ile Ala Ala Ala
 325 330 335

005607-100000

gat tgg cca agc caa aat ctg ctg agc ttc cgc ggt aaa gtg cag gaa 355
Asp Trp Pro Ser Gln Asn Leu Leu Ser Phe Arg Gly Lys Val Gln Glu

gcc acc atc gga tca ggt gtt gcg gcg atg gcc ggt tgc gaa att atc 691
Ala Thr Ile Gly Ser Gly Val Ala Ala Met Ala Gly Ser Glu Ile Ile
185 190 195

aac gcg cca ctg acc caa tcc acg cag tcc acg ctg tat ttc tac gcc 739
Asn Ala Pro Leu Thr Gln Ser Thr Gln Ser Thr Leu Tyr Phe Tyr Ala
200 205 210

gcg gaa atg gtc tcc cac gcc tgg att ttc aac gcc gct gtc cac cgc 787
Arg Glu Met Val Ser His Ala Trp Ile Phe Asn Gly Ala Val His Arg
215 220 225

ccc aac agc gcc gcg acg ccg acg gcg ttc gga aat aca aat acc tta 835
Pro Asn Ser Gly Arg Thr Pro Thr Ala Phe Gly Asn Thr Asn Thr Leu
230 235 240 245

aaa gat gct ttt cga cgt gga ctc aca cca aca act ttc tcc gat tta 883
Lys Asp Ala Phe Arg Arg Gly Leu Thr Pro Thr Thr Phe Ser Asp Leu
250 255 260

gtc caa ctc tcc cac acc aac ccg ctt gca cga cag atc ctc aac gag 931
Val Gln Leu Ser His Thr Asn Pro Leu Ala Arg Gln Ile Leu Asn Glu
265 270 275

gcg gcc cac aaa ctt gcc gac gcc gta acc acc gcc gtt gat gtt gtc 979
Arg Ala His Lys Leu Ala Asp Ala Val Thr Thr Ala Val Asp Val Val
280 285 290

gac ccc gaa gcc gtc gtc ttc gcc gcc gaa gcc ttc acc ctg gat ccg 1027
Asp Pro Glu Ala Val Val Phe Ala Gly Glu Ala Phe Thr Leu Asp Pro
295 300 305

gaa act ctt gcg att gtg gtg acc cag ctc cga gca aac acc gcc agc 1075
Glu Thr Leu Arg Ile Val Val Thr Gln Leu Arg Ala Asn Thr Gly Ser
310 315 320 325

caa ctg aga atc caa cgc gca gac gcc tac att ctc gcg acc gcg gcc 1123
Gln Leu Arg Ile Gln Arg Ala Asp Ala Tyr Ile Leu Arg Thr Ala Ala
330 335 340

atc cag gtg gcg ctg cat ccg atc cgt caa gat ccg ttg gca ttt gtg 1171
Ile Gln Val Ala Leu His Pro Ile Arg Gln Asp Pro Leu Ala Phe Val
345 350 355

taattaccac ccatgttgcg ggg 1194

<210> 192
<211> 357
<212> PRT
<213> Corynebacterium glutamicum

<400> 192
Val Phe Met Leu Ala Gln Arg Thr Leu Pro Ile His Ile Thr Ala Pro
1 5 10 15
His Leu Pro Val Ala Arg Val Phe His Gln Ile Arg Ala Thr Asp Ala
20 25 30
Asp Arg Thr Ser Leu Gln Arg Asp Leu Glu Leu Ser Gln Ala Gly Ile

00503074.052300

35										40										45											
Thr	Arg	His	Val	Ser	Ala	Leu	Ile	Asp	Ala	Gly	Leu	Val	Glu	Glu	Thr	Arg	Val	Asp	Ser	Gly	Ala	Arg	Ser	Gly	Arg	Pro	Arg	Thr	Lys	Leu	Gly
50										55										60											
65										70										75											
Ile	Asp	Gly	Arg	His	Leu	Thr	Ala	Trp	Gly	Val	His	Ile	Gly	Leu	Arg	Asn	Phe	Val	Ala	His	Arg	Leu	Gln	Thr	Leu	Ser	Ala	Gly	Leu	Pro	Glu
85										90										95											
Ser	Thr	Asp	Phe	Ala	Val	Cys	Asp	Leu	Ala	Gly	Arg	Val	Ile	Arg	Tyr	Pro	Arg	Thr	Lys	Leu	Gly	Asn	Phe	Val	Ala	His	Arg	Leu	Gln	Thr	Leu
100										105										110											
Glu	Arg	Val	Asp	His	Glu	Val	Ser	His	Ser	Thr	Pro	Ser	Glu	Thr	Leu	Asn	Phe	Val	Ala	His	Arg	Leu	Gln	Thr	Leu	Ser	Ala	Gly	Leu	Pro	Glu
115										120										125											
Pro	Arg	Asn	Val	Gly	Val	Ala	Leu	Ser	Ala	His	Leu	Ser	Ala	Asn	Gly	Pro	Arg	Asn	Val	Gly	Val	Ala	Leu	Ser	Ala	His	Leu	Ser	Ala	Asn	Gly
130										135										140											
Thr	Val	Thr	Ser	Glu	Asp	Tyr	Gly	Trp	Ser	Glu	Val	Glu	Ile	Gly	Ala	Thr	Val	Thr	Ser	Glu	Asp	Tyr	Gly	Trp	Ser	Glu	Val	Glu	Ile	Gly	Ala
145										150										155											
His	Leu	Pro	Phe	Pro	Ala	Thr	Ile	Gly	Ser	Gly	Val	Ala	Ala	Met	Ala	His	Leu	Pro	Phe	Pro	Ala	Thr	Ile	Gly	Ser	Gly	Val	Ala	Ala	Met	Ala
160										165										170											
Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr	Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr
175										180										185											
Leu	Tyr	Phe	Tyr	Ala	Arg	Glu	Met	Val	Ser	His	Ala	Trp	Ile	Phe	Asn	Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr
190										195										200											
Gly	Ala	Val	His	Arg	Pro	Asn	Ser	Gly	Arg	Thr	Pro	Thr	Ala	Phe	Gly	Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr
205										210										215											
Asn	Thr	Asn	Thr	Leu	Lys	Asp	Ala	Phe	Arg	Arg	Gly	Leu	Thr	Pro	Thr	Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr
220										225										230											
Thr	Phe	Ser	Asp	Leu	Val	Gln	Leu	Ser	His	Thr	Asn	Pro	Leu	Ala	Arg	Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr
235										240										245											
Gln	Ile	Leu	Asn	Glu	Arg	Ala	His	Lys	Leu	Ala	Asp	Ala	Val	Thr	Thr	Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr
250										255										260											
Ala	Val	Asp	Val	Val	Asp	Pro	Glu	Ala	Val	Val	Phe	Ala	Gly	Glu	Ala	Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr
265										270										275											
Phe	Thr	Leu	Asp	Pro	Glu	Thr	Leu	Arg	Ile	Val	Val	Thr	Gln	Leu	Arg	Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln	Ser	Thr	Gln	Ser	Thr
280										285										290											
Ala	Asn	Thr	Gly	Ser	Gln	Leu	Arg	Ile	Gln	Arg	Ala	Asp	Ala	Tyr	Ile	Gly	Ser	Glu	Ile	Ile	Asn	Ala	Pro	Leu	Thr	Gln					

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<220>  
<221> CDS  
<222> (101)..(1264)  
<223> RXA01935
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Ile Ala Gly Arg Leu Asn Tyr Gln Phe Ser Val Pro Ala Thr Val Ala			
185	190	195	
tca gca att cct gcc atc gca gct tct gaa ctg cag gct tcc cca ctt			739
Ser Ala Ile Pro Ala Ile Ala Ala Ser Glu Leu Gln Ala Ser Pro Leu			
200	205	210	
ccc cac cct gag cag cca act ccc atc acc ttg acc ttc tac gcc gat			787
Pro His Pro Glu Gln Pro Thr Pro Ile Thr Leu Thr Phe Tyr Ala Asp			
215	220	225	
gac tct gtg ggc gcg gcc tac agc aat gat ttg gga gta cat gtc att			835
Asp Ser Val Gly Ala Ala Tyr Ser Asn Asp Leu Gly Val His Val Ile			
230	235	240	
gga cca ctg gct aca act cgt gga tca ggt ttg gat act ttg gcc atg			883
Gly Pro Leu Ala Thr Thr Arg Gly Ser Gly Leu Asp Thr Leu Gly Met			
250	255	260	
gct gcc gaa gat gcg ctg agc acc caa ggt ttc tta agc agg gtt tct			931
Ala Ala Glu Asp Ala Leu Ser Thr Gln Gly Phe Leu Ser Arg Val Ser			
265	270	275	
gat cag ggt atc ttt gcc aac agc ctt ggt gag cta gtc acc att gct			979
Asp Gln Gly Ile Phe Ala Asn Ser Leu Gly Glu Leu Val Thr Ile Ala			
280	285	290	
aaa gac aat gaa acc gca cgg gaa ttc ctc aac gat cgc gcg acc ctg			1027
Lys Asp Asn Glu Thr Ala Arg Glu Phe Leu Asn Asp Arg Ala Thr Leu			
295	300	305	
ctg gct cac act gcc gca gaa gct gcc gaa aca gtt aag cca tcc acc			1075
Leu Ala His Thr Ala Ala Glu Ala Ala Glu Thr Val Lys Pro Ser Thr			
310	315	320	
ctg gtt ctc tcg gga tcg gcg ttt tcc gaa gat cca caa ggt cgg tcg			1123
Leu Val Leu Ser Gly Ser Ala Phe Ser Glu Asp Pro Gln Gly Arg Ser			
330	335	340	
gtg ttc gct tcc caa ttg aag aag gaa tac gac gca gac att gag ctc			1171
Val Phe Ala Ser Gln Leu Lys Lys Glu Tyr Asp Ala Asp Ile Glu Leu			
345	350	355	
cgg ttg atc ccc acc cac cgg gaa aac gtc cgc gca gca gct cga gca			1219
Arg Leu Ile Pro Thr His Arg Glu Asn Val Arg Ala Ala Ala Arg Ala			
360	365	370	
gtc gca ett gat cga cta ctc aac gag cca ctt act ctc gta ccc			1264
Val Ala Leu Asp Arg Leu Leu Asn Glu Pro Leu Thr Leu Val Pro			
375	380	385	
taacctcact taagctcagt gct			1287

<210> 194

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

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<400> 194

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Met Ile Gly Tyr Gly Leu Pro Met Pro Asn Gln Ala His Phe Ser Ala
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Ser Phe Ala Arg Pro Ser Thr Pro Ala Ala Lys Cys Met His His Ile
20 25 30

Arg Leu Gly Gln Gln Leu Ile Arg Asn Glu Leu Val Glu Ala Thr Gly
35 40 45

Leu Ser Gln Pro Thr Val Thr Arg Ala Val Thr Ala Leu Met Gln Ala
50 55 60

Gly Leu Val Arg Glu Arg Pro Asp Leu Thr Leu Ser Ser Gly Pro Gly
65 70 75 80

Arg Pro Asn Ile Pro Leu Glu Leu Ala Pro Ser Pro Trp Ile His Ala
85 90 95

Gly Val Ala Ile Gly Thr Lys Ser Ser Tyr Val Ala Leu Phe Asp Thr
100 105 110

Lys Gly Arg Thr Leu Arg Asp Ala Met Leu Glu Ile Ser Ala Ala Asp
115 120 125

Leu Asp Pro Asp Thr Phe Ile Glu His Leu Ile Ala Gly Val Asn Arg
130 135 140

Leu Thr Thr Gly Leu Asp Leu Pro Leu Val Gly Ile Gly Val Ala Thr
145 150 155 160

Ser Gly Lys Val Thr Asn Ala Gly Val Val Thr Ala Ser Asn Leu Gly
165 170 175

Trp Asp Gly Val Asp Ile Ala Gly Arg Leu Asn Tyr Gln Phe Ser Val
180 185 190

Pro Ala Thr Val Ala Ser Ala Ile Pro Ala Ile Ala Ala Ser Glu Leu
195 200 205

Gln Ala Ser Pro Leu Pro His Pro Glu Gln Pro Thr Pro Ile Thr Leu
210 215 220

Thr Phe Tyr Ala Asp Asp Ser Val Gly Ala Ala Tyr Ser Asn Asp Leu
225 230 235 240

Gly Val His Val Ile Gly Pro Leu Ala Thr Thr Arg Gly Ser Gly Leu
245 250 255

Asp Thr Leu Gly Met Ala Ala Glu Asp Ala Leu Ser Thr Gln Gly Phe
260 265 270

Leu Ser Arg Val Ser Asp Gln Gly Ile Phe Ala Asn Ser Leu Gly Glu
275 280 285

Leu Val Thr Ile Ala Lys Asp Asn Glu Thr Ala Arg Glu Phe Leu Asn
290 295 300

Asp Arg Ala Thr Leu Leu Ala His Thr Ala Ala Glu Ala Ala Glu Thr
305 310 315 320

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Val Lys Pro Ser Thr Leu Val Leu Ser Gly Ser Ala Phe Ser Glu Asp
325 330 335

Pro Gln Gly Arg Ser Val Phe Ala Ser Gln Leu Lys Lys Glu Tyr Asp
340 345 350

Ala Asp Ile Glu Leu Arg Leu Ile Pro Thr His Arg Glu Asn Val Arg
355 360 365

Ala Ala Ala Arg Ala Val Ala Leu Asp Arg Leu Leu Asn Glu Pro Leu
370 375 380

Thr Leu Val Pro
385

<210> 195

<211> 744

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(721)

<223> RXN02270

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gcacgcgtat tgggcgcgcgt cgcttctggg gtggcgggtg atg gat cag gcg cgg 115
Met Asp Gln Ala Arg
1 5

cgc aat cga acg cac tac gcc atg gtt gag ctg gag cag cat ggt ttt 163
Pro Asn Arg Thr His Tyr Ala Met Val Glu Leu Glu Gln His Gly Phe
10 15 20

tta agt ggt gtg gtc acc caa aat gtc gat ggt tta cac gcg gaa gca 211
Leu Ser Gly Val Val Thr Gln Asn Val Asp Gly Leu His Ala Glu Ala
25 30 35

ggc acg aaa aac ctg gtc gcg ctg cat ggt gat ctc gcc cat gtg atg 259
Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp Leu Ala His Val Met
40 45 50

tgt ttg aac tgc ggt ttc ggg gag gat cga cac ctc ttt gat gaa cgt 307
Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His Leu Phe Asp Glu Arg
55 60 65

ctc gaa gcc gcc aac ccc ggc tac gtc gct tcc att cgc ctg gaa ccg 355
Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser Ile Arg Leu Glu Pro
70 75 80 85

ggc gca gtc aac ccc gac ggc gac gtc ttc ctc gac gaa gaa caa gta 403
Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu Asp Glu Glu Gln Val
90 95 100

cgc cgc ttc acc atg atc ggc tgc ttg cgc tgc ggc tgc ctc atg ctc 451
Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys Gly Ser Leu Met Leu
105 110 115

Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser
130 135 140

aaa cca gac gtg gtt tac ttc ggc gaa ccc gtg ccc gcc gcg cgc aaa 499
Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val Pro Ala Ala Arg Lys
120 125 130

aaa gat tta aaa aag ctt ctc gac gcc tcc tcc agc ctc tta atc gcc 547
 Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser Ser Leu Leu Ile Ala
 135 140 145
 ggc tcc tcc cta gcc gtc atg agt gga tac cgg atc gtc atc gaa gcg 595
 Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg Ile Val Ile Glu Ala
 150 155 160 165
 caa cgt caa gga aaa caa gtg tct gtc atc aac gcc gcc cca ggt cgg 643
 Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn Gly Gly Pro Gly Arg
 170 175 180
 gcg gat tcc cgc gtg gac att ttg tgg cgc acc cgc gtt gca cgg gcc 691
 Ala Asp Ser Arg Val Asp Ile Leu Trp Arg Thr Arg Val Ala Pro Ala
 185 190 195
 ttt gat gac att ttg gac gcg ctg gac ctt tagacttttg gtggcttaag 741
 Phe Asp Asp Ile Leu Asp Ala Leu Asp Leu
 200 205
 ttc 744
 <210> 198
 <211> 207
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 198
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 20 25 30
 Leu His Ala Glu Ala Gly Thr Lys Asn Leu Val Ala Leu His Gly Asp
 35 40 45
 Leu Ala His Val Met Cys Leu Asn Cys Gly Phe Gly Glu Asp Arg His
 50 55 60
 Leu Phe Asp Glu Arg Leu Glu Ala Ala Asn Pro Gly Tyr Val Ala Ser
 65 70 75 80
 Ile Arg Leu Glu Pro Gly Ala Val Asn Pro Asp Gly Asp Val Phe Leu
 85 90 95
 Asp Glu Glu Gln Val Arg Arg Phe Thr Met Ile Gly Cys Leu Arg Cys
 100 105 110
 Gly Ser Leu Met Leu Lys Pro Asp Val Val Tyr Phe Gly Glu Pro Val
 115 120 125
 Pro Ala Ala Arg Lys Lys Asp Leu Lys Lys Leu Leu Asp Ala Ser Ser
 130 135 140
 Ser Leu Leu Ile Ala Gly Ser Ser Leu Ala Val Met Ser Gly Tyr Arg
 145 150 155 160
 Ile Val Ile Glu Ala Gln Arg Gln Gly Lys Gln Val Ser Val Ile Asn

cgc

603

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<210> 200
<211> 160
<212> PRT
<213> Corynebacterium glutamicum
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400> 200
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Ala Thr Gln Ala Lys Ser Lys Ala Pro Gln Ala Gly Val His Asp Pro
20 25 30
Glu Leu Ala Gly Gln Thr Ser Phe Val Pro Val Val Gly Lys Ile Ala
35 40 45
Ala Gly Ser Pro Ile Thr Ala Glu Gln Asn Ile Glu Glu Tyr Tyr Pro
50 55 60
Leu Pro Ala Glu Ile Val Gly Asp Gly Asp Leu Phe Met Leu Gln Val
65 70 75 80
Val Gly Glu Ser Met Arg Asp Ala Gly Ile Leu Thr Gly Asp Trp Val
85 90 95
Val Val Arg Ser Gln Pro Val Ala Glu Gln Gly Glu Phe Val Ala Ala
100 105 110
Met Ile Asp Gly Glu Ala Thr Val Lys Glu Phe His Lys Asp Ser Ser
115 120 125
Gly Ile Trp Leu Leu Pro His Asn Asp Thr Phe Ala Pro Ile Pro Ala
130 135 140
Glu Asn Ala Glu Ile Met Gly Lys Val Val Ser Val Met Arg Lys Leu
145 150 155 160

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<210> 201
<211> 777
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(754)  
<223> RXA02127
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<400> 203
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actgtttaaat gtgttaaacc tgcccagact gctgtaccgg gtg tat gag cgc cgt															115
Val Tyr Glu Arg Arg 1 5															
ctt tta aga gaa cta gac ggc gcc aaa cag ccc ggt cac gtt gcc atc	163														
Leu Leu Arg Glu Leu Asp Gly Ala Lys Gln Pro Gly His Val Ala Ile															
10 15 20															
atg tgt gat ggc aac cga cgc tgg gcc cgg gaa gcg ggc ttc act gat	211														
Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu Ala Gly Phe Thr Asp															
25 30 35															
gtc agc cat ggg cac cga gtg ggt gcc aaa aag atc ggc gag atg gtc	259														
Val Ser His Gly His Arg Val Gly Ala Lys Lys Ile Gly Glu Met Val															
40 45 50															
cgc tgg tgt gat gat gta gac gtc aat ctc gtg acc gtt tat ttg ctg	307														
Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val Thr Val Tyr Leu Leu															
55 60															
tct atg gaa aac ctt ggg cga tcc tcc gaa gag ctg caa ttg ctg ttc	355														
Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu Leu Gln Leu Leu Phe															
70 75 80 85															
gat atc atc gcc gat gtc gct gat gaa ctc gcg cgt cct gaa acc aac	403														
Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala Arg Pro Glu Thr Asn															
90 95 100															
tgt cga gtc cgc ctc gtt ggt cat tta gat ctg ctc cca gac cca gtt	451														
Cys Arg Val Arg Leu Val Gly His Leu Asp Leu Leu Pro Asp Pro Val															
105 110 115															
get tgt cgt tta cgc aaa gct gaa gaa gct acc gtt aac aac aca ggc	499														
Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr Val Asn Asn Thr Gly															
120 125 130															
atc gca gtc aac atg gct gtc ggt tat ggc gga cgc cag gaa atc gtt	547														
Ile Ala Val Asn Met Ala Val Gly Tyr Gly Gly Arg Gln Glu Ile Val															
135 140 145															
gat gcc gtg caa aaa ctt ctg acc atc ggc aag gac gag gcc cta agc	595														
Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys Asp Glu Gly Leu Ser															
150 155 160 165															
gtt gat gaa ctg atc gaa tcc gtc aag gta gat gcg atc tcc act cac	643														
Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp Ala Ile Ser Thr His															
170 175 180															
ctg tac acc tct ggc caa cca gac cca gac ctg gtg atc cgc acc tct	691														
Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu Val Ile Arg Thr Ser															
185 190 195															
ggg gag cag cga ctt tcc gga ttc atg ctg tgg caa tct gcc tac tcc	739														
Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp Gln Ser Ala Thr Ser															
200 205 210															
gaa atc tgg ttc aca gac acc tac tgg cca gcc ttc cga cgc atc gac	787														
Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala Phe Arg Arg Ile Asp															
215 220 225															

ttc etc cgc gcc att cgc gac tac tcg cag cgc agc aga aga ttc ggt 835
 Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg Ser Arg Arg Phe Gly
 230 235 240 245

aaa taactatttc tccaaggaga gac 861
 Lys

<210> 204
 <211> 246
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 204
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 1 5 10 15
 Gly His Val Ala Ile Met Cys Asp Gly Asn Arg Arg Trp Ala Arg Glu
 20 25 30
 Ala Gly Phe Thr Asp Val Ser His Gly His Arg Val Gly Ala Lys Lys
 35 40 45
 Ile Gly Glu Met Val Arg Trp Cys Asp Asp Val Asp Val Asn Leu Val
 50 55 60
 Thr Val Tyr Leu Leu Ser Met Glu Asn Leu Gly Arg Ser Ser Glu Glu
 65 70 75 80
 Leu Gln Leu Leu Phe Asp Ile Ile Ala Asp Val Ala Asp Glu Leu Ala
 85 90 95
 Arg Pro Glu Thr Asn Cys Arg Val Arg Leu Val Gly His Leu Asp Leu
 100 105 110
 Leu Pro Asp Pro Val Ala Cys Arg Leu Arg Lys Ala Glu Glu Ala Thr
 115 120 125
 Val Asn Asn Thr Gly Ile Ala Val Asn Met Ala Val Gly Tyr Gly Gly
 130 135 140
 Arg Gln Glu Ile Val Asp Ala Val Gln Lys Leu Leu Thr Ile Gly Lys
 145 150 155 160
 Asp Glu Gly Leu Ser Val Asp Glu Leu Ile Glu Ser Val Lys Val Asp
 165 170 175
 Ala Ile Ser Thr His Leu Tyr Thr Ser Gly Gln Pro Asp Pro Asp Leu
 180 185 190
 Val Ile Arg Thr Ser Gly Glu Gln Arg Leu Ser Gly Phe Met Leu Trp
 195 200 205
 Gln Ser Ala Tyr Ser Glu Ile Trp Phe Thr Asp Thr Tyr Trp Pro Ala
 210 215 220
 Phe Arg Arg Ile Asp Phe Leu Arg Ala Ile Arg Asp Tyr Ser Gln Arg
 225 230 235 240
 Ser Arg Arg Phe Gly Lys

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245

<210> 205

<211> 582

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> {101}..(559)

<223> RXA00592

<400> 205

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aacctgtgc	ttacatgaag	cgtagggtgg	cttagttctt	atg	gct	tct	aat	tcc	115
				Met	Ala	Ser	Asn	Ser	
				1				5	

gaa	cgc	ctt	gca	gag	ctg	ggc	att	tct	ctt	cct	tcc	ggt	gca	gcg	cct	163
Glu	Arg	Leu	Ala	Glu	Leu	Gly	Ile	Ser	Leu	Pro	Ser	Val	Ala	Ala	Pro	
			10						15					20		

ggt	gct	gcg	tat	ggt	cct	gcg	att	cag	acc	ggt	aac	cag	gtg	tgg	act	211
Val	Ala	Ala	Tyr	Val	Pro	Ala	Ile	Gln	Thr	Gly	Asn	Gln	Val	Trp	Thr	
			25					30					35			

tct	ggt	cag	ctg	cct	ttc	ggt	gat	ggt	cag	ctt	ccg	gcc	acc	ggc	aag	259
Ser	Gly	Gln	Leu	Pro	Phe	Val	Asp	Gly	Gln	Leu	Pro	Ala	Thr	Gly	Lys	
			40				45					50				

ggt	ggc	gct	gag	ggt	tcc	gct	gag	gat	gcg	gag	aag	ttg	gct	cgt	gcg	307
Val	Gly	Ala	Glu	Val	Ser	Ala	Glu	Asp	Ala	Glu	Lys	Leu	Ala	Arg	Ala	
		55				60						65				

gct	gcg	cta	aac	gct	ctt	gct	gcg	att	gat	gcg	ctt	ggt	ggc	att	gat	355
Ala	Ala	Leu	Asn	Ala	Leu	Ala	Ala	Ile	Asp	Ala	Leu	Val	Gly	Ile	Asp	
		70			75					80				85		

aag	gtc	act	cgc	ggt	ttg	aag	att	ggt	ggt	ttc	gtg	gcg	tct	gct	gat	403
Lys	Val	Thr	Arg	Val	Leu	Lys	Ile	Val	Gly	Phe	Val	Ala	Ser	Ala	Asp	
			90						95					100		

gat	ttc	agt	ggt	cag	cct	gct	gtc	gtc	aac	ggt	gct	tcc	aat	ttg	atg	451
Asp	Phe	Ser	Gly	Gln	Pro	Ala	Val	Val	Asn	Gly	Ala	Ser	Asn	Leu	Met	
			105					110						115		

ggt	gag	ggt	ttc	ggc	gag	gct	ggg	gcg	cat	gcg	cgt	tct	gct	gtg	ggc	499
Gly	Glu	Val	Phe	Gly	Glu	Ala	Gly	Ala	His	Ala	Arg	Ser	Ala	Val	Gly	
		120				125								130		

gtg	gcg	gag	ttg	ccg	ctc	aac	tcg	cct	gtc	gag	gtc	gag	ggt	atc	gtc	547
Val	Ala	Glu	Leu	Pro	Leu	Asn	Ser	Pro	Val	Glu	Val	Glu	Val	Ile	Val	
		135					140					145				

gag	atc	gcg	cag	tagcacgctt	ttcgacgcaa	aat	582
Glu	Ile	Ala	Gln				
							150

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<210> 206
 <211> 153
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 206
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 Ser Val Ala Ala Pro Val Ala Ala Tyr Val Pro Ala Ile Gln Thr Gly
 20 25 30
 Asn Gln Val Trp Thr Ser Gly Gln Leu Pro Phe Val Asp Gly Gln Leu
 35 40 45
 Pro Ala Thr Gly Lys Val Gly Ala Glu Val Ser Ala Glu Asp Ala Glu
 50 55 60
 Lys Leu Ala Arg Ala Ala Ala Leu Asn Ala Leu Ala Ala Ile Asp Ala
 65 70 75 80
 Leu Val Gly Ile Asp Lys Val Thr Arg Val Leu Lys Ile Val Gly Phe
 85 90 95
 Val Ala Ser Ala Asp Asp Phe Ser Gly Gln Pro Ala Val Val Asn Gly
 100 105 110
 Ala Ser Asn Leu Met Gly Glu Val Phe Gly Glu Ala Gly Ala His Ala
 115 120 125
 Arg Ser Ala Val Gly Val Ala Glu Leu Pro Leu Asn Ser Pro Val Glu
 130 135 140
 Val Glu Val Ile Val Glu Ile Ala Gln
 145 150

<210> 207
 <211> 182
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(159)
 <223> RXA00630

<400> 207
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 Ala Lys Ile Leu Asp Asn Val Trp His Tyr Asp Phe Gly Gly Asp Gly
 1 5 10 15
 aac gtc gtg gaa tcc tac atc tcc tac ctg cgc cgc aag gtg gac acc 96
 Asn Val Val Glu Ser Tyr Ile Ser Tyr Leu Arg Arg Lys Val Asp Thr
 20 25 30
 cag gat ccg cag cta att cag act gtt cgt ggc gtt gga tat gtt ctg 144
 Gln Asp Pro Gln Leu Ile Gln Thr Val Arg Gly Val Gly Tyr Val Leu
 35 40 45
 cgc acc cca cgt agc taaattctcc tatggaaaat cct 182

00000-123000

agc cca gtt ctg tac ctc acc gca aag gat gcc gtg gag cac cgc atc 403

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<210> 210
<211> 128
<212> PRT
<213> Corynebacterium glutamicum
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<210> 211
<211> 1251
<212> DNA
<213> Corynebacterium glutamicum
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<400> 211
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aactagtcgt aattagtcgg attttaagga ggctcaagcc  atg ggc att gag ttt      115
               Met Gly Ile Glu Phe

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1 5

aag cgt tca ccg cga ccc acc ctg ggc gtt gag tgg gaa att gca ctt 163
 Lys Arg Ser Pro Arg Pro Thr Leu Gly Val Glu Trp Glu Ile Ala Leu
 10 15 20

gtt gat cca gaa aca cgt gat cta gcc ccg cgc gct gca gaa ata cta 211
 Val Asp Pro Glu Thr Arg Asp Leu Ala Pro Arg Ala Ala Glu Ile Leu
 25 30 35

gag att gtg gcc aag aac cac cct gag gtg cac ctg gag cgc gaa ttc 259
 Glu Ile Val Ala Lys Asn His Pro Glu Val His Leu Glu Arg Glu Phe
 40 45 50

ctc caa aac acc gtg gag ctt gtc acc gga gtg tgc gac acc gtc ccc 307
 Leu Gln Asn Thr Val Glu Leu Val Thr Gly Val Cys Asp Thr Val Pro
 55 60 65

gaa gcg gtg gca gag ctt tcc cac gat cta gat gcg ctg aaa gaa gca 355
 Glu Ala Val Ala Glu Leu Ser His Asp Leu Asp Ala Leu Lys Glu Ala
 70 75 80 85

gcg gat tct ctc ggg ctt cgg ttg tgg acc tct gga tcc cac cca ttt 403
 Ala Asp Ser Leu Gly Leu Arg Leu Trp Thr Ser Gly Ser His Pro Phe
 90 95 100

tcg gat ttc cgc gaa aac cca gta tct gaa aaa ggc tcc tac gac gag 451
 Ser Asp Phe Arg Glu Asn Pro Val Ser Glu Lys Gly Ser Tyr Asp Glu
 105 110 115

atc atc gcg cgc acc caa tac tgg gga aac cag atg ttg att tgg ggc 499
 Ile Ile Ala Arg Thr Gln Tyr Trp Gly Asn Gln Met Leu Ile Trp Gly
 120 125 130

att cac gtc cac gtg ggc atc agc cat gaa gat cgc gtg tgg ccg atc 547
 Ile His Val His Val Gly Ile Ser His Glu Asp Arg Val Trp Pro Ile
 135 140 145

atc aat gcg ctg ctg aca aat tac cca cat ctg ttg gca ctt tct gca 595
 Ile Asn Ala Leu Leu Thr Asn Tyr Pro His Leu Leu Ala Leu Ser Ala
 150 155 160 165

agc tct cca gca tgg gac gga ctt gat acc ggt tat gcc tcc aac cgg 643
 Ser Ser Pro Ala Trp Asp Gly Leu Asp Thr Gly Tyr Ala Ser Asn Arg
 170 175 180

acg atg ctc tac caa cag ctg cct aca gcc gga ctg cca tac caa ttc 691
 Thr Met Leu Tyr Gln Gln Leu Pro Thr Ala Gly Leu Pro Tyr Gln Phe
 185 190 195

caa agc tgg gat gaa tgg tgc agc tac atg gcg gat caa gat aaa tcc 739
 Gln Ser Trp Asp Glu Trp Cys Ser Tyr Met Ala Asp Gln Asp Lys Ser
 200 205 210

ggt gtc atc aac cac acc gga tcc atg cac ttt gat atc cgc ccc gca 787
 Gly Val Ile Asn His Thr Gly Ser Met His Phe Asp Ile Arg Pro Ala
 215 220 225

tcc aaa tgg gga acc atc gaa gtc cgc gtg gcc gat tct acc tcc aac 835
 Ser Lys Trp Gly Thr Ile Glu Val Arg Val Ala Asp Ser Thr Ser Asn
 230 235 240 245

03503374-062300

Gly Ser His Pro Phe Ser Asp Phe Arg Glu Asn Pro Val Ser Glu Lys
 100 105 110
 Gly Ser Tyr Asp Glu Ile Ile Ala Arg Thr Gln Tyr Trp Gly Asn Gln
 115 120 125
 Met Leu Ile Trp Gly Ile His Val His Val Gly Ile Ser His Glu Asp
 130 135 140
 Arg Val Trp Pro Ile Ile Asn Ala Leu Leu Thr Asn Tyr Pro His Leu
 145 150 155 160
 Leu Ala Leu Ser Ala Ser Ser Pro Ala Trp Asp Gly Leu Asp Thr Gly
 165 170 175
 Tyr Ala Ser Asn Arg Thr Met Leu Tyr Gln Gln Leu Pro Thr Ala Gly
 180 185 190
 Leu Pro Tyr Gln Phe Gln Ser Trp Asp Glu Trp Cys Ser Tyr Met Ala
 195 200 205
 Asp Gln Asp Lys Ser Gly Val Ile Asn His Thr Gly Ser Met His Phe
 210 215 220
 Asp Ile Arg Pro Ala Ser Lys Trp Gly Thr Ile Glu Val Arg Val Ala
 225 230 235 240
 Asp Ser Thr Ser Asn Leu Arg Glu Leu Ser Ala Ile Val Ala Leu Thr
 245 250 255
 His Cys Leu Val Val His Tyr Asp Arg Met Ile Asp Ala Gly Glu Glu
 260 265 270
 Leu Pro Ser Leu Gln Gln Trp His Val Ser Glu Asn Lys Trp Arg Ala
 275 280 285
 Ala Arg Tyr Gly Leu Asp Ala Glu Ile Ile Ile Ser Arg Asp Thr Asp
 290 295 300
 Glu Ala Met Val Gln Asp Glu Leu Arg Arg Leu Val Ala Gln Leu Met
 305 310 315 320
 Pro Leu Ala Asn Glu Leu Gly Cys Ala Arg Glu Leu Glu Leu Val Leu
 325 330 335
 Glu Ile Leu Glu Arg Gly Gly Gly Tyr Glu Arg Gln Arg Arg Val Phe
 340 345 350
 Lys Glu Thr Gly Ser Trp Lys Ala Ala Val Asp Leu Ala Cys Asp Glu
 355 360 365
 Leu Asn Asp Leu Lys Ala Leu Asp
 370 375

<210> 213

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(664)

<223> RXA01450

<400> 213

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gcctcctgat taggttctta cccaacgatt gctaggatat gtg cct gtg acc ctt 115
 Val Pro Val Thr Leu
 1 5

act ctt gga atc gtc ggc ctg ccc aac gtt ggc aag tcc acc ctg ttc 163
 Thr Leu Gly Ile Val Gly Leu Pro Asn Val Gly Lys Ser Thr Leu Phe
 10 15 20

aac gcc ctg act cgc aat gac gtg ctc gca gcg aac tac ccg ttc gcc 211
 Asn Ala Leu Thr Arg Asn Asp Val Leu Ala Ala Asn Tyr Pro Phe Ala
 25 30 35

acc atc gag cca aac gtg ggc ctt gtc gag ctt cca gac gct cgc ctt 259
 Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu Pro Asp Ala Arg Leu
 40 45 50

gaa cgc ctt tct gaa atc ttc ggc tct gag cgc atc ctg cca gca acc 307
 Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg Ile Leu Pro Ala Thr
 55 60 65

gtg tct ttc gtt gac atc gcc gga atc gtt aag gga gct tcc gaa gcc 355
 Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys Gly Ala Ser Glu Gly
 70 75 80 85

gaa gga atg ggc aac gct ttc ctt gcc aac atc cgc gaa gca gac gct 403
 Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile Arg Glu Ala Asp Ala
 90 95 100

atc tgt cag gtt gtg cgc gca ttc gct gac gaa aac gtc att cac gtc 451
 Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu Asn Val Ile His Val
 105 110 115

gat ggt gaa gtt aac cca gca acc gat atc tct gtg atc aac acc gag 499
 Asp Gly Glu Val Asn Pro Ala Thr Asp Ile Ser Val Ile Asn Thr Glu
 120 125 130

ctg atc ctc gcc gac ctg cag acc gtg gaa aaa gca ctc cca cgc ctc 547
 Leu Ile Leu Ala Asp Leu Gln Thr Val Glu Lys Ala Leu Pro Arg Leu
 135 140 145

gaa aag gat gca cgc aaa gac aag gga ctt ggc gaa gtc gta gat gag 595
 Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly Glu Val Val Asp Glu
 150 155 160 165

acc aaa aaa gcc ctt gcg atc ttg agc gat gac cgc acc ttg ttt ctc 643
 Thr Lys Lys Ala Leu Ala Ile Leu Ser Asp Asp Arg Thr Leu Phe Leu
 170 175 180

tgc agc aaa agc tgg cga cat tgatctggcc ctctgcgcg atc 687
 Cys Ser Lys Ser Trp Arg His
 185

<210> 214
 <211> 188
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 214
 Val Pro Val Thr Leu Thr Leu Gly Ile Val Gly Leu Pro Asn Val Gly
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 Lys Ser Thr Leu Phe Asn Ala Leu Thr Arg Asn Asp Val Leu Ala Ala
 20 25 30
 Asn Tyr Pro Phe Ala Thr Ile Glu Pro Asn Val Gly Leu Val Glu Leu
 35 40 45
 Pro Asp Ala Arg Leu Glu Arg Leu Ser Glu Ile Phe Gly Ser Glu Arg
 50 55 60
 Ile Leu Pro Ala Thr Val Ser Phe Val Asp Ile Ala Gly Ile Val Lys
 65 70 75 80
 Gly Ala Ser Glu Gly Glu Gly Met Gly Asn Ala Phe Leu Ala Asn Ile
 85 90 95
 Arg Glu Ala Asp Ala Ile Cys Gln Val Val Arg Ala Phe Ala Asp Glu
 100 105 110
 Asn Val Ile His Val Asp Gly Glu Val Asn Pro Ala Thr Asp Ile Ser
 115 120 125
 Val Ile Asn Thr Glu Leu Ile Leu Ala Asp Leu Gln Thr Val Glu Lys
 130 135 140
 Ala Leu Pro Arg Leu Glu Lys Asp Ala Arg Lys Asp Lys Gly Leu Gly
 145 150 155 160
 Glu Val Val Asp Glu Thr Lys Lys Ala Leu Ala Ile Leu Ser Asp Asp
 165 170 175
 Arg Thr Leu Phe Leu Cys Ser Lys Ser Trp Arg His
 180 185

<210> 215
 <211> 690
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> {101}..(667)
 <223> RXA01451

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 Met Thr Ala Pro Cys
 1 5
 ttc tct gca gca aaa gct ggc gac att gat ctg gcc ctc ctg cgc gat 163

Phe Ser Ala Ala Lys Ala Gly Asp Ile Asp Leu Ala Leu Leu Arg Asp
 10 15 20
 ctc cac ctg atg aca gca aag cct ttc ctc tac gtc ttc aac tcc gac 211
 Leu His Leu Met Thr Ala Lys Pro Phe Leu Tyr Val Phe Asn Ser Asp
 25 30 35
 gaa aaa gtg ctc acc gac gac gcc aag aag gac gaa ctc cgc gca cta 259
 Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp Glu Leu Arg Ala Leu
 40 45 50
 gtc gcg cca gca gac tgc gta ttc ctt gac gca caa act gaa acc gaa 307
 Val Ala Pro Ala Asp Cys Val Phe Leu Asp Ala Gln Thr Glu Thr Glu
 55 60 65
 ctt ctt gaa ctc gaa gaa gac gaa gca gca gaa ctc ctc gaa gct gta 355
 Leu Leu Glu Leu Glu Glu Asp Glu Ala Ala Glu Leu Leu Glu Ala Val
 70 75 80 85
 ggc caa acg gaa cca ggc cta cac tcc ctc gca cgt gca gga ttt gaa 403
 Gly Gln Thr Glu Pro Gly Leu His Ser Leu Ala Arg Ala Gly Phe Glu
 90 95 100
 acc ctc gga cta cag acc tac ctc acc gcg ggt cct aag gaa tca cgc 451
 Thr Leu Gly Leu Gln Thr Tyr Leu Thr Ala Gly Pro Lys Glu Ser Arg
 105 110 115
 gcc tgg acc atc cac aag ggc gac acc gct cca cag gca gca ggc gtt 499
 Ala Trp Thr Ile His Lys Gly Asp Thr Ala Pro Gln Ala Ala Gly Val
 120 125 130
 atc cat tct gac ttc gaa cgc ggc ttc atc aag gct gaa atc gtc tcc 547
 Ile His Ser Asp Phe Glu Arg Gly Phe Ile Lys Ala Glu Ile Val Ser
 135 140 145
 ttc gaa gat ctt gac gct gct ggt tcc atg gcg gaa gcc aag gcc cag 595
 Phe Glu Asp Leu Asp Ala Ala Gly Ser Met Ala Glu Ala Lys Ala Gln
 150 155 160 165
 ggc aaa gtc cgc caa gaa ggt aag gac tac gtg atg gtc gat ggc gac 643
 Gly Lys Val Arg Gln Glu Gly Lys Asp Tyr Val Met Val Asp Gly Asp
 170 175 180
 gtt gtg gag ttc cgg ttt aac gtc tagcgttatt gacgctcctc gtt 690
 Val Val Glu Phe Arg Phe Asn Val
 185

 <210> 216
 <211> 189
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 216
 Met Thr Ala Pro Cys Phe Ser Ala Ala Lys Ala Gly Asp Ile Asp Leu
 1 5 10 15
 Ala Leu Leu Arg Asp Leu His Leu Met Thr Ala Lys Pro Phe Leu Tyr
 20 25 30
 Val Phe Asn Ser Asp Glu Lys Val Leu Thr Asp Asp Ala Lys Lys Asp

att gag aag caa ttc gga tgg ccc gtg ttc att atc tcc gca gtg gca 1075
 ile glu lys gln phe gly trp pro val phe ile ile ser ala val ala
 310 315 320 325

cgc aag ggc ttg gat cct ttg aag tac aag ctg ctg gaa atc gtc cag 1123
 arg lys gly leu lys asp pro leu lys tyr lys leu leu glu ile val gln
 330 335 340

gat gcc cga aag aag cgt cca aag gag aag gct gag tct gtc atc att 1171
 asp ala arg lys lys arg pro lys glu lys ala glu ser val ile ile
 345 350 355

aag cct aag gct gtt gat cac cgc act aag ggg cag ttc cag atc aag 1219
 lys pro lys ala val asp his arg thr lys gly gln phe gln ile lys
 360 365 370

cct gac cca gag gtt cag ggc gga ttc atc atc acc ggc gaa aag cca 1267
 pro asp pro glu val gln gly gly phe ile ile thr gly glu lys pro
 375 380 385

gag cgc tgg att ttg cag acc gac ttt gaa aac gac gaa gca gtt ggc 1315
 glu arg trp ile leu gln thr asp phe glu asn asp glu ala val gly
 390 395 400 405

tac ctg gct gac cgt ctg gcc aag ttg ggc att gag gac ggg ctt cgt 1363
 tyr leu ala asp arg leu ala lys leu gly ile glu asp gly leu arg
 410 415 420

aag gca gga gca cat gtg ggt gca aac gtc acc atc gga ggc att tcc 1411
 lys ala gly ala his val gly ala asn val thr ile gly gly ile ser
 425 430 435

ttc gag tgg gag cca atg acc acc gct ggc gac gat cca gtc ctt acc 1459
 phe glu trp glu pro met thr thr ala gly asp asp pro val leu thr
 440 445 450

gga cgt ggc acc gat gtg cgc ctt gaa cag acc tct cgt atc tct gct 1507
 gly arg gly thr asp val arg leu glu gln thr ser arg ile ser ala
 455 460 465

gca gag cgt aaa cgc gca tct cag gta cgt cgt ggc ctc atc gat gag 1555
 ala glu arg lys arg ala ser gln val arg arg gly leu ile asp glu
 470 475 480 485

ttg gat tat ggc gag gac caa gag gct tcc cgc gaa cgc tgg gaa gga 1603
 leu asp tyr gly glu asp gln glu ala ser arg glu arg trp glu gly
 490 495 500

taaaaccgag cacttttcag gtc 1626

<210> 218
 <211> 501
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 218
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 1 5 10 15

0060874.062000

Gly	Gly	Asn	Gly	Cys	Val	Ser	Val	His	Arg	Glu	Lys	Phe	Lys	Pro	Leu
		20							25				30		
Gly	Gly	Pro	Asp	Gly	Gly	Asn	Gly	Gly	His	Gly	Gly	Asp	Ile	Ile	Leu
		35					40					45			
Glu	Val	Thr	Ala	Gln	Val	His	Thr	Leu	Leu	Asp	Phe	His	Phe	His	Pro
	50					55					60				
His	Val	Lys	Ala	Glu	Arg	Gly	Ala	Asn	Gly	Ala	Gly	Asp	His	Arg	Asn
	65				70					75					80
Gly	Ala	Arg	Gly	Lys	Asp	Leu	Val	Leu	Glu	Val	Pro	Pro	Gly	Thr	Val
			85					90						95	
Val	Leu	Asn	Glu	Lys	Gly	Glu	Thr	Leu	Ala	Asp	Leu	Thr	Ser	Val	Gly
			100					105					110		
Met	Lys	Phe	Ile	Ala	Ala	Ala	Gly	Gly	Asn	Gly	Gly	Leu	Gly	Asn	Ala
	115						120					125			
Ala	Leu	Ala	Ser	Lys	Ala	Arg	Lys	Ala	Pro	Gly	Phe	Ala	Leu	Ile	Gly
	130					135					140				
Glu	Pro	Gly	Glu	Ala	His	Asp	Leu	Ile	Leu	Glu	Leu	Lys	Ser	Met	Ala
	145				150					155					160
Asp	Val	Gly	Leu	Val	Gly	Phe	Pro	Ser	Ala	Gly	Lys	Ser	Ser	Leu	Ile
			165						170					175	
Ser	Val	Met	Ser	Ala	Ala	Lys	Pro	Lys	Ile	Gly	Asp	Tyr	Pro	Phe	Thr
		180						185					190		
Thr	Leu	Gln	Pro	Asn	Leu	Gly	Val	Val	Asn	Val	Gly	His	Glu	Thr	Phe
	195						200					205			
Thr	Met	Ala	Asp	Val	Pro	Gly	Leu	Ile	Pro	Gly	Ala	Ser	Glu	Gly	Lys
	210					215					220				
Gly	Leu	Gly	Leu	Asp	Phe	Leu	Arg	His	Ile	Glu	Arg	Thr	Ser	Val	Leu
	225				230					235					240
Val	His	Val	Val	Asp	Thr	Ala	Thr	Met	Asp	Pro	Gly	Arg	Asp	Pro	Ile
				245					250					255	
Ser	Asp	Ile	Glu	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Ala	Tyr	Gln	Ser	Ala
			260					265					270		
Leu	Asp	Glu	Asp	Thr	Gly	Leu	Gly	Asp	Leu	Ser	Gln	Arg	Pro	Arg	Leu
		275					280					285			
Val	Val	Leu	Asn	Lys	Ala	Asp	Val	Pro	Glu	Ala	Glu	Glu	Leu	Ala	Glu
	290					295					300				
Phe	Leu	Lys	Glu	Asp	Ile	Glu	Lys	Gln	Phe	Gly	Trp	Pro	Val	Phe	Ile
	305				310					315					320
Ile	Ser	Ala	Val	Ala	Arg	Lys	Gly	Leu	Asp	Pro	Leu	Lys	Tyr	Lys	Leu
			325						330					335	
Leu	Glu	Ile	Val	Gln	Asp	Ala	Arg	Lys	Lys	Arg	Pro	Lys	Glu	Lys	Ala

340					345					350						
Glu	Ser	Val	Ile	Ile	Lys	Pro	Lys	Ala	Val	Asp	His	Arg	Thr	Lys	Gly	
355					360					365						
Gln	Phe	Gln	Ile	Lys	Pro	Asp	Pro	Glu	Val	Gln	Gly	Gly	Phe	Ile	Ile	
370					375					380						
Thr	Gly	Glu	Lys	Pro	Glu	Arg	Trp	Ile	Leu	Gln	Thr	Asp	Phe	Glu	Asn	
385					390					395					400	
Asp	Glu	Ala	Val	Gly	Tyr	Leu	Ala	Asp	Arg	Leu	Ala	Lys	Leu	Gly	Ile	
405					410					415						
Glu	Asp	Gly	Leu	Arg	Lys	Ala	Gly	Ala	His	Val	Gly	Ala	Asn	Val	Thr	
420					425					430						
Ile	Gly	Gly	Ile	Ser	Phe	Glu	Trp	Glu	Pro	Met	Thr	Thr	Ala	Gly	Asp	
435					440					445						
Asp	Pro	Val	Leu	Thr	Gly	Arg	Gly	Thr	Asp	Val	Arg	Leu	Glu	Gln	Thr	
450					455					460						
Ser	Arg	Ile	Ser	Ala	Ala	Glu	Arg	Lys	Arg	Ala	Ser	Gln	Val	Arg	Arg	
465					470					475					480	
Gly	Leu	Ile	Asp	Glu	Leu	Asp	Tyr	Gly	Glu	Asp	Gln	Glu	Ala	Ser	Arg	
485					490					495						
Glu	Arg	Trp	Glu	Gly												
500																

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<210> 219
<211> 605
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (1)..(582)
<223> RXA01065
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Ile	Leu	Glu	Ala	Val	Arg	Lys	Val	Ser	Pro	Lys	Thr	Pro	Ile	Leu	Gly	
1				5					10					15		
atc	atc	acc	aaa	gca	gac	agc	gtc	tca	cgt	gac	ttg	gtt	gcg	gcc	caa	96
Ile	Ile	Thr	Lys	Ala	Asp	Ser	Val	Ser	Arg	Asp	Leu	Val	Ala	Ala	Gln	
			20					25					30			
ctg	atg	gct	gtc	cat	gag	ctg	ctc	ggc	gga	aac	agc	gag	gta	gtc	cca	144
Leu	Met	Ala	Val	His	Glu	Leu	Glu	Gly	Gly	Asn	Ser	Glu	Val	Val	Pro	
			35				40					45				
gtg	tct	tcc	acc	tcg	ggg	gaa	aac	gtc	gaa	acg	ctt	att	aag	gtc	atg	192
Val	Ser	Ser	Thr	Ser	Gly	Glu	Asn	Val	Glu	Thr	Leu	Ile	Lys	Val	Met	
	50					55					60					
acc	gac	ctg	ctg	cct	gaa	ggc	ccc	aag	ttc	tac	ccg	gat	gat	cac	atc	240

Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile
 65 70 75 80
 acc gat gag gac acc aac acc cgc atc gcg gaa gcc atc cgc gaa gca 288
 Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala
 85 90 95
 gca ctg tct ggc ttg aag aac gaa ctg cgc cac tcc gtc gca gtt gag 336
 Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu
 100 105 110
 gtt gat gaa atc ctg cca gac cca gaa cgc aac ggt gtc ctg gct gtg 384
 Val Asp Glu Ile Leu Pro Asp Pro Glu Arg Asn Gly Val Leu Ala Val
 115 120 125
 cac gcc atc atc tac gtc gag cgt gtt ggt cag aaa gac atc atc gtc 432
 His Ala Ile Ile Tyr Val Glu Arg Val Gly Gln Lys Asp Ile Ile Val
 130 135 140
 gga cac aag gga cag cgc ctg ggg cgc atc atc cac acc tca cgc caa 480
 Gly His Lys Gly Gln Arg Leu Gly Arg Ile Ile His Thr Ser Arg Gln
 145 150 155 160
 gac atc atc aag atc ctc ggc caa aac gta ttc ctt gac ctg cgc atc 528
 Asp Ile Ile Lys Ile Leu Gly Gln Asn Val Phe Leu Asp Leu Arg Ile
 165 170 175
 aag gtg ctg aag aac tgg caa tcc gat cca aag gct ttg aac cgc ctg 576
 Lys Val Leu Lys Asn Trp Gln Ser Asp Pro Lys Ala Leu Asn Arg Leu
 180 185 190
 ggc ttc tagctttaag ggggtgagtt cat 605
 Gly Phe

<210> 220

<211> 194

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 220

Ile Leu Glu Ala Val Arg Lys Val Ser Pro Lys Thr Pro Ile Leu Gly
 1 5 10 15

Ile Ile Thr Lys Ala Asp Ser Val Ser Arg Asp Leu Val Ala Gln
 20 25 30

Leu Met Ala Val His Glu Leu Leu Gly Gly Asn Ser Glu Val Val Pro
 35 40 45

Val Ser Ser Thr Ser Gly Glu Asn Val Glu Thr Leu Ile Lys Val Met
 50 55 60

Thr Asp Leu Leu Pro Glu Gly Pro Lys Phe Tyr Pro Asp Asp His Ile
 65 70 75 80

Thr Asp Glu Asp Thr Asn Thr Arg Ile Ala Glu Ala Ile Arg Glu Ala
 85 90 95

Ala Leu Ser Gly Leu Lys Asn Glu Leu Pro His Ser Val Ala Val Glu

gcc agc ctt gcg gaa ctt gca gcg ttg gct gat acc gcc ggc get gag	451
Ala Ser Leu Ala Glu Leu Ala Ala Leu Ala Asp Thr Ala Gly Ala Glu	
105 110 115	
ggt att gaa acg ctg tac caa aag cgc gat aaa cca gat cct gga acc	499
Val Ile Glu Thr Leu Tyr Gln Lys Arg Asp Lys Pro Asp Pro Gly Thr	
120 125 130	
tac att ggt tcc ggc aag gtt cgg gag tta aag gag atc atc gaa gcc	547
Tyr Ile Gly Ser Gly Lys Val Arg Glu Leu Lys Glu Ile Ile Glu Ala	
135 140 145	
act agt gca gat acc gtg gtg tgc gat ggt gaa ctt agc cct tcc cag	595
Thr Ser Ala Asp Thr Val Val Cys Asp Gly Glu Leu Ser Pro Ser Gln	
150 155 160 165	
ctc gtg gca tta gag cgc gaa ctt gat atc aag gtc att gac cgc acc	643
Leu Val Ala Leu Glu Arg Glu Leu Asp Ile Lys Val Ile Asp Arg Thr	
170 175 180	
atg ctg att ctg gat atc ttc gcc cag cac gct aaa tcg cgc gaa ggt	691
Met Leu Ile Leu Asp Ile Phe Ala Gln His Ala Lys Ser Arg Glu Gly	
185 190 195	
aaa gcc caa gtc gcg ttg gcg cag atg gaa tac ctg att agc cgt gtg	739
Lys Ala Gln Val Ala Leu Ala Gln Met Glu Tyr Leu Ile Ser Arg Val	
200 205 210	
cgt ggt tgg ggt gga aac ctc tcc agg cag gcc ggt ggt cgt gca ggt	787
Arg Gly Trp Gly Gly Asn Leu Ser Arg Gln Ala Gly Gly Arg Ala Gly	
215 220 225	
tct aat ggt ggt gtg ggt ctg cgt ggt cca ggt gaa acc aaa att gaa	835
Ser Asn Gly Gly Val Gly Leu Arg Gly Pro Gly Glu Thr Lys Ile Glu	
230 235 240 245	
gca gac cgc cgt cgt ctt cga tcg gat atg gct cgc ctg cgc agg gaa	883
Ala Asp Arg Arg Arg Leu Arg Ser Asp Met Ala Arg Leu Arg Arg Glu	
250 255 260	
ctt tcg ggg ctg gat acg tcg aga agc att aaa aga gcg caa cgc gca	931
Leu Ser Gly Leu Asp Thr Ser Arg Ser Ile Lys Arg Ala Gln Arg Ala	
265 270 275	
gcc tcc ctg gtg ccg cag atc gcc atc gct ggc tac acg aac gcc ggc	979
Ala Ser Leu Val Pro Gln Ile Ala Ile Ala Gly Tyr Thr Asn Ala Gly	
280 285 290	
aaa tct tcg ctg att aac gcg atg acc ggc cgc ggt gtg ctg gtg gag	1027
Lys Ser Ser Ser Leu Ile Asn Ala Met Thr Gly Ala Gly Val Leu Val Glu	
295 300 305	
aac gcg ctg ttc gcc acg ctt gat cca aca acc aga aaa gcc gac ctt	1075
Asn Ala Leu Phe Ala Thr Leu Asp Pro Thr Thr Arg Lys Ala Glu Leu	
310 315 320 325	
gcc gac ggc cga cac gtc gtg ttc acg gac acc gtc ggc ttt gtg cga	1123
Ala Asp Gly Arg His Val Val Phe Thr Asp Thr Val Gly Phe Val Arg	
330 335 340	

cac ctg ccg acc tct ctg gtt gag gcg ttc aaa tct acg ctg gaa gaa 1171
 His Leu Pro Thr Ser Leu Val Glu Ala Phe Lys Ser Thr Leu Glu Glu
 345 350 355
 gtc gtg gag gcg gac ctc atg ctg cac gtg gtg gat gga tcc gat ccg 1219
 Val Val Glu Ala Asp Leu Met Leu His Val Val Asp Gly Ser Asp Pro
 360 365 370
 ttc ccg ctg aag cag atc gac gct gtg aac acc gtg att agc gat att 1267
 Phe Pro Leu Lys Gln Ile Asp Ala Val Asn Thr Val Ile Ser Asp Ile
 375 380 385
 gtg cga tcc acc ggt gcg gtg cca cca cca gag atc atc gtg gtg aac 1315
 Val Arg Ser Thr Gly Ala Val Pro Pro Glu Ile Ile Val Val Asn
 390 395 400 405
 aaa att gac caa gct gat ccg ctg acg ctg gca gaa cta cgc cac gcc 1363
 Lys Ile Asp Gln Ala Asp Pro Leu Thr Leu Ala Glu Leu Arg His Ala
 410 415 420
 gtc gac gat gtg gtg ttt gtc tct gcg ctg aca ggg gag gga att aag 1411
 Val Asp Asp Val Val Phe Val Ser Ala Leu Thr Gly Glu Gly Ile Lys
 425 430 435
 gag ctg gaa gct cgc atc gaa cta ttc ctc aac tcc agg gac gcg cac 1459
 Glu Leu Glu Ala Arg Ile Glu Leu Phe Leu Asn Ser Arg Asp Ala His
 440 445 450
 cta ctg ctg aaa atc ccg ttc acc cgt gcc gat att gtg tcc cgc ctg 1507
 Leu Leu Leu Lys Ile Pro Phe Thr Arg Gly Asp Ile Val Ser Arg Leu
 455 460 465
 cac cag cat gcc acc gtt ctc agc gaa gac tac gcc gaa gac gcc acc 1555
 His Gln His Gly Thr Val Leu Ser Glu Asp Tyr Ala Glu Asp Gly Thr
 470 475 480 485
 ttg atg gat gtg cgt atc ccc acc caa ttg gcc caa gag ctg cag agt 1603
 Leu Met Asp Val Arg Ile Pro Thr Gln Leu Ala Gln Glu Leu Gln Ser
 490 495 500
 tac gtt gta gaa ccc acc tct gcc taactgtcga ttcccaaga gcc 1650
 Tyr Val Val Glu Pro Thr Ser Ala
 505

<210> 222

<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

Met Asp Glu Lys Lys Asn Leu Ser His Asp Glu Leu Leu Ala Gln Ala
 1 5 10 15

Phe Arg Gly His Lys Asn Thr Val Arg Pro Gly Ser Asp Glu Thr Ser
 20 25 30

Gly Phe Asp Leu Ser Gly Phe Ile Arg Ala Glu Glu Pro Ser Thr Gly
 35 40 45

Asp Leu Asp Leu Glu Ala Arg Asp Ala Gln Arg Arg Arg Asp Thr Glu

50					55					60					
Ile	His	Ala	Asp	Glu	Ala	Ala	Asp	Gly	Tyr	Glu	Val	Glu	Tyr	Arg	Lys
65					70					75					80
Leu	Arg	Leu	Glu	Arg	Val	Ile	Leu	Val	Gly	Val	Trp	Thr	Glu	Gly	Thr
				85					90					95	
Thr	Ala	Glu	Ile	Asp	Ala	Ser	Leu	Ala	Glu	Leu	Ala	Ala	Leu	Ala	Asp
				100				105					110		
Thr	Ala	Gly	Ala	Glu	Val	Ile	Glu	Thr	Leu	Tyr	Gln	Lys	Arg	Asp	Lys
		115					120					125			
Pro	Asp	Pro	Gly	Thr	Tyr	Ile	Gly	Ser	Gly	Lys	Val	Arg	Glu	Leu	Lys
	130					135					140				
Glu	Ile	Ile	Glu	Ala	Thr	Ser	Ala	Asp	Thr	Val	Val	Cys	Asp	Gly	Glu
145				150							155				160
Leu	Ser	Pro	Ser	Gln	Leu	Val	Ala	Leu	Glu	Arg	Glu	Leu	Asp	Ile	Lys
				165					170					175	
Val	Ile	Asp	Arg	Thr	Met	Leu	Ile	Leu	Asp	Ile	Phe	Ala	Gln	His	Ala
			180					185					190		
Lys	Ser	Arg	Glu	Gly	Lys	Ala	Gln	Val	Ala	Leu	Ala	Gln	Met	Glu	Tyr
		195					200					205			
Leu	Ile	Ser	Arg	Val	Arg	Gly	Trp	Gly	Gly	Asn	Leu	Ser	Arg	Gln	Ala
	210					215					220				
Gly	Gly	Arg	Ala	Gly	Ser	Asn	Gly	Gly	Val	Gly	Leu	Arg	Gly	Pro	Gly
225				230					235					240	
Glu	Thr	Lys	Ile	Glu	Ala	Asp	Arg	Arg	Arg	Leu	Arg	Ser	Asp	Met	Ala
			245						250					255	
Arg	Leu	Arg	Arg	Glu	Leu	Ser	Gly	Leu	Asp	Thr	Ser	Arg	Ser	Ile	Lys
			260					265					270		
Arg	Ala	Gln	Arg	Ala	Ala	Ser	Leu	Val	Pro	Gln	Ile	Ala	Ile	Ala	Gly
		275					280					285			
Tyr	Thr	Asn	Ala	Gly	Lys	Ser	Ser	Leu	Ile	Asn	Ala	Met	Thr	Gly	Ala
	290					295					300				
Gly	Val	Leu	Val	Glu	Asn	Ala	Leu	Phe	Ala	Thr	Leu	Asp	Pro	Thr	Thr
305				310					315					320	
Arg	Lys	Ala	Glu	Leu	Ala	Asp	Gly	Arg	His	Val	Val	Phe	Thr	Asp	Thr
			325					330					335		
Val	Gly	Phe	Val	Arg	His	Leu	Pro	Thr	Ser	Leu	Val	Glu	Ala	Phe	Lys
			340					345					350		
Ser	Thr	Leu	Glu	Glu	Val	Val	Glu	Ala	Asp	Leu	Met	Leu	His	Val	Val
		355					360					365			
Asp	Gly	Ser	Asp	Pro	Phe	Pro	Leu	Lys	Gln	Ile	Asp	Ala	Val	Asn	Thr
	370					375					380				

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<210> 224
<211> 57
<212> PRT
<213> Corynebacterium glutamicum
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1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

<400> 224

Thr Thr Val Thr Leu Ala Lys Ala Arg Ser Leu Ser Leu Asp Glu Ala
 1 5 10 15

Leu Glu Phe Cys Gly Val Asp Glu Cys Val Glu Val Thr Pro Asp Val
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Leu Arg Ile Arg Lys Val Ile Leu Asn Ala Thr Glu Arg Gly Arg Ala
 35 40 45

Arg Ser Arg Ala Lys Ser Leu Asn Lys
 50 55

<210> 225

<211> 469

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(469)

<223> FRXA00839

<400> 225

cacaatgtgc ggaacgggagc ataatgcgag tacagtgata ccgttctaaa acaatggact 60

cggtttacaa gtctccata cttctttatc cggcaggaga atg ccc cca gtg acc 115
 Met Pro Pro Val Thr
 1 5

cac cca gag ttt cgt aac gta gcg att gtc gcg cac gtt gac cac gga 163
 His Pro Glu Phe Arg Asn Val Ala Ile Val Ala His Val Asp His Gly
 10 15 20

aag acc aca ctc gtt aat gcc atg ctt gaa cag tct gcc gta ttc agt 211
 Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln Ser Gly Val Phe Ser
 25 30 35

gac cac ggt gaa gta gcc gac cgt gtg atg gac tcc ggt gac ctg gaa 259
 Asp His Gly Glu Val Ala Asp Arg Val Met Asp Ser Gly Asp Leu Glu
 40 45 50

aag gaa aag ggc atc acc atc ctt gcc aag aac acc gcg att cgt cgt 307
 Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile Arg Arg
 55 60 65

aaa ggc gct ggc aag gac ggc aat gac ctg att atc aac gtc att gac 355
 Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile Ile Asn Val Ile Asp
 70 75 80 85

acc cca ggc cac gct gac ttc ggt ggc gaa gtt gag cgc gca ctg tcc 403
 Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val Glu Arg Ala Leu Ser
 90 95 100

atg gtt gac ggc gtt gtc ctt ctg gtt gac gca tct gaa ggc cca ctg 451
 Met Val Asp Gly Val Val Leu Leu Val Asp Ala Ser Glu Gly Pro Leu
 105 110 115

cct cag acc cga ttc gtg 469
 Pro Gln Thr Arg Phe Val

00220 1720000

120

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<210> 226
<211> 123
<212> PRT
<213> Corynebacterium glutamicum
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<400> 226
Met Pro Pro Val Thr His Pro Glu Phe Arg Asn Val Ala Ile Val Ala
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His Val Asp His Gly Lys Thr Thr Leu Val Asn Ala Met Leu Glu Gln
20 25 30

Ser Gly Val Phe Ser Asp His Gly Glu Val Ala Asp Arg Val Met Asp
35 40 45

Ser Gly Asp Leu Glu Lys Glu Lys Gly Ile Thr Ile Leu Ala Lys Asn
50 55 60

Thr Ala Ile Arg Arg Lys Gly Ala Gly Lys Asp Gly Asn Asp Leu Ile
65 70 75 80

Ile Asn Val Ile Asp Thr Pro Gly His Ala Asp Phe Gly Gly Glu Val
85 90 95

Glu Arg Ala Leu Ser Met Val Asp Gly Val Val Leu Leu Val Asp Ala
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Ser Glu Gly Pro Leu Pro Gln Thr Arg Phe Val
115 120

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<211> 903
<212> DNA
<213> Corynebacterium glutamicum
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<222> (1)..(903)  
<223> FRXA00845
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ttg cgt aag ggc cag cag gtt gca tgg att cac tac gat gaa gaa ggt 96
Leu Arg Lys Gly Gln Gln Val Ala Trp Ile His Tyr Asp Glu Glu Gly
20 25 30

aac cag cac acc aag acc gct aag atc gca gag ctt ctg gct acc gtt 144
Asn Gln His Thr Lys Thr Ala Lys Ile Ala Glu Leu Leu Ala Thr Val
35 40 45

ggc gtt gcc cgc gtt cct gct acc gaa gtt gtt gca ggt gac atc gct 192
Gly Val Ala Arg Val Pro Ala Thr Glu Val Val Ala Gly Asp Ile Ala
50 55 60

gct atc tcc ggc atc gaa gac atc atg att ggc gat acc ctc gcg gat 240
 Ala Ile Ser Gly Ile Glu Asp Ile Met Ile Gly Asp Thr Leu Ala Asp
 65 70 75 80

cct gag aac cca gtt gca ctg cct cgc atc acc gtt gat gag cca gca 288
 Pro Glu Asn Pro Val Ala Leu Pro Arg Ile Thr Val Asp Glu Pro Ala
 85 90 95

ctg tcc atg acc atc ggt gtg aac acc tca cca atg gct ggt cgt ggc 336
 Leu Ser Met Thr Ile Gly Val Asn Thr Ser Pro Met Ala Gly Arg Gly
 100 105 110

ggc gga gac aag ctg acc gca cgt gtg gtc aag gct cgt ctt gag aac 384
 Gly Gly Asp Lys Leu Thr Ala Arg Val Val Lys Ala Arg Leu Glu Asn
 115 120 125

gaa ctg atc ggt aac gtg tcc ctg aag gtc aac cca act gag cgc cca 432
 Glu Leu Ile Gly Asn Val Ser Leu Lys Val Asn Pro Thr Glu Arg Pro
 130 135 140

gat acc tgg gaa gtt cag ggt cgt ggc gaa atg gct ctg tcc atc ctc 480
 Asp Thr Trp Glu Val Gln Gly Arg Gly Glu Met Ala Leu Ser Ile Leu
 145 150 155 160

gtt gag acc atg cgt cgc gaa ggc ttc gag ctc acc gtt ggt aag cca 528
 Val Glu Thr Met Arg Arg Glu Gly Phe Glu Leu Thr Val Gly Lys Pro
 165 170 175

cag gtt gtt acc cag acc atc gac ggc aag ctg cac gag cct tac gag 576
 Gln Val Val Thr Gln Thr Ile Asp Gly Lys Leu His Glu Pro Tyr Glu
 180 185 190

atc atc gtc atc gac gtt cct tcc gag tac cag ggc aac gtg acc cag 624
 Ile Ile Val Ile Asp Val Pro Ser Glu Tyr Gln Gly Asn Val Thr Gln
 195 200 205

ctg ctg gct acc cgc aag ggc ctc atg cag tcc atg tcc acc acc cca 672
 Leu Leu Ala Thr Arg Lys Gly Leu Met Gln Ser Met Ser Thr Thr Pro
 210 215 220

ggt tcc gac tgg atc cgc atg gaa ttc cgt att cct gct cgt ggc ctg 720
 Gly Ser Asp Trp Ile Arg Met Glu Phe Arg Ile Pro Ala Arg Gly Leu
 225 230 235 240

att ggt ttc cgt acc cag ttc atg act gaa acc cgt ggt acc ggt atc 768
 Ile Gly Phe Arg Thr Gln Phe Met Thr Glu Thr Arg Gly Thr Gly Ile
 245 250 255

gct aac tcc tac tct gac ggc atg gat gtt tgg gct ggc gaa atc aag 816
 Ala Asn Ser Tyr Ser Asp Gly Met Asp Val Trp Ala Gly Glu Ile Lys
 260 265 270

ggc cgc gca cac ggt tcc ttg gtt gct gac cgt tcc ggc cag atc acc 864
 Gly Arg Ala His Gly Ser Leu Val Ala Asp Arg Ser Gly Gln Ile Thr
 275 280 285

gct tac gct ctg acc cag ctg gca gac cgt ggt agc ttc 903
 Ala Tyr Ala Leu Thr Gln Leu Ala Asp Arg Gly Ser Phe
 290 295 300

UNRECORDED

<210> 228
 <211> 301
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 228
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 Leu Arg Lys Gly Gln Gln Val Ala Trp Ile His Tyr Asp Glu Gly
 20 25 30
 Asn Gln His Thr Lys Thr Ala Lys Ile Ala Glu Leu Leu Ala Thr Val
 35 40 45
 Gly Val Ala Arg Val Pro Ala Thr Glu Val Val Ala Gly Asp Ile Ala
 50 55 60
 Ala Ile Ser Gly Ile Glu Asp Ile Met Ile Gly Asp Thr Leu Ala Asp
 65 70 75 80
 Pro Glu Asn Pro Val Ala Leu Pro Arg Ile Thr Val Asp Glu Pro Ala
 85 90 95
 Leu Ser Met Thr Ile Gly Val Asn Thr Ser Pro Met Ala Gly Arg Gly
 100 105 110
 Gly Gly Asp Lys Leu Thr Ala Arg Val Val Lys Ala Arg Leu Glu Asn
 115 120 125
 Glu Leu Ile Gly Asn Val Ser Leu Lys Val Asn Pro Thr Glu Arg Pro
 130 135 140
 Asp Thr Trp Glu Val Gln Gly Arg Gly Glu Met Ala Leu Ser Ile Leu
 145 150 155 160
 Val Glu Thr Met Arg Arg Glu Gly Phe Glu Leu Thr Val Gly Lys Pro
 165 170 175
 Gln Val Val Thr Gln Thr Ile Asp Gly Lys Leu His Glu Pro Tyr Glu
 180 185 190
 Ile Ile Val Ile Asp Val Pro Ser Glu Tyr Gln Gly Asn Val Thr Gln
 195 200 205
 Leu Leu Ala Thr Arg Lys Gly Leu Met Gln Ser Met Ser Thr Thr Pro
 210 215 220
 Gly Ser Asp Trp Ile Arg Met Glu Phe Arg Ile Pro Ala Arg Gly Leu
 225 230 235 240
 Ile Gly Phe Arg Thr Gln Phe Met Thr Glu Thr Arg Gly Thr Gly Ile
 245 250 255
 Ala Asn Ser Tyr Ser Asp Gly Met Asp Val Trp Ala Gly Glu Ile Lys
 260 265 270
 Gly Arg Ala His Gly Ser Leu Val Ala Asp Arg Ser Gly Gln Ile Thr
 275 280 285
 Ala Tyr Ala Leu Thr Gln Leu Ala Asp Arg Gly Ser Phe

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<223> RXA02365																
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	1			5					10							
ggt	ggc	atg	gac	tac	ctt	tcg	gag	gac	cgc	gtg	gag	ctg	cgc	tac	acc	99
Gly	Gly	Met	Asp	Tyr	Leu	Ser	Glu	Asp	Arg	Val	Glu	Leu	Arg	Tyr	Thr	
		15						20					25			
atg	cct	tgg	ggt	gag	atc	atc	ttt	gac	ttc	ttc	gat	atg	ttg	aag	tct	147
Met	Pro	Leu	Gly	Glu	Ile	Ile	Phe	Asp	Phe	Phe	Asp	Met	Leu	Lys	Ser	
		30					35					40				
cgc	acc	aag	ggt	tac	gct	tcg	ctg	aac	tac	gag	gaa	gct	ggc	gag	cag	195
Arg	Thr	Lys	Gly	Tyr	Ala	Ser	Leu	Asn	Tyr	Glu	Met	Ala	Gly	Glu	Gln	
	45					50					55					
act	gcc	gac	ctg	gtc	aag	gta	gat	atc	ttg	ctc	caa	ggt	gaa	cct	gtg	243
Thr	Ala	Asp	Leu	Val	Lys	Val	Asp	Ile	Leu	Leu	Gln	Gly	Glu	Pro	Val	
	60				65				70					75		
gat	gca	ttc	tct	gcg	atc	gtg	cac	cgc	gat	aat	gcg	cag	tggt	tac	gga	291
Asp	Ala	Phe	Ser	Ala	Ile	Val	His	Arg	Asp	Asn	Ala	Gln	Trp	Tyr	Gly	
				80					85					90		
aac	aag	atg	act	gtg	aag	ctg	aag	gaa	ctg	atc	cct	cgc	cag	cag	ttc	339
Asn	Lys	Met	Thr	Val	Lys	Leu	Lys	Glu	Leu	Ile	Pro	Arg	Gln	Gln	Phe	
			95					100					105			
gaa	gtt	cct	gtg	cag	gca	gcc	att	ggt	tcc	aag	gtt	atc	gct	cggt	gaa	387
Glu	Val	Pro	Val	Gln	Ala	Ala	Ile	Gly	Ser	Lys	Val	Ile	Ala	Arg	Glu	
		110				115						120				
aac	att	cggt	gca	ctg	cgct	aag	gac	gtg	ttg	gcg	aag	tgt	tac	gggt	ggc	435
Asn	Ile	Arg	Ala	Leu	Arg	Lys	Asp	Val	Leu	Ala	Lys	Cys	Tyr	Gly	Gly	
	125					130					135					
gat	att	tcc	cggt	aag	cgct	aag	ctt	ctg	gaa	aag	cag	aag	gct	gggt	aag	483
Asp	Ile	Ser	Arg	Lys	Arg	Lys	Leu	Leu	Glu	Lys	Gln	Lys	Ala	Gly	Lys	
	140				145				150					155		
aag	cgct	atg	aag	aac	atc	gggt	tcg	gtc	gag	gtt	cct	cag	gaa	gca	ttc	531
Lys	Arg	Met	Lys	Asn	Ile	Gly	Ser	Val	Glu	Val	Pro	Gln	Glu	Ala	Phe	
			160													

tag

581

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 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Ile Ile Phe Asp Phe Phe Asp Met Leu Lys Ser Arg Thr Lys Gly Tyr
 35 40 45
 Ala Ser Leu Asn Tyr Glu Glu Ala Gly Glu Gln Thr Ala Asp Leu Val
 50 55 60
 Lys Val Asp Ile Leu Leu Gln Gly Glu Pro Val Asp Ala Phe Ser Ala
 65 70 75 80
 Ile Val His Arg Asp Asn Ala Gln Trp Tyr Gly Asn Lys Met Thr Val
 85 90 95
 Lys Leu Lys Glu Leu Ile Pro Arg Gln Gln Phe Glu Val Pro Val Gln
 100 105 110
 Ala Ala Ile Gly Ser Lys Val Ile Ala Arg Glu Asn Ile Arg Ala Leu
 115 120 125
 Arg Lys Asp Val Leu Ala Lys Cys Tyr Gly Gly Asp Ile Ser Arg Lys
 130 135 140
 Arg Lys Leu Leu Glu Lys Gln Lys Ala Gly Lys Lys Arg Met Lys Asn
 145 150 155 160
 Ile Gly Ser Val Glu Val Pro Gln Glu Ala Phe Val Ala Ala Leu Ser
 165 170 175
 Thr Asp Glu Ala
 180

<210> 231
 <211> 1360
 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <221> CDS
 <222> (101)..(1360)
 <223> FRXA02392

<400> 231
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000001 123CP 123CP 123CP

Met Ala Glu Lys Phe
1 5

gca gaa aca aca ttt acg gat cca gcc agg att cgt aac ttc tgc atc 163
Ala Glu Thr Thr Phe Thr Asp Pro Ala Arg Ile Arg Asn Phe Cys ile
10 15 20

att gcc cac att gac cac ggt aaa tct acg ctc gct gac cgt atc ctg 211
Ile Ala His Ile Asp His Gly Lys Ser Thr Leu Ala Asp Arg Ile Leu
25 30 35

cag ctg tct aac gtt gtg gat gcc cgc gat atg cgt gat cag tac ctg 259
Gln Leu Ser Asn Val Val Asp Ala Arg Asp Met Arg Asp Gln Tyr Leu
40 45 50

gac aac atg gac atc gaa cgt gaa cgt gcc att acc att aag gct cag 307
Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile Thr Ile Lys Ala Gln
55 60 65

aac gtt cgc ctg cca tgg att cct cgc agt ggt gag tac gag gcc cag 355
Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly Glu Tyr Glu Gly Gln
70 75 80 85

cag atc gtc atg cag atg atc gat acg cca gcc cac gtg gac ttc acc 403
Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly His Val Asp Phe Thr
90 95 100

tat gaa gtg tct cgg gcg ctt gaa gcg tgt gaa gcc gcg att ttg ctt 451
Tyr Glu Val Ser Arg Ala Leu Glu Ala Cys Glu Gly Ala Ile Leu Leu
105 110 115

gtt gat gca gcg cag gcc att gaa gcc cag acc ttg gca aac ttg tat 499
Val Asp Ala Ala Gln Gly Ile Glu Ala Gln Thr Leu Ala Asn Leu Tyr
120 125 130

ttg gct atg gaa aac gat ctt gag atc atc cct gtg ctg aac aag att 547
Leu Ala Met Glu Asn Asp Leu Glu Ile Ile Pro Val Leu Asn Lys Ile
135 140 145

gac ctt cca gcg gcg gat cca gac aag tac gcg ttg gag atc gcc aac 595
Asp Leu Pro Ala Ala Asp Pro Asp Lys Tyr Ala Leu Glu Ile Ala Asn
150 155 160 165

att gtg ggt tgt gaa cct gaa gat gtg ttg cgc gtg tcc ggt aaa act 643
Ile Val Gly Cys Glu Pro Glu Asp Val Leu Arg Val Ser Gly Lys Thr
170 175 180

ggc atg ggt gtc cct gag ctt ctg gat aag gtc gtt gaa ctt atc cca 691
Gly Met Gly Val Pro Glu Leu Leu Asp Lys Val Val Glu Leu Ile Pro
185 190 195

gca cct acc tct gaa ttt gag gaa gac gcc cca gct cgt gcg atg att 739
Ala Pro Thr Ser Glu Phe Glu Glu Asp Ala Pro Ala Arg Ala Met Ile
200 205 210

ttc gac tct gtc tat gac acc tac cgc gcc gtg gtt acc tac atc cgc 787
Phe Asp Ser Val Tyr Asp Thr Tyr Arg Gly Val Val Thr Tyr Ile Arg
215 220 225

atg atg gac gcc aag ctg aca cct cgc caa aag atc aag atg atg tcc 835
Met Met Asp Gly Lys Leu Thr Pro Arg Gln Lys Ile Lys Met Met Ser

0062387-062300

Arg Asp Gln Tyr Leu Asp Asn Met Asp Ile Glu Arg Glu Arg Gly Ile
 50 55 60
 Thr Ile Lys Ala Gln Asn Val Arg Leu Pro Trp Ile Pro Arg Ser Gly
 65 70 75 80
 Glu Tyr Glu Gly Gln Gln Ile Val Met Gln Met Ile Asp Thr Pro Gly
 85 90 95
 His Val Asp Phe Thr Tyr Glu Val Ser Arg Ala Leu Glu Ala Cys Glu
 100 105 110
 Gly Ala Ile Leu Leu Val Asp Ala Ala Gln Gly Ile Glu Ala Gln Thr
 115 120 125
 Leu Ala Asn Leu Tyr Leu Ala Met Glu Asn Asp Leu Glu Ile Ile Pro
 130 135 140
 Val Leu Asn Lys Ile Asp Leu Pro Ala Ala Asp Pro Asp Lys Tyr Ala
 145 150 155 160
 Leu Glu Ile Ala Asn Ile Val Gly Cys Glu Pro Glu Asp Val Leu Arg
 165 170 175
 Val Ser Gly Lys Thr Gly Met Gly Val Pro Glu Leu Leu Asp Lys Val
 180 185 190
 Val Glu Leu Ile Pro Ala Pro Thr Ser Glu Phe Glu Glu Asp Ala Pro
 195 200 205
 Ala Arg Ala Met Ile Phe Asp Ser Val Tyr Asp Thr Tyr Arg Gly Val
 210 215 220
 Val Thr Tyr Ile Arg Met Met Asp Gly Lys Leu Thr Pro Arg Gln Lys
 225 230 235 240
 Ile Lys Met Met Ser Thr Gly Ala Thr His Glu Leu Leu Glu Ile Gly
 245 250 255
 Ile Val Ser Pro Thr Pro Lys Lys Cys Val Gly Leu Gly Pro Gly Glu
 260 265 270
 Val Gly Tyr Leu Ile Thr Gly Val Lys Asp Val Arg Gln Ser Lys Val
 275 280 285
 Gly Asp Thr Val Thr Trp Ala Ile His Gly Ala Glu Gln Pro Leu Arg
 290 295 300
 Gly Tyr Gln Glu Pro Thr Pro Met Val Tyr Ser Gly Leu Phe Pro Ile
 305 310 315 320
 Ser Gln Ala Asp Phe Pro Asp Leu Arg Asp Ala Leu Glu Lys Leu Gln
 325 330 335
 Leu Asn Asp Ala Ser Leu Thr Tyr Glu Pro Glu Thr Ser Val Ala Leu
 340 345 350
 Gly Phe Gly Phe Arg Cys Gly Phe Leu Gly Leu Leu His Met Glu Ile
 355 360 365

Thr Arg Asp Arg Leu Glu Arg Glu Phe Gly Leu Asp Leu Ile Ser Thr
 370 375 380

Ala Pro Ser Val Asn Tyr Arg Val Ile Asp Glu Ala Gly Lys Glu Phe
 385 390 395 400

Arg Val His Asn Pro Ser Asp Trp Pro Gly Gly Lys Leu Ser Glu Val
 405 410 415

Tyr Glu Pro Ile
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<210> 233

<211> 2205

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2182)

<223> RXA01573

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aaaaaccggc gcattgccgg tattttttcca ggagaattta atg aag agg ctt tcc 115
 Met Lys Arg Leu Ser
 1 5

cgt gca gcc ctc gca gtg gtc gcc acc acc gca gtt agc ttc agc gca 163
 Arg Ala Ala Leu Ala Val Val Ala Thr Thr Ala Val Ser Phe Ser Ala
 10 15 20

ctc gca gtt cca gct ttc gca gac gaa gca agc aat gtt gag ctc aac 211
 Leu Ala Val Pro Ala Phe Ala Asp Glu Ala Ala Ser Asn Val Glu Leu Asn
 25 30 35

atc ctc ggt gtc acc gac ttc cac gga cac atc gag cag aag gct gtt 259
 Ile Leu Gly Val Thr Asp Phe His Gly His Ile Glu Gln Lys Ala Val
 40 45 50

aaa gat gat aag gga gta atc acc ggt tac tca gaa atg ggt gcc agt 307
 Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser Glu Met Gly Ala Ser
 55 60 65

ggc gtt gcc tgc tac gtc gac gct gaa cgc gcg gac aac cca aac acc 355
 Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala Asp Asn Pro Asn Thr
 70 75 80 85

cgc ttc atc acc gtt ggt gac aac att ggt gga tcc cca ttc gtg tcc 403
 Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly Ser Pro Phe Val Ser
 90 95 100

tcc atc ctg aag gat gag cca acc ttg caa gcc ctc agc gcc atc ggt 451
 Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala Leu Ser Ala Ile Gly
 105 110 115

gtt gac gca tcc gca ctg ggc aat cac gaa ttc gac cag ggc tac tca 499
 Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe Asp Gln Gly Tyr Ser
 120 125 130

gtc aac gac gcg acc atc ctg aac gct gac atc ggc atc atg aac gca 1267
Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile Gly Ile Met Asn Ala
375 380 385

ggc ggc gtg cgt gcg gac ctc gaa gca ggc gaa gtt acc ttc gca gat 1315
Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu Val Thr Phe Ala Asp
390 395 400 405

gca tac gca acc cag aac ttc tcc aac acc tac ggc gta cgt gaa gtg 1363
Ala Tyr Ala Thr Gln Asn Phe Ser Asn Thr Tyr Gly Val Arg Glu Val
410 415 420

tct ggt gcg cag ttc aaa gaa gca ctg gaa cag cag tgg aag gaa acc 1411
Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln Gln Trp Lys Glu Thr
425 430 435

ggc gac cgc cca cgt ctg gca ttg gga ctg tcc agc aac gtc cag tac 1459
Gly Asp Arg Pro Arg Leu Ala Leu Gly Leu Ser Ser Asn Val Gln Tyr
440 445 450

tcc tac gac gag acc cgc gaa tac ggc gac cgc atc acc cac atc acc 1507
Ser Tyr Asp Glu Thr Arg Glu Tyr Gly Asp Arg Ile Thr His Ile Thr
455 460 465

ttc aac ggt gag cca atg gat atg aag gag acc tac cgc gtc aca gga 1555
Phe Asn Gly Glu Pro Met Asp Met Lys Glu Thr Tyr Arg Val Thr Gly
470 475 480 485

tca tcc ttc ctg ctc gca ggt ggc gac tcc ttc act gca ttc gct gaa 1603
Ser Ser Phe Leu Leu Ala Gly Gly Asp Ser Phe Thr Ala Phe Ala Glu
490 495 500

ggc ggc cca atc gct gaa acc ggc atg gtt gac att gac ctg ttc aac 1651
Gly Gly Pro Ile Ala Glu Thr Gly Met Val Asp Ile Asp Leu Phe Asn
505 510 515

aac tac atc gca gct cac cca gat gca cca att cgt gca aat cag agc 1699
Asn Tyr Ile Ala Ala His Pro Asp Ala Pro Ile Arg Ala Asn Gln Ser
520 525 530

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Ser Val Gly Ile Ala Leu Ser Gly Pro Ala Val Ala Glu Asp Gly Thr
535 540 545

ttg gtc cct ggt gaa gag ctg acc gtc gat ctt tct tcc ctc tcc tac 1795
Leu Val Pro Gly Glu Glu Leu Thr Val Asp Leu Ser Ser Leu Ser Tyr
550 555 560 565

acc gga cct gaa gct aag cca acc acc gtt gag gtg acc gtt ggt act 1843
Thr Gly Pro Glu Ala Lys Pro Thr Thr Val Glu Val Thr Val Gly Thr
570 575 580

gag aag aag act gcg gac gtc gat aac acc atc gtt cct cag ttt gac 1891
Glu Lys Lys Thr Ala Asp Val Asp Asn Thr Ile Val Pro Gln Phe Asp
585 590 595

agc acc ggc aag gca act gtc acc ctg act gtt cct gag gga gct acc 1939
Ser Thr Gly Lys Ala Thr Leu Thr Val Pro Glu Gly Ala Thr
600 605 610

tct gtc aag atc gca act gac aat ggc act acc ttt gaa ctg cca gta 1987

Ser Val Lys Ile Ala Thr Asp Asn Gly Thr Thr Phe Glu Leu Pro Val
 615 620 625

acc gta aac ggt gaa ggc aac aat gat gac gat gat aag gag cag 2035
 Thr Val Asn Gly Glu Gly Asn Asn Asp Asp Asp Asp Lys Glu Gln
 630 635 640 645

cag tcc tcc gga tcc tcc gac gcc ggt tcc ctt gta gca gtt ctc ggt 2083
 Gln Ser Ser Gly Ser Ser Asp Ala Gly Ser Leu Val Ala Val Leu Gly
 650 655 660

gtt ctt gga gca ctc ggt ggc ctg gtg gcg ttc ttc ctg aac tct gcg 2131
 Val Leu Gly Ala Leu Gly Gly Leu Val Ala Phe Phe Leu Asn Ser Ala
 665 670 675

cag gcc gca cca ttc ttg gct cag ctt cag gct atg ttt gcg cag ttc 2179
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 680 685 690

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 Met

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 <211> 694
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 234
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Asn Val Glu Leu Asn Ile Leu Gly Val Thr Asp Phe His Gly His Ile
 35 40 45

Glu Gln Lys Ala Val Lys Asp Asp Lys Gly Val Ile Thr Gly Tyr Ser
 50 55 60

Glu Met Gly Ala Ser Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala
 65 70 75 80

Asp Asn Pro Asn Thr Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly
 85 90 95

Ser Pro Phe Val Ser Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala
 100 105 110

Leu Ser Ala Ile Gly Val Asp Ala Ser Ala Leu Gly Asn His Glu Phe
 115 120 125

Asp Gln Gly Tyr Ser Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser
 130 135 140

Gly Ser Ala Lys Phe Pro Tyr Leu Gly Ala Asn Val Glu Gly Gly Thr
 145 150 155 160

Pro Ala Pro Ala Lys Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile

00220-102000

165 170 175

Ala Tyr Val Gly Ala Val Thr Glu Glu Thr Ala Thr Leu Val Ser Pro
180 185 190

Ala Gly Ile Glu Gly Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn
195 200 205

Ala Glu Ala Asp Arg Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile
210 215 220

Ala Leu Ile His Ala Glu Ala Ala Pro Thr Asp Leu Phe Ser Asn Asn
225 230 235 240

Val Asp Val Val Phe Ser Gly His Thr His Phe Asp Tyr Val Ala Glu
245 250 255

Gly Glu Ala Arg Gly Asp Lys Gln Pro Leu Val Val Ile Gln Gly His
260 265

Glu Tyr Gly Lys Val Ile Ser Asp Val Glu Ile Ser Tyr Asp Arg Glu
275 280 285

Ala Gly Lys Ile Thr Asn Ile Glu Ala Lys Asn Val Ser Ala Thr Asp
290 295 300

Val Val Glu Asn Cys Glu Thr Pro Asn Thr Ala Val Asp Ala Ile Val
305 310 315 320

Ala Ala Ala Val Glu Ala Ala Glu Glu Ala Gly Asn Glu Val Val Ala
325 330 335

Thr Ile Asp Asn Gly Phe Tyr Arg Gly Ala Asp Glu Glu Gly Thr Thr
340 345

Gly Ser Asn Arg Gly Val Glu Ser Ser Leu Ser Asn Leu Ile Ala Glu
355 360 365

Ala Gly Leu Trp Ala Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile
370 375 380

Gly Ile Met Asn Ala Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu
385 390 395

Val Thr Phe Ala Asp Ala Tyr Ala Thr Gln Asn Phe Ser Asn Thr Tyr
405 410 415

Gly Val Arg Glu Val Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln
420 425 430

Gln Trp Lys Glu Thr Gly Asp Arg Pro Arg Leu Ala Leu Gly Leu Ser
435 440 445

Ser Asn Val Gln Tyr Ser Tyr Asp Glu Thr Arg Glu Tyr Gly Asp Arg
450 455 460

Ile Thr His Ile Thr Phe Asn Gly Glu Pro Met Asp Met Lys Glu Thr
465 470 475 480

Tyr Arg Val Thr Gly Ser Ser Phe Leu Leu Ala Gly Gly Asp Ser Phe
485 490 495

Thr Ala Phe Ala Glu Gly Gly Pro Ile Ala Glu Thr Gly Met Val Asp
500 505 510

Ile Asp Leu Phe Asn Asn Tyr Ile Ala Ala His Pro Asp Ala Pro Ile
515 520 525

Arg Ala Asn Gln Ser Ser Val Gly Ile Ala Leu Ser Gly Pro Ala Val
530 535 540

Ala Glu Asp Gly Thr Leu Val Pro Gly Glu Glu Leu Thr Val Asp Leu
545 550 555 560

Ser Ser Leu Ser Tyr Thr Gly Pro Glu Ala Lys Pro Thr Thr Val Glu
565 570 575

Val Thr Val Gly Thr Glu Lys Lys Thr Ala Asp Val Asp Asn Thr Ile
580 585 590

Val Pro Gln Phe Asp Ser Thr Gly Lys Ala Thr Val Thr Leu Thr Val
595 600 605

Pro Glu Gly Ala Thr Ser Val Lys Ile Ala Thr Asp Asn Gly Thr Thr
610 615 620

Phe Glu Leu Pro Val Thr Val Asn Gly Glu Gly Asn Asn Asp Asp Asp
625 630 635 640

Asp Asp Lys Glu Gln Gln Ser Ser Gly Ser Ser Asp Ala Gly Ser Leu
645 650 655

Val Ala Val Leu Gly Val Leu Gly Ala Leu Gly Gly Leu Val Ala Phe
660 665 670

Phe Leu Asn Ser Ala Gln Gly Ala Pro Phe Leu Ala Gln Leu Gln Ala
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Met Phe Ala Gln Phe Met
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<213> Corynebacterium glutamicum

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Met Ile Pro Leu Ile
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aat gta cgt ttt ccc gtt gcc gcc tta cct ctc gca tta gtg gcg act 163
Asn Val Arg Phe Pro Val Ala Ala Leu Pro Leu Ala Leu Val Ala Thr
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gta tgg ctt aat gct tgg gca gac cat ctt ctc cta act ggt ttt att 211
 Val Trp Leu Asn Ala Trp Ala Asp His Leu Leu Leu Thr Gly Phe Ile
 25 30 35

gtt tat ctt gct gtg gaa tac gca aca agc cgt ggg cgc ttc gct ctc 259
 Val Tyr Leu Ala Val Glu Tyr Ala Thr Ser Arg Gly Arg Phe Ala Leu
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gca ttg att ttg gga gtt gaa tgg atc tta att gct tat ggg gta gct 307
 Ala Leu Ile Leu Gly Val Glu Trp Ile Leu Ile Ala Tyr Gly Val Ala
 55 60 65

ttg gaa agg cct ctt gag gct aaa gac tct cca tct ctc att acc gaa 355
 Leu Glu Arg Pro Leu Glu Ala Lys Asp Ser Pro Ser Leu Ile Thr Glu
 70 75 80 85

att ttg ctc ata ctt gta gca gct ggc aca ggg gca ggt cgg tgg aaa 403
 Ile Leu Leu Ile Leu Val Ala Ala Gly Thr Gly Ala Gly Arg Trp Lys
 90 95 100

att ttg agt gaa cgc aag caa cgt gca att act cag cag gaa atc atc 451
 Ile Leu Ser Glu Arg Lys Gln Arg Ala Ile Thr Gln Gln Glu Ile Ile
 105 110 115

aaa aaa atc cgt act gat ata gcg cac tat ttg cat gac agt atg gca 499
 Lys Lys Ile Arg Thr Asp Ile Ala His Tyr Leu His Asp Ser Met Ala
 120 125 130

aga tgg ttg gca ata atg ata gtt caa tca aag ctg act gaa cta gag 547
 Arg Ser Leu Ala Ile Met Ile Val Gln Ser Lys Leu Thr Glu Leu Glu
 135 140 145

cct gat cca aaa aag att caa gaa aaa cta aac agt att gcc aaa att 595
 Pro Asp Pro Lys Lys Ile Gln Glu Lys Leu Asn Ser Ile Ala Lys Ile
 150 155 160 165

gga caa gag gca gtg gct gat ttg cat caa tta gtt aga cac ctc gtg 643
 Gly Gln Glu Ala Val Ala Asp Leu His Gln Leu Val Arg His Leu Val
 170 175 180

gtc gag gag tct gct gaa aaa gcc aca gcg ttt gga gca tgg gct gca 691
 Val Glu Glu Ser Ala Glu Lys Ala Thr Ala Phe Gly Ala Trp Ala Ala
 185 190 195

gtt tct att cat gac acg gtt aat tct gcc att cag tta tta gta gat 739
 Val Ser Ile His Asp Thr Val Asn Ser Ala Ile Gln Leu Leu Val Asp
 200 205 210

gca gga cat gtc gtt tcc ttt gac agt aga aaa aag aac tat aag ctg 787
 Ala Gly His Val Val Ser Phe Asp Ser Arg Lys Lys Asn Tyr Lys Leu
 215 220 225

gac cat att gct gaa acg gcg ttt gct tta gcc ttc aat gag gca gtc 835
 Asp His Ile Ala Glu Thr Ala Phe Ala Leu Ala Phe Asn Glu Ala Val
 230 235 240 245

tgt aat gca att aaa cat tct ccg ccc aag gca aac gtt act att cgc 883
 Cys Asn Ala Ile Lys His Ser Pro Pro Lys Ala Asn Val Thr Ile Arg
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4000> 236

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Leu	Thr	Gly	Phe	Ile	Val	Tyr	Leu	Ala	Val	Glu	Tyr	Ala	Thr	Ser	Arg
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Ser	Leu	Ile	Thr	Glu	Ile	Leu	Leu	Ile	Leu	Val	Ala	Ala	Gly	Thr	Gly
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Ala	Gly	Arg	Trp	Lys	Ile	Leu	Ser	Glu	Arg	Lys	Gln	Arg	Ala	Ile	Thr
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Ser	Ile	Ala	Lys	Ile	Gly	Gln	Glu	Ala	Val	Ala	Asp	Leu	His	Gln	Leu
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Val	Arg	His	Leu	Val	Val	Glu	Glu	Ser	Ala	Glu	Lys	Ala	Thr	Ala	Phe

2024

55 60 65

gtg ctg agt ttg ttg tgg gcg agc ctg att tgg gat gga ccg gag cct 355
Val Leu Ser Leu Leu Trp Ala Ser Leu Ile Trp Asp Gly Pro Glu Pro 85
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gcg tat ttg gtg ttt ccg atg ttt ttc ctc gca gtg ttg atc acg aca 403
Ala Tyr Leu Val Phe Pro Met Phe Phe Leu Ala Val Leu Ile Thr Thr 100
90 95

ccg ctg aaa tcc gcg atc atc att gca ata ctg acg gcg atc gcg gtg 451
Pro Leu Lys Ser Ala Ile Ile Ile Ala Ile Leu Thr Ala Ile Ala Val 115
105 110

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Val Thr Leu Ala Met His Leu Gly Phe Ser Val Gly Val Val Thr Gly 130
120 125

ccg atc ctt ggc gcg ttg gtg gcg tgg gta atg ggt acg tgt ttt cag 547
Pro Ile Leu Gly Ala Leu Val Ala Trp Val Met Gly Thr Cys Phe Gln 145
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Leu Leu Ala Gln Ala Leu Lys Glu Leu Val Asp Ala Arg Ala Ser Ala 165
150 155 160

atc cgg gcg tgc aaa agc gct ggc gag cag gca gaa cga gcc cgc ata 643
Ile Arg Ala Ser Lys Ser Ala Gly Glu Gln Ala Glu Arg Ala Arg Ile 180
170 175

gcg ggc gaa ata cat gac act gtg gcg cag ggg ttg tcc tgc att cag 691
Ala Gly Glu Ile His Asp Thr Val Ala Gln Gly Leu Ser Ser Ile Gln 195
185 190

atg ttg ttg cat gcg gcg gaa aaa cgg gtg gat gat ccg cag gcg tta 739
Met Leu Leu His Ala Ala Glu Lys Arg Val Asp Asp Pro Gln Ala Leu 210
200 205

agc cat ata cgg ttg gcc agg caa acg aca gct gat aat ttg gcg gag 787
Ser His Ile Arg Leu Ala Arg Gln Thr Thr Ala Asp Asn Leu Ala Glu 225
215 220

acc agg cag atc att gct gcg ctg caa ccg act cca ctc att ggg gcg 835
Thr Arg Gln Ile Ile Ala Ala Leu Gln Pro Thr Pro Leu Ile Gly Ala 245
230 235 240

gat ctg ccg gtg gcg ttg gcc aga ctg tgc tgc acc acc ccg atg gga 883
Asp Leu Pro Val Ala Leu Ala Arg Leu Ser Ser Thr Thr Pro Met Gly 260
250 255

cag aac atc acg ttt gaa gtc gac gga tcc cca cgg gta tta cct gat 931
Gln Asn Ile Thr Phe Glu Val Asp Gly Ser Pro Arg Val Leu Pro Asp 275
265 270

gcg atg gag gca gag atc gta cga att gcc caa acg ctg ctg gga aat 979
Ala Met Glu Ala Glu Ile Val Arg Ile Ala Gln Thr Leu Leu Gly Asn 290
280 285

gtg gtg cgg cat gca cag gca gat tct gca aaa atg acc ctg aca tat 1027
Val Val Arg His Ala Gln Ala Asp Ser Ala Lys Met Thr Leu Thr Tyr 305
295 300

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 Gln Asp Asp Gln Ile Leu Leu Asp Val Ile Asp Asn Gly Gln Gly Phe
 310 315 320 325

gat gtg gca gaa gtg atc cgt aaa aaa tcc att gga ctg ccc aca gcg 1123
 Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile Gly Leu Pro Thr Ala
 330 335 340

caa cgc cgg gct gaa ggg ctg ggc gga aca ata att att gaa tct aca 1171
 Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile Ile Ile Gly Ser Thr
 345 350 355

atc gga tgc gga act gga att tcc gcc cgt ttt ccc tat cca caa aag 1219
 Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe Pro Tyr Pro Gln Lys
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<212> PRT

<213> Corynebacterium glutamicum

<400> 238

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Arg Ala Ser His Trp Gly Val Trp Val Leu Ala Phe Gly Tyr Gly Val
 35 40 45

Val Tyr Val Ala Gly Val Val Pro Asn Ser Pro Phe Lys Asn His Pro
 50 55 60

Met Ala Trp Phe Leu Val Leu Ser Leu Leu Trp Ala Ser Leu Ile Trp
 65 70 75 80

Asp Gly Pro Glu Pro Ala Tyr Leu Val Phe Pro Met Phe Phe Leu Ala
 85 90 95

Val Leu Ile Thr Thr Pro Leu Lys Ser Ala Ile Ile Ile Ala Ile Leu
 100 105 110

Thr Ala Ile Ala Val Val Thr Leu Ala Met His Leu Gly Phe Ser Val
 115 120 125

Gly Val Val Thr Gly Pro Ile Leu Gly Ala Leu Val Ala Trp Val Met
 130 135 140

Gly Thr Cys Phe Gln Leu Leu Ala Gln Ala Leu Lys Glu Leu Val Asp
 145 150 155 160

Ala Arg Ala Ser Ala Ile Arg Ala Ser Lys Ser Ala Gly Glu Gln Ala
 165 170 175

Glu Arg Ala Arg Ile Ala Gly Glu Ile His Asp Thr Val Ala Gln Gly
180 185 190

Leu Ser Ser Ile Gln Met Leu Leu His Ala Ala Glu Lys Arg Val Asp
195 200 205

Asp Pro Gln Ala Leu Ser His Ile Arg Leu Ala Arg Gln Thr Thr Ala
210 215 220

Asp Asn Leu Ala Glu Thr Arg Gln Ile Ile Ala Ala Leu Gln Pro Thr
225 230 235 240

Pro Leu Ile Gly Ala Asp Leu Pro Val Ala Leu Ala Arg Leu Ser Ser
245 250 255

Thr Thr Pro Met Gly Gln Asn Ile Thr Phe Glu Val Asp Gly Ser Pro
260 265 270

Arg Val Leu Pro Asp Ala Met Glu Ala Glu Ile Val Arg Ile Ala Gln
275 280 285

Thr Leu Leu Gly Asn Val Val Arg His Ala Gln Ala Asp Ser Ala Lys
290 295 300

Met Thr Leu Thr Tyr Gln Asp Asp Gln Ile Leu Leu Asp Val Ile Asp
305 310 315 320

Asn Gly Gln Gly Phe Asp Val Ala Glu Val Ile Arg Lys Lys Ser Ile
325 330 335

Gly Leu Pro Thr Ala Gln Arg Arg Ala Glu Gly Leu Gly Gly Thr Ile
340 345 350

Ile Ile Glu Ser Thr Ile Gly Ser Gly Thr Gly Ile Ser Ala Arg Phe
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Pro Tyr Pro Gln Lys Asp Gln Asp Lys
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<222> (1)..(339)

<223> RXN03071

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aac gag cag atc acc gaa gcc ttc gag cgc gac gtc gtc cca tac gcg 96
Asn Glu Gln Ile Thr Glu Ala Phe Glu Arg Asp Val Val Pro Tyr Ala 30
20 25

gag ctt ttc gac gcc tcc ggc cag att cct tca tcg cag gag ttc ttc 144
Glu Leu Phe Asp Ala Ser Gly Gln Ile Pro Ser Ser Gln Glu Phe Phe

35	40	45	
cgc gtg tca ctc acc gga	cag tat ctt cca gac agt	gag gtt ttg ctg	192
Arg Val Ser Leu Thr Gly	Gln Tyr Leu Pro Asp	Ser Glu Val Leu Leu	
50	55	60	
cgc ctt cgc ccc gtc gac	tcc ggc cca gca ttc	caa tgc tta acc ccc	240
Arg Leu Arg Pro Val Asp	Ser Gly Pro Ala Phe	Gln Ser Leu Thr Pro	
65	70	75	80
ttc gaa ctt gaa aac gga	cag att gtc ctc gtc	aac cgt ggt tac gaa	288
Phe Glu Leu Glu Asn Gly	Gln Ile Val Leu Val	Asn Arg Gly Tyr Glu	
85	90	95	
tca tca gag ggc aca atc	gtc cca gag atc gag	cct gct cct tca cac	336
Ser Ser Glu Gly Thr Ile	Val Pro Glu Ile Glu	Pro Ala Pro Ser His	
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Gln			

<210> 240

<211> 113

<212> PRT

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<400> 240

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			20						25					30	

Glu	Leu	Phe	Asp	Ala	Ser	Gly	Gln	Ile	Pro	Ser	Ser	Gln	Glu	Phe	Phe
	35						40						45		

Arg	Val	Ser	Leu	Thr	Gly	Gln	Tyr	Leu	Pro	Asp	Ser	Glu	Val	Leu	Leu
	50					55						60			

Arg	Leu	Arg	Pro	Val	Asp	Ser	Gly	Pro	Ala	Phe	Gln	Ser	Leu	Thr	Pro
	65					70				75				80	

Phe	Glu	Leu	Glu	Asn	Gly	Gln	Ile	Val	Leu	Val	Asn	Arg	Gly	Tyr	Glu
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Gln

<210> 241

<211> 558

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(535)

<223> RXN03072

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ggattcgccg caagaacgag ggccctccagg ttctgcacct atg gaa gac agc ggc 115
 Met Glu Asp Ser Gly
 1 5

tac acc cag gtc tac gga att aac acc gaa cag atc agt gac gtc acc 163
 Tyr Thr Gln Val Tyr Gly Ile Asn Thr Glu Gln Ile Ser Asp Val Thr
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ggc ctt gat ctt ggc acc gac tac gtc cag gtc gca gaa ggc gaa cct 211
 Gly Leu Asp 25 Gly Thr Asp Tyr Val Gln Val Ala Glu Gly Glu Pro
 30 35

ggt gtt ttg aac cca atg cca ctg cct caa atg gac cgc ggt aac cac 259
 Gly Val Leu Asn Pro Met Pro Leu Pro Gln Met Asp Arg Gly Asn His
 40 45 50

ctc tca tac ggc ttc cag tgg atc gcc ttc ggc atc atg gca cct tta 307
 Leu Ser Tyr Gly Phe Gln Trp Ile Ala Phe Gly Ile Met Ala Pro Leu
 55 60 65

ggg ctt gga tac ttc atc tgg gct gaa atg cgc gaa cga cgc cgc gac 355
 Gly Leu Gly Tyr Phe Ile Trp Ala Glu Met Arg Glu Arg Arg Arg Asp
 70 75 80 85

aaa gca gaa cgc gaa cag atg gcc gag cta aac act ctt gaa cca gtg 403
 Lys Ala Glu Arg Glu Gln Met Ala Glu Leu Asn Thr Leu Glu Pro Val
 90 95 100

gtg gaa acc cct gaa gtt gtt gaa act gca gaa cca acc atc acc ccg 451
 Val Glu Thr Pro Glu Val Val Glu Thr Ala Glu Pro Thr Ile Thr Pro
 105 110 115

gct gca tcc aaa cga cgt tca cgc tac ggc gat caa cac cgc aat cac 499
 Ala Ala Ser Lys Arg Arg Ser Arg Tyr Gly Asp Gln His Arg Asn His
 120 125 130

tac gag aag atc tcc aaa cga gac caa gag cgc ttc taagcccgtc 545
 Tyr Glu Lys Ile Ser Lys Arg Asp Gln Glu Arg Phe
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tcatttttgc acc 558

<210> 242

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

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Ile Ser Asp Val Thr Gly Leu Asp Leu Gly Thr Asp Tyr Val Gln Val
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UNRECORDED

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 <222> (101)..(1321)
 <223> RXN03090

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gggacgacga ctaactaacc cctgaggcac ttctctatttc atg gct aaa tca act 115
                               Met Ala Lys Ser Thr
                               1 5

cct ttg att gca tcg cta cgc tgg cga att gtc ctg tgg atg aca gcg 163
Pro Leu Ile Ala Ser Leu Arg Trp Arg Ile Val Leu Trp Met Thr Ala
                               10 15 20

gtt gtt ttc ttg acc cta gcc agc gtt gtg atc att acc cgt tcg gtg 211
Val Val Phe Leu Thr Leu Ala Ser Val Val Ile Ile Thr Arg Ser Val
                               25 30 35

ctg ctt tca gag gta acc aac acc gcg aac tcg gca gtt gag cag gaa 259
Leu Leu Ser Glu Val Thr Asn Thr Ala Asn Ser Ala Val Glu Gln Glu
                               40 45 50

att gag gag ttt cgt cgc ttt gca gcc gaa gga att gat cca aca act 307
Ile Glu Glu Phe Arg Arg Phe Ala Ala Glu Gly Ile Asp Pro Thr Thr
                               55 60 65

gcg cag cct ttt gag tca ggt cat cgc ctg atg gag gtt tac ctg tcg 355
Ala Gln Pro Phe Glu Ser Gly His Arg Leu Met Glu Val Tyr Leu Ser
                               70 75 80 85

agg cag att ccg gat gaa aat gaa gcc att gtc ggc att ttc ccc gga 403
Arg Gln Ile Pro Asp Glu Asn Glu Ala Ile Val Gly Ile Phe Pro Gly
                               90 95 100

gag ctc att cag gtt gat tac tcc cag ctc agt ggc gcc cat ccg ctt 451
Glu Leu Ile Gln Val Asp Tyr Ser Gln Leu Ser Gly Ala His Pro Leu
                               105 110 115

cct ttg gaa cac tcc gat ccg ttg att tcg gaa atc cga cag acc acg 499
Pro Leu Glu His Ser Asp Pro Leu Ile Ser Glu Ile Arg Gln Thr Thr
                               120 125 130

ctg aat tct gga gtt ttc agc gat ctt gaa cgc gga acc act cac tgg 547
Leu Asn Ser Gly Val Phe Ser Asp Leu Glu Arg Gly Thr Thr His Trp
                               135 140 145

gga aag gtg aat ttc caa act gct tcc ggt gag gcc gat ggt gag ttc 595
Gly Lys Val Asn Phe Gln Thr Ala Ser Gly Glu Ala Asp Gly Glu Phe
                               150 155 160 165

gtt gtc gca ttc ttc gct gat aat ctt aaa gac cag gtc aac ggc cag 643
Val Val Ala Phe Phe Ala Asp Asn Leu Lys Asp Gln Val Asn Gly Gln
                               170 175 180

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 185 190 195

ctg att gct tgg ttg att gcg ggc cag atc att gcc ccg atc cgc aaa 739
 Leu Ile Ala Trp Leu Ile Ala Gly Gln Ile Ile Ala Pro Ile Arg Lys
 200 205 210

ttg agt tcc gtg tcc gca aag atc agt aat tgc gat ctc acc tgg cgc 787
 Leu Ser Ser Val Ser Ala Lys Ile Ser Asn Ser Asp Leu Thr Trp Arg
 215 220 225

gtc cct gtg gag ggt cgt gat gag att gcg cag ctg gcc agg act ttt 835
 Val Pro Val Glu Gly Arg Asp Glu Ile Ala Gln Leu Ala Arg Thr Phe
 230 235 240 245

aat gcc atg ttg gat cgc atc gaa atc gcg tat aac gat cag cgc cag 883
 Asn Ala Met Leu Asp Arg Ile Glu Ile Ala Tyr Asn Asp Gln Arg Gln
 250 255 260

ttc gtt gat gat gcc ggc cac gag ctg cgc acc ccg atc aca gtg gtg 931
 Phe Val Asp Asp Ala Gly His Glu Leu Arg Thr Pro Ile Thr Val Val
 265 270 275

cgt ggc cag tta gag ctt ctc gcc acc acc ccg ccg gag gaa caa gcg 979
 Arg Gly Gln Leu Glu Leu Leu Ala Thr Thr Pro Pro Glu Glu Gln Ala
 280 285 290

cgg tgc att gag ctg gcc acc act gag ttg gat cga atg tgc cga atg 1027
 Arg Ser Ile Glu Leu Ala Thr Thr Glu Leu Asp Arg Met Ser Arg Met
 295 300 305

gtc aat gat ctg ctc acc ctc gca gtc gcc gat tct ggc acc ttc atc 1075
 Val Asn Asp Leu Leu Thr Leu Ala Val Ala Asp Ser Gly Thr Phe Ile
 310 315 320 325

cac gcc cac ccc acg gat gtc acg gat tta aca atc gat atc gaa gac 1123
 His Ala His Pro Thr Asp Val Thr Asp Leu Thr Ile Asp Ile Glu Asp
 330 335 340

aaa gcc cgc acc atc agc gac cga att ttg ctt gtc gac gcc cgc ccg 1171
 Lys Ala Arg Thr Ile Ser Asp Arg Ile Leu Leu Val Asp Ala Arg Pro
 345 350 355

agg gcc tgc tca gcc tgc acg agc agc ggg tca ccg agg cag tgc ttg 1219
 Arg Ala Ser Ser Ala Ser Thr Ser Ser Gly Ser Pro Arg Gln Cys Leu
 360 365 370

gag ttg ttc ggc aat gcg ttg cgc tac agc gat gat gtg gtg gag ttg 1267
 Glu Leu Phe Gly Asn Ala Leu Arg Tyr Ser Asp Asp Val Val Glu Leu
 375 380 385

ggt tca gga ttt caa ggg gtc tgg ccc cca ccg cat ttt tgc cat ttg 1315
 Gly Ser Gly Phe Gln Gly Val Trp Pro Pro His Phe Ser His Leu
 390 395 400 405

ggt tgc tgacaaagga aacggtgttg ata 1344
 Gly Ser

400> 246																			
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Leu	Trp	Met	Thr	Ala	Val	Val	Phe	Leu	Thr	Leu	Ala	Ser	Val	Val	Ile				
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Ile	Thr	Arg	Ser	Val	Leu	Leu	Ser	Glu	Val	Thr	Asn	Thr	Ala	Asn	Ser				
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Ala	Val	Glu	Gln	Glu	Ile	Glu	Glu	Phe	Arg	Arg	Phe	Ala	Ala	Glu	Gly				
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Ile	Asp	Pro	Thr	Thr	Ala	Gln	Pro	Phe	Glu	Ser	Gly	His	Arg	Leu	Met				
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Glu	Val	Tyr	Leu	Ser	Arg	Gln	Ile	Pro	Asp	Glu	Asn	Glu	Ala	Ile	Val				
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Gly	Ile	Phe	Pro	Gly	Glu	Leu	Ile	Gln	Val	Asp	Tyr	Ser	Gln	Leu	Ser				
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Gly	Ala	His	Pro	Leu	Pro	Leu	Glu	His	Ser	Asp	Pro	Leu	Ile	Ser	Glu				
	115						120					125							
Ile	Arg	Gln	Thr	Thr	Leu	Asn	Ser	Gly	Val	Phe	Ser	Asp	Leu	Glu	Arg				
	130					135					140								
Gly	Thr	Thr	His	Trp	Gly	Lys	Val	Asn	Phe	Gln	Thr	Ala	Ser	Gly	Glu				
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Gln	Val	Asn	Gly	Gln	Ile	Gln	Ile	Leu	Ile	Leu	Ile	Gly	Thr	Gly	Gly				
			180					185					190						
Leu	Ile	Ala	Ser	Ile	Leu	Ile	Ala	Trp	Leu	Ile	Ala	Gly	Gln	Ile	Ile				
	195						200					205							
Ala	Pro	Ile	Arg	Lys	Leu	Ser	Ser	Val	Ser	Ala	Lys	Ile	Ser	Asn	Ser				
	210					215					220								
Asp	Leu	Thr	Trp	Arg	Val	Pro	Val	Glu	Gly	Arg	Asp	Glu	Ile	Ala	Gln				
	225				230				235					240					
Leu	Ala	Arg	Thr	Phe	Asn	Ala	Met	Leu	Asp	Arg	Ile	Glu	Ile	Ala	Tyr				
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Asn	Asp	Gln	Arg	Gln	Phe	Val	Asp	Asp	Ala	Gly	His	Glu	Leu	Arg	Thr				
			260					265					270						
Pro	Ile	Thr	Val	Val	Arg	Gly	Gln	Leu	Glu	Leu	Leu	Ala	Thr	Thr	Pro				
	275					280						285							
Pro	Glu	Glu	Gln	Ala	Arg	Ser	Ile	Glu	Leu	Ala	Thr	Thr	Glu	Leu	Asp	</			

4000> 247	tacagcgcgatg atgtggtgga gttgggttca ggatttcaag gggttetggcc cccaccgcgat	60
	ttttcgcatt tgggttcgtg acaaaggaag cggttgtgat atg gat gaa caa gaa	115
	Met Asp Glu Gln Glu	
	1 5	
	gcc ctg ttc gat cgc ttc tcc aga ggc tcc caa aaa aat tca cgg cgt	163
	Ala Leu Phe Asp Arg Phe Ser Arg Gly Ser Gln Lys Asn Ser Arg Arg	
	10 15 20	
	ccc ggt ggc gct ggc ctg gga tta tcc att gtc aag gcg atc ggc gaa	211
	Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val Lys Ala Ile Gly Glu	
	25 30 35	
	gcc cac gtc ggc cga gct ttc gtc aat tcc aca cca ggt cta gga tcc	259
	Ala His Val Gly Arg Ala Phe Val Asn Ser Thr Pro Gly Leu Gly Ser	
	40 45 50	
	att ttc ggc ctg gaa atc ccc gca cca gaa caa tca aag gaa tac acc	307
	Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln Ser Lys Glu Tyr Thr	
	55 60 65	
	cat gag caa gat cct gct cgc tgaagatgac gccggcatcg cag	351
	His Glu Gln Asp Pro Ala Arg	
	70 75	

<210> 248

<211> 76

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 248

Met Asp Glu Gln Glu Ala Leu Phe Asp Arg Phe Ser Arg Gly Ser Gln
1 5 10 15

Lys Asn Ser Arg Arg Pro Gly Gly Ala Gly Leu Gly Leu Ser Ile Val
20 25 30

Lys Ala Ile Gly Glu Ala His Val Gly Arg Ala Phe Val Asn Ser Thr
35 40 45

Pro Gly Leu Gly Ser Ile Phe Gly Leu Glu Ile Pro Ala Pro Glu Gln
50 55 60

Ser Lys Glu Tyr Thr His Glu Gln Asp Pro Ala Arg
65 70 75

<210> 249

<211> 720

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (697)

<223> RXN02990

<400> 249

gaagactaag caccagtttt aacaaagcag ggacaatcca cacacttaaa ccatgatgtg 60

gcttgttcct gctttttcgt caacgaaggg caacaacgcg atg gat atc caa gcc 115
Met Asp Ile Gln Ala
1 5

gaa aag att gaa aag ctc aga aaa gca ctc gac aac ttt gaa cgc gct 163
Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp Asn Phe Glu Arg Ala
10 15 20

cat gcg cga ggc gaa tca gac ttc ttt gac cat gaa aaa gaa gaa aag 211
His Ala Arg Gly Glu Ser Asp Phe Phe Asp His Glu Lys Glu Glu Lys
25 30 35

aaa gcc aac gta cgc aga cgt gcc ctg ctg ctg ctt aac caa cgc gca 259
Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu Asn Gln Arg Ala
40 45 50

cga tca gtc aac gaa cta agc acc aga ctt aaa gca ctg gag ttt gag 307
Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys Ala Leu Glu Phe Glu
55 60 65

gaa gac atc atc aat gag gtc att ggc gat ctc acc aga tcc aaa ctg 355
Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu Thr Arg Ser Lys Leu
70 75 80 85

ctt gat gat qaa gtt ttt gcc act gag tgg gtt cgg caa cgt gct gcc 403

Glu Leu Gln Glu Lys Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu
115 120 125

[illegible]

Glu Gln Ile Asp Gln Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala
130 135 140

Val Lys Lys Ala Arg Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp
145 150 155 160

Tyr Asp Lys Ala Leu Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly
165 170 175

Phe Pro Ala Gly Met Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala
180 185 190

Arg Ile Glu Asp Leu Lys Asn
195

<210> 251

<211> 341

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(318)

<223> RXN03100

<400> 251

ctc tac ggc cag gac aaa gtg acc tcc gat ccg atg gaa gct gct tac 48
Leu Tyr Gly Gln Asp Lys Val Thr Ser Asp Pro Met Glu Ala Ala Tyr
1 5 10 15

act agc ctc tac ctc tgg aaa gaa atg gta gag aag gcc gat tcc ttt 96
Thr Ser Leu Tyr Leu Trp Lys Glu Met Val Glu Lys Ala Asp Ser Phe
20 25 30

gat gtc gcc gca att caa gca gcc gcc gac gga acc act ttt gat gca 144
Asp Val Ala Ala Ile Gln Ala Ala Ala Asp Gly Thr Thr Phe Asp Ala
35 40 45

cca gaa gga acc gtg gtg gtt ggc ggc gat aac cac cac atc tcc aaa 192
Pro Glu Gly Thr Val Val Val Gly Gly Asp Asn His His Ile Ser Lys
50 55 60

aca ccg cgc atc ggt cga atc cgc ccg gat gga ttg atc gac acc att 240
Thr Pro Arg Ile Gly Arg Ile Arg Pro Asp Gly Leu Ile Asp Thr Ile
65 70 75 80

tgg gaa acc gat tcc cca gtt gat ccg gac cca tac ttg tct tcc tat 288
Trp Glu Thr Asp Ser Pro Val Asp Pro Asp Pro Tyr Leu Ser Ser Tyr
85 90 95

gac tgg gcc aag acc acc gct cgc act tcc taagagataa aaatcatgga 338
Asp Trp Ala Lys Thr Thr Ala Ala Thr Ser
100 105

cat

341

<210> 252

<211> 106

00220 1111111111

<213> *Corynebacterium glutamicum*

<400> 252
Leu Tyr Gly Gln Asp Lys Val Thr Ser Asp Pro Met Glu Ala Ala Tyr
1 5 10 15

Thr Ser Leu Tyr Leu Trp Lys Glu Met Val Glu Lys Ala Asp Ser Phe
20 25 30

Asp Val Ala Ala Ile Gln Ala Ala Ala Asp Gly Thr Thr Phe Asp Ala
35 40 45

Pro Glu Gly Thr Val Val Val Gly Gly Asp Asn His His Ile Ser Lys
50 55 60

Thr Pro Arg Ile Gly Arg Ile Arg Pro Asp Gly Leu Ile Asp Thr Ile
65 70 75 80

Trp Glu Thr Asp Ser Pro Val Asp Pro Asp Pro Tyr Leu Ser Ser Tyr
85 90 95

Asp Trp Ala Lys Thr Thr Ala Ala Thr Ser
100 105

<211> 525

<213> *Corynebacterium glutamicum*

<221> CDS

<223> RXN00031

<400> 253
cacacatcgc ctcgtcatcc ttagacacgc caaatcttcc tggtcacacg gagtactcga 60

ccataaacgc ccacttaatc aacgtgggct tcgcgatggc gtg gca gct ggc caa 115
Val Ala Ala Gly Gln
1 5

tgg cta gct ggc aac atc ggc gaa att gat cat gtg ctg tgt tca gat 163
Trp Leu Ala Gly Asn Ile Gly Glu Ile Asp His Val Leu Cys Ser Asp
 10 15 20

gcc acc cgc aca caa tta acg tgg gaa cgc gtc cag ctt ggt ggc gca 211
Ala Thr Arg Thr Gln Leu Thr Trp Glu Arg Val Gln Leu Gly Gly Ala
25 30 35

acc gcc aaa ggc tct agc ttc cac aat gac atc tat gaa aac caa gtg 259
Thr Ala Lys Gly Ser Ser Phe His Asn Asp Ile Tyr Glu Asn Gln Val
40 45 50

tct gaa ttt aaa cat tta ata aca ggg ctc cca gat gta gtt ggt acc 307
Ser Glu Phe Lys His Leu Ile Thr Gly Leu Pro Asp Val Val Gly Thr
55 60 65

gcc cta ctc atc ggg cac tgg cca ggc gtg gaa gaa cta gcc cat tat 355
Ala Leu Leu Ile Gly His Trp Pro Gly Val Glu Glu Leu Ala His Tyr

Chlorine is a greenish-yellow gas with a strong, irritating odor. It is highly toxic and can cause severe respiratory distress and lung damage. Chlorine is commonly used in water treatment and as a disinfectant.

<400> 255

aatgtcgtgt tccgcgctca gacatgagac aattgttgcc gtg act gaa ctc atc 115
Val Thr Glu Leu Ile
1 5

cag aat gaa tcc caa gaa atc gct gag ctg gaa gcc ggc cag cag gtt 163
Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu Ala Gly Gln Gln Val
10 15 20

gca ttg cgt gaa ggt tat ctt cct gcg gtg atc aca gtg agc ggt aaa 211
Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile Thr Val Ser Gly Lys
25 30 35

gac cgc cca ggt gtg act gcc gcg ttc ttt agg gtc ttg tcc gct aat 259
Asp Arg Pro Gly Val Thr Ala Phe Phe Arg Val Leu Ser Ala Asn
40 45 50

cag gtt cag gtc ttg gac gtt gag cag tca atg ttc cgt ggc ttt ttg 307
Gln Val Gln Val Leu Asp Val Glu Gln Ser Met Phe Arg Gly Phe Leu
55 60 65

aac ttg gcg gcg ttt gtg ggt atc gca cct gag cgt gtc gag acc gtc 355
Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu Arg Val Glu Thr Val
70 75 80 85

acc aca ggc ctg act gac acc ctc aag gtg cat gga cag tcc gtg gtg 403
Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His Gly Gln Ser Val Val
90 95 100

gtg gag ctg cag gaa act gtg cag tcg tcc cgt cct cgt tct tcc cat 451
Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg Pro Arg Ser Ser His
105 110 115

ggt gtt gtg gtg ttg ggt gat ccg gtt gat gcg ttg gat att tcc cgc 499
Val Val Val Val Leu Gly Asp Pro Val Asp Ala Leu Asp Ile Ser Arg
120 125 130

att ggt cag acc ctg gcg gat tac gat gcc aac att gac acc att cgt 547
Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn Ile Asp Thr Ile Arg
135 140 145

ggt att tgg gat tac cct gtg acc ggc ctg gag ctg aag gtg act gtg 595
Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu Leu Lys Val Thr Val
150 155 160 165

ccg gat gtc agc cct ggt ggt ggt gaa gcg atg cgt aag gcg ctt gct 643
Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met Arg Lys Ala Leu Ala
170 175 180

gct ctt acc tct gag ctg aat gtg gat att gcg att gag cgt tct ggt 691
Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala Ile Glu Arg Ser Gly
185 190 195

ttg ctg cgt cgt tct aag cgt ctg gtg tgc ttc gat tgt gat tcc acg 739
Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe Asp Cys Asp Ser Thr
200 205 210

ttg atc act ggt gag gtc att gag atg ctg gcg gct cac gcg ggc aag 787
 Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala Ala His Ala Gly Lys
 215 220 225

gaa gct gaa gtt gcg gca gtt act gag cgt gcg atg cgc ggt gag ctg 835
 Glu Ala Glu Val Ala Val Thr Glu Arg Ala Met Arg Gly Glu Leu
 230 235 240 245

gat ttc gag gag tct ctg cgt gag cgt gtg aag gcg ttg gct ggt ttg 883
 Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys Ala Leu Ala Gly Leu
 250 255 260

gat gcg tcg gtg atc gat gag gtc gct gcc gct att gag ctg acc cct 931
 Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala Ile Glu Leu Thr Pro
 265 270 275

ggt gcg cgc acc acg atc cgt acg ctg aac cgc atg ggt tac cag acc 979
 Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg Met Gly Tyr Gln Thr
 280 285 290

gct gtt gtt tcc ggt ggt ttc atc cag gtg ttg gaa ggt ttg gct gag 1027
 Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu Glu Gly Leu Ala Glu
 295 300 305

gag ttg gag ttg gat tat gtc cgc gcc aac act ttg gaa atc gtt gat 1075
 Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr Leu Glu Ile Val Asp
 310 315 320 325

ggc aag ctg acc ggc aac gtc acc gga aag atc gtt gac cgc gct gcg 1123
 Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile Val Asp Arg Ala Ala
 330 335 340

aag gct gag ttc ctc cgt gag ttc gct gcg gat tct ggc ctg aag atg 1171
 Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp Ser Gly Leu Lys Met
 345 350 355

tac cag act gtc gct gtc ggt gat ggc gct aat gac atc gat atg ctg 1219
 Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn Asp Ile Asp Met Leu
 360 365 370

tcc gct gcg ggt ctg ggt gtt gct ttc aac gcg aag cct gcg ctg aag 1267
 Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala Lys Pro Ala Leu Lys
 375 380 385

gag att gcg gat act tcc gtg aac cac cca ttc ctc gac gag gtt ttg 1315
 Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe Leu Asp Glu Val Leu
 390 395 400 405

cac atc atg ggc att tcc cgc gac gag atc gat ctg gcg gat cag gaa 1363
 His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp Leu Ala Asp Gln Glu
 410 415 420

gag ggc act ttc cac cgc gtt cca ttg acc aat gcc taaagattcg 1409
 Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn Ala
 425 430

tttctcgacg ccc 1422

<210> 256

<211> 433

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 256

Val Thr Glu Leu Ile Gln Asn Glu Ser Gln Glu Ile Ala Glu Leu Glu
 1 5 10 15
 Ala Gly Gln Gln Val Ala Leu Arg Glu Gly Tyr Leu Pro Ala Val Ile
 20 25 30
 Thr Val Ser Gly Lys Asp Arg Pro Gly Val Thr Ala Ala Phe Phe Arg
 35 40 45
 Val Leu Ser Ala Asn Gln Val Gln Val Leu Asp Val Glu Gln Ser Met
 50 55 60
 Phe Arg Gly Phe Leu Asn Leu Ala Ala Phe Val Gly Ile Ala Pro Glu
 65 70 75 80
 Arg Val Glu Thr Val Thr Thr Gly Leu Thr Asp Thr Leu Lys Val His
 85 90 95
 Gly Gln Ser Val Val Val Glu Leu Gln Glu Thr Val Gln Ser Ser Arg
 100 105 110
 Pro Arg Ser Ser His Val Val Val Leu Gly Asp Pro Val Asp Ala
 115 120 125
 Leu Asp Ile Ser Arg Ile Gly Gln Thr Leu Ala Asp Tyr Asp Ala Asn
 130 135 140
 Ile Asp Thr Ile Arg Gly Ile Ser Asp Tyr Pro Val Thr Gly Leu Glu
 145 150 155 160
 Leu Lys Val Thr Val Pro Asp Val Ser Pro Gly Gly Gly Glu Ala Met
 165 170 175
 Arg Lys Ala Leu Ala Ala Leu Thr Ser Glu Leu Asn Val Asp Ile Ala
 180 185 190
 Ile Glu Arg Ser Gly Leu Leu Arg Arg Ser Lys Arg Leu Val Cys Phe
 195 200 205
 Asp Cys Asp Ser Thr Leu Ile Thr Gly Glu Val Ile Glu Met Leu Ala
 210 215 220
 Ala His Ala Gly Lys Glu Ala Glu Val Ala Ala Val Thr Glu Arg Ala
 225 230 235 240
 Met Arg Gly Glu Leu Asp Phe Glu Glu Ser Leu Arg Glu Arg Val Lys
 245 250 255
 Ala Leu Ala Gly Leu Asp Ala Ser Val Ile Asp Glu Val Ala Ala Ala
 260 265 270
 Ile Glu Leu Thr Pro Gly Ala Arg Thr Thr Ile Arg Thr Leu Asn Arg
 275 280 285
 Met Gly Tyr Gln Thr Ala Val Val Ser Gly Gly Phe Ile Gln Val Leu
 290 295 300

000250 42000000

Glu Gly Leu Ala Glu Glu Leu Glu Leu Asp Tyr Val Arg Ala Asn Thr
305 310 315 320

Leu Glu Ile Val Asp Gly Lys Leu Thr Gly Asn Val Thr Gly Lys Ile
325 330 335

Val Asp Arg Ala Ala Lys Ala Glu Phe Leu Arg Glu Phe Ala Ala Asp
340 345 350

Ser Gly Leu Lys Met Tyr Gln Thr Val Ala Val Gly Asp Gly Ala Asn
355 360 365

Asp Ile Asp Met Leu Ser Ala Ala Gly Leu Gly Val Ala Phe Asn Ala
370 375 380

Lys Pro Ala Leu Lys Glu Ile Ala Asp Thr Ser Val Asn His Pro Phe
385 390 395 400

Leu Asp Glu Val Leu His Ile Met Gly Ile Ser Arg Asp Glu Ile Asp
405 410 415

Leu Ala Asp Gln Glu Asp Gly Thr Phe His Arg Val Pro Leu Thr Asn
420 425 430

Ala

<210> 257

<211> 738

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(715)

<223> RXN00978

<400> 257

tctctgggtag catgggctta tgagcaactga tagccaaaac cctgtaagaa aatcctgcgc 60

acagccacat tcttggtccc aagaggtgcg attgaaagcg atg tcc agg tca ccg 115
Met Ser Arg Ser Pro 5

ctt act aaa ggt cta aat caa ctt gaa cac ctc gag tta gat aag tca 163
Leu Thr Lys Gly Leu Asn Gln Leu Glu His Leu Glu Leu Asp Lys Ser 20

cta act gcg tgg tgg gca gaa gat gat cct ttg tac ctc gca ggt 211
Leu Thr Ala Trp Ser Trp Ala Glu Asp Asp Pro Leu Tyr Leu Ala Gly 35

gag aac tta aac ggc agt tac ctc att gtc gca gga cga gtg cgg gtc 259
Glu Asn Leu Asn Gly Ser Tyr Leu Ile Val Ala Gly Arg Val Arg Val 50

tct cgc gac acc atc gac ggg aaa gaa ctc acc gtt gat att gca acg 307
Ser Arg Asp Thr Ile Asp Gly Lys Glu Leu Thr Val Asp Ile Ala Thr 60

00250-123CP

400> 259	agttgtcagc tgggatttgc cgatggtgtt atctttgata ttacacctaa ccccgtttct	60
aattcagctt ttctcgttac ccgaagaggaa ttgatcgatt	atg gcg aca tca cgt Met Ala Thr Ser Arg 1 5	115
cga gat gcc gaa aac ata gac cag gcc ggt agc gaa ttc att gaa tct	Gly Ser Glu Phe Ile Glu Ser 15 20	163
Arg Asp Ala Glu Asn Ile Asp Gln Ala		
gat tca gga cac acc gca acc cct gaa gag gta gta gcc acc gct ctg	Glu Val Val Ala Thr Ala Leu 30 35	211
Asp Ser Gly His Thr Ala Thr Pro		
aca ttt ttt gca gag gat ggt ttt agc gaa acc aaa ttg gag aaa atc	Leu Glu Lys Ile 40 45 50	259
Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr Lys		
gcg aag gca tct ggc atg tcc aag cgc atg atc cac tat cac ttt ggc	His Tyr His Phe Gly 55 60 65	307
Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile		
gat aag aaa ggc ctg tac atc aag gct gtt tcc tac gcg ttg cga ttg	Ala Val Ser Tyr Ala Leu Arg Leu 70 75 80 85	355
Asp Lys Lys Gly Leu Tyr Ile Lys Ala		
ctg cgc cca gag gct gaa gcg atg caa ctt gat tcc gcg gta cca gtt	Ala Val Pro Val 90 95	403
Leu Arg Pro Glu Ala Glu Ala Met Gln Leu Asp Ser Ala Val Pro Val		

90	95	100	
gat ggt gtc cgc aaa atc gtc gag gct tta tat acc tgc atc acc aag Asp Gly Val Arg Lys Ile Val Glu Ala Leu Tyr Thr Cys Ile Thr Lys 105 110 115			451
cac cca gaa gca gtg cgc ctg cta ttg atg gaa aac ctg cat agc caa His Pro Glu Ala Val Arg Leu Leu Leu Met Glu Asn Leu His Ser Gln 120 125 130			499
gac agc gtg gat tcc acc gcg gca tat tcc gat gaa tcc aat gtg ctg Asp Ser Val Asp Ser Thr Ala Ala Tyr Ser Asp Glu Ser Asn Val Leu 135 140 145			547
ctc aac ctg gat aag ctg ctc atg ctt ggc cag gat gcc ggc gcc ttc Leu Asn Leu Asp Lys Leu Leu Met Leu Gly Gln Asp Ala Gly Ala Phe 150 155 160 165			595
cgt cct gga atc tcc gca gaa gac gta ctg gtt ctt att agc tcc ctg Arg Pro Gly Ile Ser Ala Glu Asp Val Leu Val Leu Ile Ser Ser Leu 170 175 180			643
gcc tac ttc cgc gta tcc aac aag gtc acg ttg aag aac ctc tac tcc Ala Tyr Phe Arg Val Ser Asn Lys Val Thr Leu Lys Asn Leu Tyr Ser 185 190 195			691
ctt gat ttg gaa tca gag gcc aat att gaa ggc atg aag cgc atc gtc Leu Asp Leu Glu Ser Glu Ala Asn Ile Glu Gly Met Lys Arg Ile Val 200 205 210			739
gtt gac acg gtg ctg gca ttc ttg acc tca aat att caa aat tct ggc Val Asp Thr Val Leu Ala Phe Leu Thr Ser Asn Ile Gln Asn Ser Gly 215 220 225			787
aac tcc agc tac ctg gtt gtt ggt ggc aag act gca gaa cca gaa act Asn Ser Ser Tyr Leu Val Val Gly Gly Lys Thr Ala Glu Pro Glu Thr 230 235 240 245			835
gat gac agc gtc tac agc ttt gat acg gac gtg ttc gaa aac Asp Asp Ser Val Tyr Ser Phe Asp Thr Asp Val Phe Glu Asn 250 255			877
taaagggtat cgagtagttt caa			900
 <210> 260 <211> 259 <212> PRT <213> Corynebacterium glutamicum			
 <400> 260 Met Ala Thr Ser Arg Arg Asp Ala Glu Asn Ile Asp Gln Ala Gly Ser 1 5 10 15 Glu Phe Ile Glu Ser Asp Ser Gly His Thr Ala Thr Pro Glu Glu Val 20 25 30 Val Ala Thr Ala Leu Thr Phe Phe Ala Glu Asp Gly Phe Ser Glu Thr 35 40 45 Lys Leu Glu Lys Ile Ala Lys Ala Ser Gly Met Ser Lys Arg Met Ile			

ctt ccc gat agg tcc cag gac tac ctg aag aca atc tgg gac atc aca 163
Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr Ile Trp Asp Ile Thr

10	15	20	
gaa ctc ctt gat gat caa cca gca gca ctc ggc gat atc gcc gaa aaa Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly Asp Ile Ala Glu Lys 25 30 35			211
atg aac cag aaa act cct acc gcc tcc gaa gca atc aaa aag ctg gcg Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala Ile Lys Lys Leu Ala 40 45 50			259
gca agg ggc ctg gtc aac cat gaa aaa tat gct ggt gtc acc ctc act Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala Gly Val Thr Leu Thr 55 60 65			307
gaa cag ggc aaa acg cta gcc atc gac atg gtg cga cgc cac cgc ctg Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val Arg Arg His Arg Leu 70 75 80 85			355
ctg gaa acc ttc ctc cac gat gtt ttg gga tac acc tgg gac gaa gtc Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr Thr Trp Asp Glu Val 90 95 100			403
cac gcc gat gca gac ctg ttg gaa cat gca gcc tct gat cag ctc atc His Ala Asp Ala Asp Leu Leu Glu His Ala Ala Ser Asp Gln Leu Ile 105 110 115			451
gaa cgc atc gat gct cac ttg ggt cgt cca cgc aaa gat ccc cac gcc Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg Lys Asp Pro His Gly 120 125 130			499
gat ccc ata cca act gcc gaa ggc gtt att gaa gag tct ccc cga acc Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu Glu Ser Pro Arg Thr 135 140 145			547
acc ctc gag gca gtt cag cca ggg gag act gtc acg att tcc agg gtc Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val Thr Ile Ser Arg Val 150 155 160 165			595
aaa gac att gat cct gaa ttg ctg cgc tac ctc gcg caa tac aac gtc Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu Ala Gln Tyr Asn Val 170 175 180			643
tca cca gga tgc cgg atc acc gtt gcg tcc gcc cca cta gct gcc atg Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly Pro Leu Ala Gly Met 185 190 195			691
gtg cat gtc gtt gta gaa gcc acc gac acc agc ttc ccc ctg gcc gaa Val His Val Val Val Glu Gly Thr Asp Thr Ser Phe Pro Leu Ala Glu 200 205 210			739
acg caa ctg cca tta att aca gtg cag gac taagcagatt catcataatg Thr Gln Leu Pro Leu Ile Thr Val Gln Asp 215 220			789
gtg			792

<210> 262

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

Met His Ile Ser Asp Leu Pro Asp Arg Ser Gln Asp Tyr Leu Lys Thr
1 5 10 15

Ile Trp Asp Ile Thr Glu Leu Leu Asp Asp Gln Pro Ala Ala Leu Gly
20 25 30

Asp Ile Ala Glu Lys Met Asn Gln Lys Thr Pro Thr Ala Ser Glu Ala
35 40 45

Ile Lys Lys Leu Ala Ala Arg Gly Leu Val Asn His Glu Lys Tyr Ala
50 55 60

Gly Val Thr Leu Thr Glu Gln Gly Lys Thr Leu Ala Ile Asp Met Val
65 70 75 80

Arg Arg His Arg Leu Leu Glu Thr Phe Leu His Asp Val Leu Gly Tyr
85 90 95

Thr Trp Asp Glu Val His Ala Asp Ala Asp Leu Leu Glu His Ala Ala
100 105 110

Ser Asp Gln Leu Ile Glu Arg Ile Asp Ala His Leu Gly Arg Pro Arg
115 120 125

Lys Asp Pro His Gly Asp Pro Ile Pro Thr Ala Glu Gly Val Ile Glu
130 135 140

Glu Ser Pro Arg Thr Thr Leu Glu Ala Val Gln Pro Gly Glu Thr Val
145 150 155 160

Thr Ile Ser Arg Val Lys Asp Ile Asp Pro Glu Leu Leu Arg Tyr Leu
165 170 175

Ala Gln Tyr Asn Val Ser Pro Gly Cys Arg Ile Thr Val Ala Ser Gly
180 185 190

Pro Leu Ala Gly Met Val His Val Val Val Glu Gly Thr Asp Thr Ser
195 200 205

Phe Pro Leu Ala Glu Thr Gln Leu Pro Leu Ile Thr Val Gln Asp
210 215 220

<210> 263

<211> 861

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (838)

<223> RXN02954

<400> 263

ttcgccacac tccaatatc taccaaaaat ggtgatctat tatacataat ggaattacca 60

aagcttcata tcacttttcc acagcctgaa agaacatact atg tcc gca gct tta 115
Met Ser Ala Ala Leu
1 5

cct	cac	aca	gca	gca	gat	ccc	gta	cac	acc	acc	cca	gcg	aaa	ccg	ctg	163
Pro	His	Thr	Ala	Ala	Asp	Pro	Val	His	Thr	Thr	Pro	Ala	Lys	Pro	Leu	
10																
ctc	gat	cat	gtc	tta	gat	tca	cta	gga	cgc	agc	atc	atc	agt	ggt	gaa	211
Leu	Asp	His	Val	Leu	Asp	Ser	Leu	Gly	Arg	Ser	Ile	Ile	Ser	Gly	Glu	
25																
atg	gaa	gcc	ggt	agc	aca	ttc	aaa	ctg	caa	gac	atc	ggt	gaa	aaa	ttc	259
Met	Glu	Ala	Gly	Ser	Thr	Phe	Lys	Leu	Gln	Asp	Ile	Gly	Glu	Lys	Phe	
40																
ggt	atc	tcc	cgc	acc	gtc	gcc	aga	gaa	gcc	atg	cgt	gcc	tta	gag	caa	307
Gly	Ile	Ser	Arg	Thr	Val	Ala	Arg	Glu	Ala	Met	Arg	Ala	Leu	Glu	Gln	
55																
ctt	ggg	ttg	gtg	gcc	tca	tcg	aga	cga	att	ggt	att	aca	gtg	ctc	tcg	355
Leu	Gly	Leu	Val	Ala	Ser	Ser	Arg	Arg	Ile	Gly	Ile	Thr	Val	Leu	Ser	
70																
cac	gag	cac	tggt	gct	gtc	ttt	gac	aaa	gcc	att	att	cgc	tggt	cggt	ctc	403
His	Glu	His	Trp	Ala	Val	Phe	Asp	Lys	Gln	Ile	Ile	Arg	Trp	Arg	Leu	
90																
gaa	gat	gag	cgt	caa	cgt	gaa	cag	caa	ctg	cag	tca	ctc	acc	gaa	ctt	451
Glu	Asp	Glu	Arg	Gln	Arg	Glu	Gln	Gln	Leu	Gln	Ser	Leu	Thr	Glu	Leu	
105																
cgt	att	gcc	att	gaa	cca	att	gct	gca	cggt	aggt	ggt	gcc	ctt	cat	gca	499
Arg	Ile	Ala	Ile	Glu	Pro	Ile	Ala	Ala	Arg	Ser	Val	Ala	Leu	His	Ala	
120																
tcg	agc	gca	gag	att	gct	atc	atc	ggt	gat	ctt	gct	gca	cga	atg	cgt	547
Ser	Ser	Ala	Glu	Ile	Ala	Ile	Ile	Gly	Asp	Leu	Ala	Ala	Arg	Met	Arg	
135																
aac	ctc	ggt	gaa	gct	ggt	cgt	ggc	gca	tca	caa	gaa	ttc	cta	gac	gca	595
Asn	Leu	Gly	Glu	Ala	Gly	Arg	Gly	Ala	Ser	Gln	Glu	Phe	Leu	Asp	Ala	
150																
gat	gtg	aaa	ttt	cat	gag	ctt	att	ttg	cag	tat	tgc	cat	aat	gag	atg	643
Asp	Val	Lys	Phe	His	Glu	Leu	Ile	Leu	Gln	Tyr	Cys	His	Asn	Glu	Met	
170																
ttc	gct	gcc	atg	gca	cca	ccc	ata	aaa	gct	gta	cta	gtc	ggg	cggt	acc	691
Phe	Ala	Ala	Met	Ala	Pro	Pro	Ile	Lys	Ala	Val	Leu	Val	Gly	Arg	Thr	
185																
aca	ctt	ggc	ctt	caa	ccc	gat	cga	cct	gcc	gaa	gaa	gtc	ttg	gac	aat	739
Thr	Leu	Gly	Leu	Gln	Pro	Asp	Arg	Pro	Ala	Glu	Glu	Val	Leu	Arg	Asn	
200																
cat	gat	gct	ctc	gca	cac	gca	cta	agt	gtt	cgt	aat	gca	gac	ctc	gcc	787
His	Asp	Ala	Leu	Ala	His	Ala	Leu	Ser	Val	Arg	Asn	Ala	Asp	Leu	Ala	
215																
gaa	aaa	gca	tcc	agg	agc	att	ctg	aat	gag	gtg	cggt	gac	gca	ctg	acc	835
Glu	Lys	Ala	Ser	Arg	Ser	Ile	Leu	Asn	Glu	Val	Arg	Asp	Ala	Leu	Thr	
230																
235																
240																
245																

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Ser

861

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<211> 246

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 264

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Pro Ala Lys Pro Leu Leu Asp His Val Leu Asp Ser Leu Gly Arg Ser
20 25 30

Ile Ile Ser Gly Glu Met Glu Ala Gly Ser Thr Phe Lys Leu Gln Asp
35 40 45

Ile Gly Glu Lys Phe Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met
50 55 60

Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Arg Arg Ile Gly
65 70 75 80

Ile Thr Val Leu Ser His Glu His Trp Ala Val Phe Asp Lys Ala Ile
85 90 95

Ile Arg Trp Arg Leu Glu Asp Glu Arg Gln Arg Glu Gln Gln Leu Gln
100 105 110

Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser
115 120 125

Val Ala Leu His Ala Ser Ser Ala Glu Ile Ala Ile Ile Gly Asp Leu
130 135 140

Ala Ala Arg Met Arg Asn Leu Gly Glu Ala Gly Arg Gly Ala Ser Gln
145 150 155 160

Glu Phe Leu Asp Ala Asp Val Lys Phe His Glu Leu Ile Leu Gln Tyr
165 170 175

Cys His Asn Glu Met Phe Ala Ala Met Ala Pro Pro Ile Lys Ala Val
180 185 190

Leu Val Gly Arg Thr Thr Leu Gly Leu Gln Pro Asp Arg Pro Ala Glu
195 200 205

Glu Val Leu Asp Asn His Asp Ala Leu Ala His Ala Leu Ser Val Arg
210 215 220

Asn Ala Asp Leu Ala Glu Lys Ala Ser Arg Ser Ile Leu Asn Glu Val
225 230 235 240

Arg Asp Ala Leu Thr Ser
245

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<211> 480
 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXN03023

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 ttatgttatat gagtaaccaa ccatcgggat cgtcgcgacc gtg cct ctg tat aaa 115
 Val Pro Leu Tyr Lys
 1 5
 cag atc gct tct ttg att gag gac tcc atc gtt gac gga acc ttg agc 163
 Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val Asp Gly Thr Leu Ser
 10 15 20
 att gat caa cgc gtg cct tct act aat gaa cta gcc gcg ttc cat cgc 211
 Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu Ala Ala Phe His Arg
 25 30 35
 att aat ccc gcc acc gca cgc aac gcc ctg acc ctc ctt gtc gaa gcc 259
 Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr Leu Leu Val Glu Ala
 40 45 50
 gcc atc ctc tat aag aag cgt gcc att gcc atg ttc gtc agc gcc cag 307
 Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met Phe Val Ser Ala Gln
 55 60 65
 gcc cca gca ctc atc cga gag cgg cga gat gcc gcc ttc gcg gct act 355
 Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala Ala Phe Ala Ala Thr
 70 75 80 85
 tat gta gca ccg ctt atc gac gaa tcc atc cac ctt ggt ttc act cgt 403
 Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His Leu Gly Phe Thr Arg
 90 95 100
 gcg cgc att cac gcc ctt tta gac cag gtc gct gaa agt agg gcc ctg 451
 Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala Glu Ser Arg Gly Leu
 105 110 115
 tac aag tagcgcttaa accctcttga cct 480
 Tyr Lys

<210> 266
 <211> 119
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 266
 Val Pro Leu Tyr Lys Gln Ile Ala Ser Leu Ile Glu Asp Ser Ile Val
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 Asp Gly Thr Leu Ser Ile Asp Gln Arg Val Pro Ser Thr Asn Glu Leu
 20 25 30

Ala Ala Phe His Arg Ile Asn Pro Ala Thr Ala Arg Asn Gly Leu Thr
35 40 45

Leu Leu Val Glu Ala Gly Ile Leu Tyr Lys Lys Arg Gly Ile Gly Met
50 55 60

Phe Val Ser Ala Gln Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala
65 70 75 80

Ala Phe Ala Ala Thr Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His
85 90 95

Leu Gly Phe Thr Arg Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala
100 105 110

Glu Ser Arg Gly Leu Tyr Lys
115

<210> 267

<211> 843

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(820)

<223> RXN03127

<400> 267

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gatatgatca gaaccatctc cagattagga agtgaacaca atg gaa agc tcc aaa 115
Met Glu Ser Ser Lys
1 5

aag act tcc cga tca agg tcc act act caa gaa gca gtg cgc gac att 163
Lys Thr Ser Arg Ser Arg Ser Thr Thr Gln Glu Ala Val Arg Asp Ile
10 15 20

aaa aaa tac att cgg gac aac cgg ctg cgt acg gga gac ctt ctt cct 211
Lys Lys Tyr Ile Arg Asp Asn Arg Leu Arg Thr Gly Asp Leu Leu Pro
25 30 35

tcc gaa gcg ttc tta tgt gag gaa ttg ggt tgt tcc cgt tct gcg atc 259
Ser Glu Ala Phe Leu Cys Glu Glu Leu Gly Cys Ser Arg Ser Ala Ile
40 45 50

agg gag gcg atc cgc gcg ctc gtg acc ttg gac atc gtc gag gtt cgc 307
Arg Glu Ala Ile Arg Ala Leu Val Thr Leu Asp Ile Val Glu Val Arg
55 60 65

cac ggc tac ggc act ttc gtg tcc agg atg tcc ctc gag ccc ctg atc 355
His Gly Tyr Gly Thr Phe Val Ser Arg Met Ser Leu Glu Pro Leu Ile
70 75 80 85

aac ggg atg gtg ttc cgc acg gtg ttg gac aat gac acc tcc gtg gaa 403
Asn Gly Met Val Phe Arg Thr Val Leu Asp Asn Asp Thr Ser Val Glu
90 95 100

aac ctt ttc tac gtg gtg gat acc cgc gaa atc ctt gac ctt tca ctt 451

Asp Thr Ser Val Glu Asn Leu Phe Tyr Val Val Asp Thr Arg Glu Ile
100 105 110

Leu Asp Leu Ser Leu Gly Glu Glu Leu Ile Glu Val Phe Thr Asp Asp
115 120 125

Asp Arg Glu Leu Leu Leu Asp Leu Val Asp Lys Met Arg Glu His Asn
130 135 140

Asp Gln Gly Glu Ser Phe Val Val Glu Asp Gln Lys Phe His Arg Ala
145 150 155 160

Leu Leu Ala Arg Thr Lys Asn Pro Leu Ile Arg Glu Leu Asn Asp Ala
165 170 175

Phe Trp Gln Ile Gln Thr Glu Ala Gln Pro Met Leu Asn Leu Ala Met
180 185 190

Pro Ala Asp Ile Asp Glu Thr Ile Lys Ala His Ser Asp Ile Val Glu
195 200 205

Ala Leu Ser Ser Gly Asn Ile Asp Asp Tyr Arg Ser Ala Val Leu Ala
210 215 220

His Tyr Ala Pro Phe Arg Arg Met Ile Ser Asn Met Leu Asp Ala His
225 230 235 240

<210> 269

<211> 1691

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1668)

<223> RXN03155

<400> 269

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Gly Tyr Pro Pro Pro Thr Ala Ser Lys Asp Ala Ala Gly Gly Leu
1 5 10 15

cca caa ctg atc aga gag ctt ctc gac gcg acc ccc atc gat cat tgg 96
Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp
20 25 30

tcc aac gat ccg cct act ctc acg ctg cca gag cat tgg gtg aca gac 144
Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp
35 40 45

atc gac att aag aac cct gtg ctt cg gaa gtc gcc tcc cat ccc ttc 192
Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe
50 55 60

ttc gat ggc tgc ccg atc gga gat tta gat gcc gat gcc ttt gtg gag 240
Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu

ttgttcagca gct

1691

<210> 270

<211> 556

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 270

Gly Tyr Pro Pro Pro Thr Ala Ser Lys Asp Ala Ala Gly Gly Leu
1 5 10 15

Pro Gln Leu Ile Arg Glu Leu Leu Asp Ala Thr Pro Ile Asp His Trp
20 25 30

Ser Asn Asp Arg Pro Thr Leu Thr Leu Pro Glu His Trp Val Thr Asp
35 40 45

Ile Asp Ile Lys Asn Pro Val Leu Arg Glu Val Ala Ser His Pro Phe
50 55 60

Phe Asp Gly Cys Pro Ile Gly Asp Leu Asp Ala Asp Ala Phe Val Glu
65 70 75 80

Asp Gly Thr Leu Ile His Glu Asn Gly Thr Leu Arg Phe Arg Ser Pro
85 90 95

Glu Glu Arg Thr Leu Val Arg Ala Ser Thr Pro Pro Ser Met Ala Arg
100 105 110

Ser Pro Arg Glu Trp Glu Ser Thr Glu Gly Gly Val Asp Lys Leu Ile
115 120 125

Ala Ala Gly Asn Leu Pro Leu Ala Arg Leu His Val Glu Glu Leu Pro
130 135 140

Arg Ala Asp Glu Gln Arg Ala Phe Leu Ala Leu Tyr Gly Gly Gln Ser
145 150 155 160

Phe Glu Ala Ala Ser Ala Ser Pro Phe Tyr Ala Leu Ala Thr Trp Asn
165 170 175

Pro Glu Ala Leu Arg Gly Asp Pro Thr Phe Asp Met Phe Ala Asp Ala
180 185 190

Leu Asp Thr Gly His Tyr Arg Glu Val Pro Arg Pro Asp Ala Pro Glu
195 200 205

Glu Ser Gln Ile His Asp Phe Ile Ser Gly Trp Leu Ala Leu Val Tyr
210 215 220

Asp Asp Pro Leu Thr Ala Arg Arg Leu Leu Ser Ser Arg Gly Pro Ser
225 230 235 240

Asp Leu Val Gly Leu Trp Gln Ser Ala Phe Leu Ala Arg Ala His Tyr
245 250 255

Val Leu Gly Glu Phe Gln Glu Ala Ser Ala Val Val Glu Arg Gly Leu
260 265 270

Ala Thr Gly Asp Arg Thr Gly Ala Ser Leu Leu Glu Pro Val His Leu

<221> CDS

Figure 1 Schematic representation of the experimental design. The subjects were divided into two groups: the control group (C) and the experimental group (E). The control group (C) was divided into two subgroups: the control group (C) and the control group (C). The experimental group (E) was divided into two subgroups: the experimental group (E) and the experimental group (E). The control group (C) was divided into two subgroups: the control group (C) and the control group (C). The experimental group (E) was divided into two subgroups: the experimental group (E) and the experimental group (E).

<222> (101)..(751)

<223> RXN01315

<400> 271

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aatattgcac tgagtgcaag ttctactag gtttacttca gtg gat att gaa gag 115
 Val Asp Ile Glu Glu
 1 5

cag ccc tcg tta aga gaa atc aag cgc caa atg acc ctg gaa gcg ata 163
 Gln Pro Ser Leu Arg Glu Ile Lys Arg Gln Met Thr Leu Glu Ala Ile
 10 15 20

gaa gat aac gca acc agg ctc att ctg gag cgt ggc ttc gac aat gtc 211
 Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg Gly Phe Asp Asn Val
 25 30 35

aca atc gaa gac atc tgc gca gag gca ggg ata tcc aag cgc aca ttc 259
 Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile Ser Lys Arg Thr Phe
 40 45 50

ttt aac tac gtg gag tcc aaa gag tct gtg gcc atc ggg cac aca gcc 307
 Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala Ile Gly His Thr Ala
 55 60 65

aag ctc cca acg gat gaa gaa cgt gaa gca ttc ctg gct acg cgt cat 355
 Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe Leu Ala Thr Arg His
 70 75 80 85

gaa aat att atc gat act gta ttt gac ctg gta atc aac ctc ttt ggc 403
 Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val Ile Asn Leu Phe Gly
 90 95 100

aac cac gac aac tcc aag tct gga gtt gca ggc gac att atg cgt cga 451
 Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly Asp Ile Met Arg Arg
 105 110 115

cgc aaa gag atc cgg gtg aag cat cca gaa ctg gca gtg caa cat ttc 499
 Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu Ala Val Gln His Phe
 120 125 130

gcc agg ttc cac caa gca cgc gaa ggg cta gaa cac cta att gtt gag 547
 Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu His Leu Ile Val Glu
 135 140 145

tac ttc gaa aaa tgg cca ggc tcc caa cat cta gat gag cct gca gat 595
 Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu Asp Glu Pro Ala Asp
 150 155 160 165

cga gaa gca atc gcc ata gtt ggc ctg ctg atc tcg gtc atg ctt caa 643
 Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile Ser Val Met Leu Gln
 170 175 180

ggt tct cgt gaa tgg cac gac atg cca caa ggc acg caa gct gat ttc 691
 Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly Thr Gln Ala Asp Phe
 185 190 195

caa gcc tgc tgt cgc aaa gca att aaa aat act ttt ctt ctt aga ggt 739
 Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr Phe Leu Leu Arg Gly
 200 205 210

0000074-0000000

gga ttt tca gaa tgacatcaca ggtcaagccg gac
 Gly Phe Ser Glu
 215

<210> 272
 <211> 217
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 272
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 Thr Leu Glu Ala Ile Glu Asp Asn Ala Thr Arg Leu Ile Leu Glu Arg
 20 25 30
 Gly Phe Asp Asn Val Thr Ile Glu Asp Ile Cys Ala Glu Ala Gly Ile
 35 40 45
 Ser Lys Arg Thr Phe Phe Asn Tyr Val Glu Ser Lys Glu Ser Val Ala
 50 55 60
 Ile Gly His Thr Ala Lys Leu Pro Thr Asp Glu Glu Arg Glu Ala Phe
 65 70 75 80
 Leu Ala Thr Arg His Glu Asn Ile Ile Asp Thr Val Phe Asp Leu Val
 85 90 95
 Ile Asn Leu Phe Gly Asn His Asp Asn Ser Lys Ser Gly Val Ala Gly
 100 105 110
 Asp Ile Met Arg Arg Arg Lys Glu Ile Arg Val Lys His Pro Glu Leu
 115 120 125
 Ala Val Gln His Phe Ala Arg Phe His Gln Ala Arg Glu Gly Leu Glu
 130 135 140
 His Leu Ile Val Glu Tyr Phe Glu Lys Trp Pro Gly Ser Gln His Leu
 145 150 155 160
 Asp Glu Pro Ala Asp Arg Glu Ala Ile Ala Ile Val Gly Leu Leu Ile
 165 170 175
 Ser Val Met Leu Gln Gly Ser Arg Glu Trp His Asp Met Pro Gln Gly
 180 185 190
 Thr Gln Ala Asp Phe Gln Ala Cys Cys Arg Lys Ala Ile Lys Asn Thr
 195 200 205
 Phe Leu Leu Arg Gly Gly Phe Ser Glu
 210 215

<210> 273
 <211> 480
 <212> DNA
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<221> CDS

<222> (101)..(457)

<223> RXN00035

<400> 273

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				Val	Pro	Leu	Tyr	Lys	
				1				5	

cag	atc	gct	tct	ttg	att	gag	gac	tcc	atc	gtt	gac	gga	acc	ttg	agc	163
Gln	Ile	Ala	Ser	Leu	Ile	Glu	Asp	Ser	Ile	Val	Asp	Gly	Thr	Leu	Ser	
				10				15						20		

att	gat	caa	cgc	gtg	cct	tct	act	aat	gaa	cta	gcc	gcg	ttc	cat	cgc	211
Ile	Asp	Gln	Arg	Val	Pro	Ser	Thr	Asn	Glu	Leu	Ala	Ala	Phe	His	Arg	
				25				30					35			

att	aat	ccc	gcc	acc	gca	cgc	aac	ggc	ctg	acc	ctc	ctt	gtc	gaa	gcc	259
Ile	Asn	Pro	Ala	Thr	Ala	Arg	Asn	Gly	Leu	Thr	Leu	Leu	Val	Glu	Ala	
				40			45						50			

ggc	atc	ctc	tat	aag	aag	cgt	ggc	att	ggc	atg	ttc	gtc	agc	gcc	cag	307
Gly	Ile	Leu	Tyr	Lys	Lys	Arg	Gly	Ile	Gly	Met	Phe	Val	Ser	Ala	Gln	
				55		60					65					

gcc	cca	gca	ctc	atc	cga	gag	cgg	cga	gat	gcc	gcc	ttc	gcg	gct	act	355
Ala	Pro	Ala	Leu	Ile	Arg	Glu	Arg	Arg	Asp	Ala	Ala	Phe	Ala	Ala	Thr	
				70		75			80					85		

tat	gta	gca	ccg	ctt	atc	gac	gaa	tcc	atc	cac	ctt	ggt	ttc	act	cgt	403
Tyr	Val	Ala	Pro	Leu	Ile	Asp	Glu	Ser	Ile	His	Leu	Gly	Phe	Thr	Arg	
				90					95					100		

gcg	cgc	att	cac	gcc	ctt	tta	gac	cag	gtc	gct	gaa	agt	agg	ggc	ctg	451
Ala	Arg	Ile	His	Ala	Leu	Leu	Asp	Gln	Val	Ala	Glu	Ser	Arg	Gly	Leu	
				105			110							115		

tac	aag	tagcgcttaa	accctottga	cct												480
Tyr	Lys															

<210> 274

<211> 119

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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			20					25					30		

Ala	Ala	Phe	His	Arg	Ile	Asn	Pro	Ala	Thr	Ala	Arg	Asn	Gly	Leu	Thr
		35				40						45			

Leu	Leu	Val	Glu	Ala	Gly	Ile	Leu	Tyr	Lys	Lys	Arg	Gly	Ile	Gly	Met
	50					55					60				

Phe Val Ser Ala Gln Ala Pro Ala Leu Ile Arg Glu Arg Arg Asp Ala
65 70 75 80

Ala Phe Ala Ala Thr Tyr Val Ala Pro Leu Ile Asp Glu Ser Ile His
85 90 95

Leu Gly Phe Thr Arg Ala Arg Ile His Ala Leu Leu Asp Gln Val Ala
100 105 110

Glu Ser Arg Gly Leu Tyr Lys
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<210> 275

<211> 810

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(787)

<223> RXN00049

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Met Pro Thr Pro Ser
1 5

cag cac aag gac gct tca aca gca caa acc gac aac cag gta cca act 163
Gln His Lys Asp Ala Ser Thr Ala Gln Thr Asp Asn Gln Val Pro Thr
10 15 20

ggc cgc cgt gca caa aaa cgc gaa caa acc cgc gcg cgc ctg atc act 211
Gly Arg Arg Ala Gln Lys Arg Glu Gln Thr Arg Ala Arg Leu Ile Thr
25 30 35

tcc gct cgc aca ctc atg gca gaa cgg ggt gtc gac aat gta gga ata 259
Ser Ala Arg Thr Leu Met Ala Glu Arg Gly Val Asp Asn Val Gly Ile
40 45 50

gct gaa atc acc gaa ggc gca aac atc gga acg gga acc ttc tac aac 307
Ala Glu Ile Thr Glu Gly Ala Asn Ile Gly Thr Gly Thr Phe Tyr Asn
55 60 65

tac ttc cca gac cgt gaa caa cta ctc caa gct gtc gca gaa gat gcc 355
Tyr Phe Pro Asp Arg Glu Gln Leu Leu Gln Ala Val Ala Glu Asp Ala
70 75 80 85

ttt gaa tcc gtg gga att gcc ctc gac cag gtg cta acc aaa tta gac 403
Phe Glu Ser Val Gly Ile Ala Leu Asp Gln Val Leu Thr Lys Leu Asp
90 95 100

gat ccg gct gaa gta ttt gca ggg tcg ctt cga cat cta gta cgg cac 451
Asp Pro Ala Glu Val Phe Ala Gly Ser Leu Arg His Leu Val Arg His
105 110 115

tcg tta gaa gat cgg att tgg ggc gga ttt ttc ata caa atg ggt gct 499
Ser Leu Glu Asp Arg Ile Trp Gly Gly Phe Phe Ile Gln Met Gly Ala

09602274-052300

tcg ctg tct gaa gtg tcc gga acg ctg aaa gtc acc tcc ttc caa tcc 403
Ser Leu Ser Glu Val Ser Gly Thr Leu Lys Val Thr Ser Phe Gln Ser
90 95 100

Figure 1

ctg ctg ttc acc ctt gcc ccg aaa gcc atc gcg cgc ctg acc gag aaa 451
 Leu Leu Phe Thr Leu Ala Pro Lys Ala Ile Ala Arg Leu Thr Glu Lys
 105 110 115

tac cca cac ctg caa gta gaa atc tcc caa cta gaa gtc acc gca gcg 499
 Tyr Pro His Leu Gln Val Glu Ile Ser Gln Leu Glu Val Thr Ala Ala
 120 125 130

ctg gaa gaa ctg cgc gcc cgc cgc gtc gac gtc gca ctg ggc gag gaa 547
 Leu Glu Glu Leu Arg Ala Arg Arg Val Asp Val Ala Leu Gly Glu Glu
 135 140 145

tac ccc gtg gaa gtc ccc ctt gtt gag gcc agc att cac cgc gaa gtc 595
 Tyr Pro Val Glu Val Pro Leu Val Glu Ala Ser Ile His Arg Glu Val
 150 155 160 165

ctg ttc gaa gac ccc atg ctg ctg gtc acc cca gca agc ggc cca tac 643
 Leu Phe Glu Asp Pro Met Leu Leu Val Thr Pro Ala Ser Gly Pro Tyr
 170 175 180

tct ggc ctg acc ctg cca gaa ctg cgc gac atc ccc atc gcc atc gat 691
 Ser Gly Leu Thr Leu Pro Glu Leu Arg Asp Ile Pro Ile Ala Ile Asp
 185 190 195

cca ccc gac ctt ccc gcg gcc gaa tgg gtc cat agg ctg tgc cgg cgc 739
 Pro Pro Asp Leu Pro Ala Gly Glu Trp Val His Arg Leu Cys Arg Arg
 200 205 210

gcc ggg ttt gag ccc cgc gtg acc ttt gaa acc agc gat ccc atg ctg 787
 Ala Gly Phe Glu Pro Arg Val Thr Phe Glu Thr Ser Asp Pro Met Leu
 215 220 225

caa gca cac ctg gtg cgt agc gcc ttg gcc gtg aca ttt tcc ccc aca 835
 Gln Ala His Leu Val Arg Ser Gly Leu Ala Val Thr Phe Ser Pro Thr
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ctg ctg acc ccg atg ctg gaa agc gtg cac atc cag ccg ctg ccc ggc 883
 Leu Leu Thr Pro Met Leu Glu Ser Val His Ile Gln Pro Leu Pro Gly
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aac ccc acg cgc acg ctg tac acc gcg gtc agg gaa ggg cgc cag ggg 931
 Asn Pro Thr Arg Thr Leu Tyr Thr Ala Val Arg Glu Gly Arg Gln Gly
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cat cca gcc att aaa gct ttt cga cga gcc ctg gcc cat gtg gcc aaa 979
 His Pro Ala Ile Lys Ala Phe Arg Arg Ala Leu Ala His Val Ala Lys
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gaa tct tat ttg gag gct cgt cta gta gag tgagttcttg tgagccttca 1029
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<223> RXN01081

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Met Thr Pro Ala Asn
1 5

gaa agt cct atg act aat cca tta ggt tct gcc ccc acc cca gcc aag 163
Glu Ser Pro Met Thr Asn Pro Leu Gly Ser Ala Pro Thr Pro Ala Lys
10 15 20

cca ctt ctt gac agt gtt ctt gat gag ctc ggt caa gat atc atc agt 211
Pro Leu Leu Asp Ser Val Leu Asp Glu Leu Gly Gln Asp Ile Ile Ser
25 30 35

ggc aag gtt gct gtc gga gat acc ttc aag ctg atg gac atc ggc gag 259
Gly Lys Val Ala Val Gly Asp Thr Phe Lys Leu Met Asp Ile Gly Glu
40 45 50

cgt ttt ggc att tcc cgc aca gtg gca cgc gaa gcg atg cgc gct ttg 307
Arg Phe Gly Ile Ser Arg Thr Val Ala Arg Glu Ala Met Arg Ala Leu
55 60 65

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Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg Ile Gly Ile Thr Val
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Leu Pro Gln Glu Glu Trp Ala Val Phe Asp Lys Ser Ile Ile Arg Trp
90 95 100

cgt ctc aat gac gaa ggt cag cgt gaa ggc cag ctt cag tct ctt acc 451
Arg Leu Asn Asp Glu Gly Gln Arg Glu Gly Gln Leu Gln Ser Leu Thr
105 110 115

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Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala Arg Ser Val Ala Leu
120 125 130

cac gcg tca acc gcc gag ctc gag aaa atc cgc gcg ctc gca aca gag 547
His Ala Ser Thr Ala Glu Leu Glu Lys Ile Arg Ala Leu Ala Thr Glu
135 140 145

atg cgt cag ttg ggt gaa tct ggt cag ggt gcg tcc cag cgc ttc ctc 595
Met Arg Gln Leu Gly Glu Ser Gly Gln Gly Ala Ser Gln Arg Phe Leu
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Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser Ala Val Leu Val Gly
185 190 195

cgc acc gag ctc ggc ctg cag cct gat ctg ccg gcg cac gag gcg cta 739
 Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro Ala His Glu Ala Leu
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 Asp Asn His Asp Lys Leu Ala Asp Ala Leu Leu Asn Arg Asp Ala Asp
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gcc gca gaa act gcg tcc cga aac atc ctc aat gag gtg cgc agc gcg 835
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<213> *Corynebacterium glutamicum*

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Met Asp Ile Gly Glu Arg Phe Gly Ile Ser Arg Thr Val Ala Arg Glu
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Ala Met Arg Ala Leu Glu Gln Leu Gly Leu Val Ala Ser Ser Arg Arg
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Ile Gly Ile Thr Val Leu Pro Gln Glu Glu Trp Ala Val Phe Asp Lys
 85 90 95

Ser Ile Ile Arg Trp Arg Leu Asn Asp Glu Gly Gln Arg Glu Gly Gln
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Leu Gln Ser Leu Thr Glu Leu Arg Ile Ala Ile Glu Pro Ile Ala Ala
 115 120 125

Arg Ser Val Ala Leu His Ala Ser Thr Ala Glu Leu Glu Lys Ile Arg
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Ala Leu Ala Thr Glu Met Arg Gln Leu Gly Glu Ser Gly Gln Gly Ala
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Ser Gln Arg Phe Leu Glu Ala Asp Val Thr Phe His Glu Leu Ile Leu
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Arg Tyr Cys His Asn Glu Met Phe Ala Ala Leu Ile Pro Ser Ile Ser
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Ala Val Leu Val Gly Arg Thr Glu Leu Gly Leu Gln Pro Asp Leu Pro

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Pro Tyr Phe Thr Arg Tyr Lys Gly Arg Thr Val Met Glu Ala Ala Arg	20								25							30											
gat ctt ggc caa ccc tcc tcc caa atc atg gaa gac ctc aac aga tta																						144					
Asp Leu Gly Gln Pro Ser Ser Gln Ile Met Glu Asp Leu Asn Arg Leu	35								40							45											
tgg atg tgt ggt ctg cca gga ctt ctt cca ggt gac ttg gtg gag ctt																						192					
Trp Met Cys Gly Leu Pro Gly Leu Leu Pro Gly Asp Leu Val Glu Leu	50								55							60											
gat cat tcc ttt aag gaa gta aaa atc cac aat gct caa ggc atg gat																						240					
Asp His Ser Phe Lys Glu Val Lys Ile His Asn Ala Gln Gly Met Asp	65								70							75						80					
aaa ccc ttg cgc ctc aca cca act gaa gcc ggt gtt ttg ctg ctg aca																						288					
Lys Pro Leu Arg Leu Thr Pro Thr Glu Ala Gly Val Leu Leu Leu Thr	85								90							95											
ctt gaa tcc ctg gaa tcc ctc ccc ggt att gcg aaa cag gaa gcg gtc																						336					
Leu Glu Ser Leu Glu Ser Leu Pro Gly Ile Ala Lys Gln Glu Ala Val	100								105							110											
gta tct gct gcg aac aag cta cgc gcc atc atg ggg gag tat tcc tcg																						384					
Val Ser Ala Ala Asn Lys Leu Arg Ala Ile Met Gly Glu Tyr Ser Ser	115								120							125											
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Thr Val Phe Asp Ser Thr Gly Glu Asp Leu Asp Ala Glu Val Leu Glu	130								135							140											
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Ile Ile Arg Asp Ala Met Asp Leu His Gln Gln Val Ser Phe Glu Tyr																											

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cat atc ttc acc cat gaa ggc gaa acc tac atc aaa gcc tgg gaa gaa				576
His Ile Phe Thr	His Glu Gly Glu Thr Tyr Ile Lys Ala Trp Glu Glu			
180	185	190		
gct gtg aac caa tgg cgg acg ttt agg ctt gat cgc atc cga agc att				624
Ala Val Asn Gln Trp Arg Thr	Phe Arg Leu Asp Arg	Ile Arg Ser Ile		
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Val Leu Leu Asp Ser Lys Ala Val His Pro Ala Arg Gly Val Ser Val				
210	215	220		
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Ser Thr Asp Asp Pro Phe Glu Phe Ala Lys Ser Ser Asp Ile Ala Thr				
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tta ttg ctg cgt gag gac gca atg tgg tta ggc aat tac atg gcc atg				768
Leu Leu Leu Arg Glu Asp Ala Met Trp	Leu Gly Asn Tyr Met Ala Met			
245	250	255		
gag gtg gat gaa acg gtg gaa ccg att cgc gat agc gac gga ttc agc				816
Glu Val Asp Glu Thr Val Glu Pro Ile Arg Asp Ser Asp Gly Phe Ser				
260	265	270		
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Trp His Thr Val Ser Phe Pro Leu Leu Ser Arg Asp Trp Phe Val Arg				
275	280	285		
ttc gcg att ggc cat gct gag cat ttg aaa gta act agt ccc gaa gat				912
Phe Ala Ile Gly His Ala Glu His Leu Lys Val Thr Ser Pro Glu Asp				
290	295	300		
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Leu Arg Lys Cys Ile Lys Gln Lys Ala Phe Ser Gly Leu Ser Ala Tyr				
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Asp His His Val Glu				
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<211> 325

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<213> Corynebacterium glutamicum

<400> 282

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			20					25					30		

Asp	Leu	Gly	Gln	Pro	Ser	Ser	Gln	Ile	Met	Glu	Asp	Leu	Asn	Arg	Leu
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                                         Met Pro Ala Gly Ile
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Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr Phe Pro Gln Ile Gln
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ctg cga cac gat gag ctc gag cgc att cat cgg ttt tac ggc acc ttt 259
Leu Arg His Asp Glu Leu Glu Arg Ile His Arg Phe Tyr Gly Thr Phe
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Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu Gly Asp Leu Phe Glu
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Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val Ser Arg Ala Ser Arg
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atc agc gat cca gca gat ttc ttc ggt gaa tac atc gga gga ctg gga 403
Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr Ile Gly Gly Leu Gly
                        90                        95                        100

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Leu Ser Ala Glu His Ala Ala Val Val Glu Gly Leu Thr Glu Lys Leu
                        105                        110                        115

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Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly Ile Ala Ser Pro Leu
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Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu Tyr Pro Phe Met Phe
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gac gct gtc ctg cgc cta acc cct gag tgg gca cag acc ctt atc ggc 643
Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala Gln Thr Leu Ile Gly
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Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr His Arg Thr Ser Trp
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 Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg Pro Arg Leu Ile Leu
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 Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg Glu Thr Thr Val Thr
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 Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val Pro Val Ile Glu Gln
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 Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys Ser Arg Val Asp Ala
 375 380 385

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cca cgt cga cgc gtt gcc ttc cac cac cca gcc gaa ttg gtc cct cac 1363
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gta cga tcc att tcc gga ctc ccc gta cac gcg cag tcc ctg atc gcc 1411
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 425 430 435

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 Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu Thr Trp Met Leu Ser

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gaa gac atg acc acc gaa ttc gaa gtc gcc tca ggt gca tca ttt cga Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser Gly Ala Ser Phe Arg 520 525 530			1699
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cga acc gtg aaa atg gtc acc cct gac aac ggc cgt acc tgg att gcc Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly Arg Thr Trp Ile Ala 650 655 660			2083
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Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala Ala Gly Arg Gln Leu 710 715 720	
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Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp Val Ser Ala Val Glu 730 735 740	
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Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr Glu Gln Gly Asn Thr 825 830 835	
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Glu His Leu Pro Val Val His Ala Ala Leu Arg Ser Pro Pro Ala Ala 840 845 850	
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Ser Gln Thr Glu Leu Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr

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Phe Tyr Gly Thr Phe Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu 50 55 60		
Gly Asp Leu Phe Glu Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val 65 70 75 80		
Ser Arg Ala Ser Arg Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr 85 90 95		
Ile Gly Gly Leu Gly Leu Ser Ala Glu His Ala Ala Val Val Glu Gly 100 105 110		
Leu Thr Glu Lys Leu Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly 115 120 125		
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His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu 145 150 155 160		
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His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala 195 200 205		
Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly 210 215 220		
Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg 225 230 235 240		
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Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu 260 265 270		
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 405 410 415
 Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala
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 465 470 475 480
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 Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro
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 515 520 525
 Gly Ala Ser Phe Arg Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser
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 His Gly Ser Pro Leu Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly
 645 650 655
 Arg Thr Trp Ile Ala Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val
 660 665 670

Abstract

Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly Met Lys Lys Ser Ala
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90 95 100

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Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val Leu Ser Leu Ser Glu
105 110 115

aaa ggc act aca tac att cag aaa aca gcc acc cgc caa aat gct ttg 499
Lys Gly Thr Thr Tyr Ile Gln Lys Thr Ala Thr Arg Gln Asn Ala Leu
120 125 130

gaa tcc gag tgg ttt ggc acc ctg acc gac atc gag cag gat tta ttg 547
Glu Ser Glu Trp Phe Gly Thr Leu Thr Asp Ile Glu Gln Asp Leu Leu
135 140 145

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Glu Ser Leu Leu Arg Lys Leu Leu Asp Ser Asn Arg Ala Ser Lys Val
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35 40 45

Arg Pro Asp Gly Leu Ser Leu Ala Ser Tyr Arg Ile Leu Phe Ser Leu
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Trp Thr Asp Gly Pro Met Ser Pro Leu Gln Val Thr Asp Lys Thr Gly
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Met Lys Lys Ser Ala Ile Ser Asn Leu Leu Lys Pro Leu Leu Ala Glu
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Ser Leu Ile Val Gln Val Thr Ala Glu Asn Asp Arg Arg Ser Lys Val
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Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp Leu Gln Asp Leu Lys					20	
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Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala Lys Leu Gln Ala Arg			30		35	
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Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile Thr Arg Pro Thr Pro			45		50	
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Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu Glu Tyr Glu Thr Ile			60		65	
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Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn Gln Ser Lys Pro Ala			75		85	
	70					
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Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu Val Phe Leu Ala Ala			90		100	
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 atc gat cac act cga gca gaa aac caa gga tgg gat tct ggt gag gac 691
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 185 190 195
 ttt gca tca tat gcg aag agt gtc ttc tcc tcc ggg gac aac cta tta 739
 Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser Gly Asp Asn Leu Leu
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 ccg gaa ttg tct ttc aaa ttt ctt ctg gag tgt ctg agc ggc gaa gct 931
 Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys Leu Ser Gly Glu Ala
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 Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro Ala Ser Leu Glu Asn
 280 285 290
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 295 300 305
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 Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr Pro Thr Glu Lys Ser
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390	395	400	405
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caa ggt ctc gat cat gag ccc gtt ttc cac acg agt ccc cgc atc gaa Gln Gly Leu Asp His Glu Pro Val Phe His Thr Ser Pro Arg Ile Glu	490	495	500
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1891			
gga caa act ggc tta aca aag act ttc gcc cgt ttt agt tcc aat tct Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg Phe Ser Ser Asn Ser	600	605	610
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1987			
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2035			645

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cct Pro	gtc Val	aca Thr	cac His 665	agc Ser	caa Gln	aca Thr	aag Lys	tgg Trp 670	gaa Glu	agc Ser	aca Thr	aag Lys	acg Thr 675	aca Thr	cta Leu	2131
gat Asp	ttc Phe	aat Asn	gac Asp 680	ttt Phe	gcc Ala	gat Asp	gga Gly 685	aac Asn	ctc Leu	cag Gln	atc Ile	aga Arg 690	ttc Phe	cct Pro	aat Asn	2179
gaa Glu	gtc Val	tat Tyr	gat Asp 695	cca Pro	aac Asn	ttg Leu 700	aaa Lys	atc Ile	att Ile	aaa Lys 705	atg Met	gtg Val	gca Ala	tac Tyr	aag Lys	2227
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 Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val Ser Phe Ile Tyr Ser
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 Gly Phe Trp Pro Ala Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu
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 His Val Tyr Asp Ala Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys

130 135 140
 Asn Gly Leu Glu Thr Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr
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 Val Gly Leu Ile Gln Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu
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 Ala Leu Val Lys Phe Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp
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 Asp Ser Gly Glu Asp Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser
 195 200 205
 Gly Asp Asn Leu Leu Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His
 210 215 220
 Ile Pro Ala Arg Ser Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr
 225 230 235 240
 Asn Trp Tyr Arg Asp Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val
 245 250 255
 Gly Thr His Gly Leu Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys
 260 265 270
 Leu Ser Gly Glu Ala Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro
 275 280 285
 Ala Ser Leu Glu Asn Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln
 290 295 300
 Ser Phe Glu Leu Ser Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala
 305 310 315
 Leu Gln Ile Pro Ala Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser
 325 330 335
 Ile Lys Val Arg Pro Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu
 340 345 350
 Tyr Arg Leu Pro Leu Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr
 355 360 365
 Pro Thr Glu Lys Ser Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn
 370 375 380
 Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu
 385 390 395 400
 Met Leu Ser Gly Asn Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile
 405 410 415
 Ile Arg Ala Arg Met Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu
 420 425 430
 Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu
 435 440 445
 Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu
 450 455 460

000000 14000000

Leu Pro Val Arg Arg Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu
 465 470 475 480
 Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr
 485 490 495
 Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln
 500 505 510
 Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr
 515 520 525
 Pro Val Glu Pro Glu Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu
 530 535 540
 Ser Asp Asp Pro Trp Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp
 545 550 555 560
 Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp
 565 570 575
 Leu Ser Leu Thr Phe Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr
 580 585 590
 Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg
 595 600 605
 Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile
 610 615 620
 Gly Leu Asp Ala Phe Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly
 625 630 635 640
 Asp Phe Pro Glu Asp Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln
 645 650 655
 Leu His Tyr Gln Val Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser
 660 665 670
 Thr Lys Thr Thr Leu Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln
 675 680 685
 Ile Arg Phe Pro Asn Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys
 690 695 700
 Met Val Ala Tyr Lys Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser
 705 710 715 720
 Lys Ile Gly Ser Ser Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys
 725 730 735
 Glu Leu Met Asp Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe
 740 745 750
 Ala Glu Ser Lys Asp Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys
 755 760 765
 Arg Thr Gly Lys Ile Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln
 770 775 780

Pro Gln Ala Ser Ser His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu
 785 790 795 800
 Ala Ala Ala Glu Ile Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg
 805 810 815
 His Thr Ser Lys Arg Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro
 820 825 830
 Leu Asp Pro Pro Ile Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu
 835 840 845
 Pro Asp Thr His Phe Val Val Gly Pro Leu Ile Val Glu Val Arg Glu
 850 855 860
 Lys Glu Phe Leu Ser Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala
 865 870 875 880
 Val Val Ala Asn Asp Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro
 885 890 895
 Phe Leu Thr His Arg Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu
 900 905 910
 Leu Pro Gln Glu Ile Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg
 915 920 925
 His Val Leu Ala Gln Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp
 930 935 940
 Phe Asp Asp Ala Thr Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala
 945 950 955 960
 Leu Asp Glu Leu Asp Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu
 965 970 975
 Ser Phe Ile Arg Ser Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp
 980 985 990
 Thr Ala Gly Asp Ile His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu
 995 1000 1005
 Met Asn Asp Leu Arg Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu
 1010 1015 1020
 Arg Ala Ile Glu Arg Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly
 1025 1030 1035 1040
 Gly Ser Glu Leu Trp Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser
 1045 1050 1055
 Leu Ala Gln Lys Cys Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg
 1060 1065 1070
 Asn Ser Gly Leu Glu Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe
 1075 1080 1085
 Ser Ala Glu Phe Ile Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu
 1090 1095 1100
 Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Gln Leu Pro Thr

03602874-153710

1105		1110		1115		1120
Leu Phe Asp Phe	Ala Glu Lys Tyr	Glu Tyr Leu Ile	Asp His Leu Gly			
	1125		1130		1135	
Asp Asp Arg Ile	Lys Val Thr Ala	Arg Glu Leu Ser	Thr Leu Ala Ser			
	1140		1145		1150	
Glu His Arg Arg	Gly Asn Ala Glu	Asn Trp Leu Tyr	Ala Pro Tyr Val			
	1155		1160		1165	
Ser Phe Ile Tyr	Ser Leu Leu Asn	Arg Met Ile Ala	His Glu Val Ile			
	1170		1175		1180	
Arg Pro Ile Ala	Gln Ile Asn Tyr	Ser Arg His Asp	Trp Ala Asn Ala			
	1185		1190		1195	1200
Ala Arg Leu Ile	Pro Arg Leu Thr	Gly Phe Asp Leu	Val Ser Ala Glu			
	1205		1210		1215	
Ala Lys Val Leu	Ser Ala Ile Asn	Asn Asn Asn Ile	Ile Pro Thr Ala			
	1220		1225		1230	

Ile

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<210> 289
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(982)  
<223> RXN02506
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<400> 289	cctttccctg aactctaagc aattgtgatc tatagtacaa atgcataaac attaacgcgcg	60
atatcatctt cttgcatacc ggccgaaagg tttagcacac	atg cac ctc aat cag Met His Leu Asn Gln 1 5	115
ctc gaa ttt ttc atc gca gta gcc caa cac gga cag atc aac cgc gcc		163
Leu Glu Phe Phe	Ile Ala Val Ala Gln His Gly Gln Ile Asn Arg Ala 10 15 20	
gcc gaa gaa ctc ctc att tcc caa ccc gct ctc agc cga cag atc tcc		211
Ala Glu Glu Leu	Leu Ile Ser Gln Pro Ala Leu Ser Arg Gln Ile Ser 25 30 35	
gca ctt gaa aaa tcc gtc gga gct cca ctc ttc gaa cgc cat tcc cgc		259
Ala Leu Glu Lys Ser Val Gly Ala	Pro Leu Phe Glu Arg His Ser Arg 40 45 50	
ggg gtc tcc ctc aca aag gcc gga gaa atc ctc cac gaa gaa gcc ctc		307
Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu His Glu Glu Ala Leu	55 60 65	
cga acg ctt agc agg atg caa tcg gta gtc gat gaa atc caa tcc ggt		355

Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp Glu Ile Gln Ser Gly
 70 75 80 85

gag cac ctc atc acc agc atc aac atc gga gtt ccc cct gga atc ccc 403
 Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val Pro Pro Gly Ile Pro
 90 95 100

atc gac tgg ttg cgc tgc caa ctc atc gat tta ggc ccc gag acc cgc 451
 Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu Gly Pro Glu Thr Arg
 105 110 115

att tca ctg atc gaa tcc ccc acc gat gat cag cta aaa ctt ctt aaa 499
 Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln Leu Lys Leu Leu Lys
 120 125 130

caa cgc gaa ctc gac atc gcc ctt tgt cga cgc caa agc gag gcc ttt 547
 Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg Gln Ser Glu Ala Phe
 135 140 145

gcc acc aca ctt gtc cac gaa caa gaa ctg gga atc gtc gtc cga aaa 595
 Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly Ile Val Val Arg Lys
 150 155 160 165

aac tcc gaa ctg cac caa aaa gtc gca gga aaa gac aac gcc aca ctc 643
 Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys Asp Asn Ala Thr Leu
 170 175 180

ttc gat ctt gaa ggg ctt cga gtc ctc gca cac tcc cgc ggt gaa gta 691
 Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His Ser Arg Gly Glu Val
 185 190 195

aga att cag gaa gaa atc ctc aaa aac gcc atg ctc gcc gca gga gtt 739
 Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met Leu Ala Ala Gly Val
 200 205 210

aat gcc acg tgg atc ttc cga aaa ttt ggg caa tat agc tca ctg atc 787
 Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln Tyr Ser Ser Leu Ile
 215 220 225

gca gac ctt gtc cag gcc gat gtc gca ctc aca aca gag gaa tcc gcc 835
 Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr Thr Glu Glu Ser Ala
 230 235 240 245

cgc acc aac ttc ccc agc tgg caa tgg gtc ccc atc gaa ggc gaa gac 883
 Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro Ile Glu Gly Glu Asp
 250 255 260

gcc tcc gga aat gac ctt gtt gtt cgc acc tgg atc acc tgg aac ccc 931
 Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp Ile Thr Trp Asn Pro
 265 270 275

caa ccc acc ccc gcg gtg aag gcc ctg atc cag aaa ttt att gac gga 979
 Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln Lys Phe Ile Asp Gly
 280 285 290

aac tgagttcttaa acagccgccca tga 1005
 Asn

<213> *Corynebacterium glutamicum*

Met His Leu Asn Gln Leu Glu Phe Phe Ile Ala Val Ala Gln His Gly
1 5 10 15

Gln Ile Asn Arg Ala Ala Glu Glu Leu Leu Ile Ser Gln Pro Ala Leu
20 25 30

Ser Arg Gln Ile Ser Ala Leu Glu Lys Ser Val Gly Ala Pro Leu Phe
35 40 45

Glu Arg His Ser Arg Gly Val Ser Leu Thr Lys Ala Gly Glu Ile Leu
50 55 60

His Glu Glu Ala Leu Arg Thr Leu Ser Arg Met Gln Ser Val Val Asp
65 70 75 80

Glu Ile Gln Ser Gly Glu His Leu Ile Thr Ser Ile Asn Ile Gly Val
85 90 95

Pro Pro Gly Ile Pro Ile Asp Trp Leu Arg Cys Gln Leu Ile Asp Leu
100 105 110

Gly Pro Glu Thr Arg Ile Ser Leu Ile Glu Ser Pro Thr Asp Asp Gln
115 120 125

Leu Lys Leu Leu Lys Gln Arg Glu Leu Asp Ile Ala Leu Cys Arg Arg
130 135 140

Gln Ser Glu Ala Phe Ala Thr Thr Leu Val His Glu Gln Glu Leu Gly
145 150 155 160

Ile Val Val Arg Lys Asn Ser Glu Leu His Gln Lys Val Ala Gly Lys
165 170 175

Asp Asn Ala Thr Leu Phe Asp Leu Glu Gly Leu Arg Val Leu Ala His
180 185 190

Ser Arg Gly Glu Val Arg Ile Gln Glu Glu Ile Leu Lys Asn Ala Met
195 200 205

Leu Ala Ala Gly Val Asn Ala Thr Trp Ile Phe Arg Lys Phe Gly Gln
210 215 220

Tyr Ser Ser Leu Ile Ala Asp Leu Val Gln Ala Asp Val Ala Leu Thr
225 230 235 240

Thr Glu Glu Ser Ala Arg Thr Asn Phe Pro Ser Trp Gln Trp Val Pro
245 250 255

Ile Glu Gly Glu Asp Ala Ser Gly Asn Asp Leu Val Val Arg Thr Trp
260 265 270

Ile Thr Trp Asn Pro Gln Pro Thr Pro Ala Val Lys Ala Leu Ile Gln
275 280 285

Lys Phe Ile Asp Gly Asn
290

[illegible]


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<210> 291
<211> 789
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(766)
<223> RXN02620
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400> 291	gaagcccgtg aaatcgatac caaataggaa ctctgcacaa ttactggcta caatctcttg	60
agatcaatag gccaaaaactt taagggaagta gaattacgct	atg gca gga gca gtg Met Ala Gly Ala Val 1 5	115
gga cgc ccc cgg aga tca gct ccg cga cgg gca ggc aag aat cct cgc	10 15 20	163
Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala Gly Lys Asn Pro Arg		
gag gag att ott gac gcc tct gct gag ctt ttc acc cgt caa ggc ttc	25 30 35	211
Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe Thr Arg Gln Gly Phe		
gca aca acc tcc acg cat caa atc gct gat gcc gtg gga atc cgc caa	40 45 50	259
Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala Val Gly Ile Arg Gln		
gcc tcg ctg tat tat cac ttc ccg tcc aag acg gaa atc ttc ctc acc	55 60 65	307
Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr Glu Ile Phe Leu Thr		
ctg ctg aaa tct act gtc gag ccg tcc act gtg ctc gcc gaa gac tta	70 75 80 85	355
Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val Leu Ala Glu Asp Leu		
agc acc ctg gac gcc gga cct gag atg cgc ctc tgg gca atc gtt gcc	90 95 100	403
Ser Thr Thr Leu Asp Ala Gly Pro Glu Met Arg Leu Trp Ala Ile Val Ala		
tcc gaa gtg cgt ctg ctg ctg tcc acc aag tgg aac gtc ggt cgc ctg	105 110 115	451
Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp Asn Val Gly Arg Leu		
tac caa ctc ccc atc gtt ggt tct gaa gag ttc gcc gag tac cac agc	120 125	499
Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe Ala Glu Tyr His Ser		
cag cgc gaa gcc ctc acc aac gtc ttc cgc gac ctc gcc acc gaa atc	135 140 145	547
Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp Leu Ala Thr Glu Ile		
gtc ggt gac gac ccc cgc gca gaa ctc ccc ttc cac atc acc atg tcg	150 155 160	595
Val Gly Asp Asp Asp Pro Arg Ala Glu Leu Pro Phe His Ile Thr Met Ser		
gtg atc gaa atg cgt cgc aac gac ggc aag att cca agc ccg ctt tcc	165 170 175	643
Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile Pro Ser Pro Leu Ser		

	170		175		180	
gca gac agc ctc ccg gag acc gca att atg ctt gcc gac gcc tcc ctc						691
Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu Ala Asp Ala Ser Leu						
	185		190		195	
gcc gtc ctc gcc gcg ccg ctg ccc gcc gac cgg gtc gaa aaa acg ctt						739
Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg Val Glu Lys Thr Leu						
	200		205		210	
gaa cta atc aag cag gct gac gcg aaa taaccatccg cgccctgcgaa						786
Glu Leu Ile Lys Gln Ala Asp Ala Lys						
	215		220			
atc						789
<210> 292						
<211> 222						
<212> PRT						
<213> Corynebacterium glutamicum						
<400> 292						
Met Ala Gly Ala Val Gly Arg Pro Arg Arg Ser Ala Pro Arg Arg Ala						
1 5 10 15						
Gly Lys Asn Pro Arg Glu Glu Ile Leu Asp Ala Ser Ala Glu Leu Phe						
20 25 30						
Thr Arg Gln Gly Phe Ala Thr Thr Ser Thr His Gln Ile Ala Asp Ala						
35 40 45						
Val Gly Ile Arg Gln Ala Ser Leu Tyr Tyr His Phe Pro Ser Lys Thr						
50 55 60						
Glu Ile Phe Leu Thr Leu Leu Lys Ser Thr Val Glu Pro Ser Thr Val						
65 70 75 80						
Leu Ala Glu Asp Leu Ser Thr Leu Asp Ala Gly Pro Glu Met Arg Leu						
85 90 95						
Trp Ala Ile Val Ala Ser Glu Val Arg Leu Leu Leu Ser Thr Lys Trp						
100 105 110						
Asn Val Gly Arg Leu Tyr Gln Leu Pro Ile Val Gly Ser Glu Glu Phe						
115 120 125						
Ala Glu Tyr His Ser Gln Arg Glu Ala Leu Thr Asn Val Phe Arg Asp						
130 135 140						
Leu Ala Thr Glu Ile Val Gly Asp Asp Pro Arg Ala Glu Leu Pro Phe						
145 150 155 160						
His Ile Thr Met Ser Val Ile Glu Met Arg Arg Asn Asp Gly Lys Ile						
165 170 175						
Pro Ser Pro Leu Ser Ala Asp Ser Leu Pro Glu Thr Ala Ile Met Leu						
180 185 190						
Ala Asp Ala Ser Leu Ala Val Leu Gly Ala Pro Leu Pro Ala Asp Arg						
195 200 205						

Val Glu Lys Thr Leu Glu Leu Ile Lys Gln Ala Asp Ala Lys
210 215 220

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<210> 293
<211> 654
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(631)
<223> RXN00826
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<400> 293
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ccgtgtccat tcagactggt ttctttaagt tcttgggcac atg atc aca gtt tta 115
Met Ile Thr Val Leu
1 5

att gat gga caa tcc ggt gcg ggc aaa acc acc ttg gcg ggt gag tta 163
Ile Asp Gly Gln Ser Gly Ala Gly Lys Thr Thr Leu Ala Gly Glu Leu
10 15 20

gct gcc cgc acc ggg ttt cag ttg gtt cat ttg gat gac ttt tat cct 211
Ala Ala Arg Thr Gly Phe Gln Leu Val His Leu Asp Asp Phe Tyr Pro
25 30 35

ggt tgg act ggc ctt gaa gcg gca tcg gag att gtt gca cgc cat gtt 259
Gly Trp Thr Gly Leu Glu Ala Ala Ser Glu Ile Val Ala Arg His Val
40 45 50

ttg gac gcg gac aac ccc ggt ttc ttc acg tgg gat tgg cac aac aat 307
 Leu Asp Ala Asp Asn Pro Gly Phe Phe Thr Trp Asp Trp His Asn Asn
 55 60 65

tgc caa ggc gat tgg atc aag ttg gag cct ggt cga agt ctc att atc 355
Cys Gln Gly Asp Trp Ile Lys Leu Glu Pro Gly Arg Ser Leu Ile Ile
70 75 80 85

gaa ggc tct gga tca atc act gct gca aca aaa cgc aag gca tcg ctg 403
Glu Gly Ser Gly Ser Ile Thr Ala Ala Thr Lys Arg Lys Ala Ser Leu
90 95 100

ttg ggc gag ctg gtg acc gtt cgt atc act ggt cct gag gct tta aga 451
Leu Gly Glu Leu Val Thr Val Arg Ile Thr Gly Pro Glu Ala Leu Arg
105 110 115

aaa cag cgc gcc ctc aac cgc gat cct gat tac gca cca ttt tgg aaa 499
Lys Gln Arg Ala Leu Asn Arg Asp Pro Asp Tyr Ala Pro Phe Trp Lys
120 125 130

gtg tgg gcg cag cag gag caa cgc cat ttc tct tta ggc gtt gag gtg 547
Val Trp Ala Gln Gln Glu Gln Arg His Phe Ser Leu Gly Val Glu Val
135 140 145

gat cat gag att gtg cta ggt tct gat gag gct tog gga cga ccc gaa 595
Asp His Glu Ile Val Leu Gly Ser Asp Glu Ala Ser Gly Arg Pro Glu
150 155 160 165

tgactagaga aca 654

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<220>  
<221> CDS  
<222> (101)..(532)  
<223> RXS00070
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1. The first step is to identify the problem. This involves understanding the symptoms and the context in which they are occurring.

<400> 295

<400> 295
ccactcgtcc tcgacatact tctcctggca ctaaacgcag ggggtgacac atctgggtag 60

actatcgaag tacattttgt gtcattgagg aggatcaacg gtg ggt atc aat cgc 115
Val Gly Ile Asn Arg
1 5

atc agc caa ggc tct gcc ccg aag ctg gga gtg cga agc acc aga cag 163
Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val Arg Ser Thr Arg Gln
10 15 20

cga aaa gcc gta att gac gtt ctt gag gaa atc gat aac ttc gct tcc 211
Arg Lys Ala Val Ile Asp Val Leu Glu Ile Asp Asn Phe Ala Ser
25 30 35

gcc aaa gaa atc cat cac gag cta tcc acc agg gaa cac aac gtc ggc 259
Ala Lys Glu Ile His His Glu Leu Ser Thr Arg Glu His Asn Val Gly
40 45 50

ctc aca acc gtc tac cga acc ctc caa tcc ctc gcc gac atc gga gca 307
Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu Ala Asp Ile Gly Ala
55 60 65

gtc gac gta ctt acc gtc acg ggt gga gaa act ctg tac cgc caa tgc 355
Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr Leu Tyr Arg Gln Cys
70 75 80 85

cac gac gag gga cac cac cat cac ctg gtc tgc acc aat tgc ggt cgc 403
His Asp Glu Gly His His His His Leu Val Cys Thr Asn Cys Gly Arg
90 95 100

aca gtc gaa atc gat ggc ggt cca gta gag aca tgg gca cag gaa att 451
Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr Trp Ala Gln Glu Ile
105 110 115

gcc act aaa aac ggc ttt gct ctc agt agt cac gag gct gaa atc ttt 499
Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His Glu Ala Glu Ile Phe
120 125 130

gga ctt tgc gct gat tgt aag gaa aaa gtt acg tagttcaagg acatatgaag 552
Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
135 140

ctg 555

<210> 296

<211> 144

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 296

<400> 296
Val Gly Ile Asn Arg Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val
1 5 10 15

Arg Ser Thr Arg Gln Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile
20 25 30

Asp Asn Phe Ala Ser Ala Lys Glu Ile His His Glu Leu Ser Thr Arg
35 40 45

Glu His Asn Val Gly Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu
50 55 60

Ala Asp Ile Gly Ala Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr
65 70 75 80

Leu Tyr Arg Gln Cys His Asp Glu Gly His His His His Leu Val Cys
85 90 95

Thr Asn Cys Gly Arg Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr
100 105 110

Trp Ala Gln Glu Ile Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His
115 120 125

Glu Ala Glu Ile Phe Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
130 135 140

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<210> 297
<211> 936
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(913)
<223> RXS00133
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<400> 297
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aatttgaagg tggataccca gcggattaaa gatgatgaag atg cta ttc gtt cgg 115
Met Leu Phe Val Arg
1 5

cgg ctg aca tcg ctg aaa acc gca aca gcc atc cca gtc acc atg ttc 163
Arg Leu Thr Ser Leu Lys Thr Ala Thr Gly Ile Pro Val Thr Met Phe
 10 15 20

gcc act gtg ttg cag gac aat cgc ctg caa att act cag tgg gtt ggg 211
Ala Thr Val Leu Gln Asp Asn Arg Leu Gln Ile Thr Gln Trp Val Gly
25 30 35

ttg cgt acc ccg gct ctg cag aat ctg gtc att gaa cca ggt gtg ggc 259
Leu Arg Thr Pro Ala Leu Gln Asn Leu Val Ile Glu Pro Gly Val Gly
40 45 50

ggt ggt gga cgc gtc gtc gca acc cgt cgt ccg gtt ggt gtg agt gat 307
Val Gly Gly Arg Val Val Ala Thr Arg Arg Pro Val Gly Val Ser Asp
55 60 65

tac acc agg gca aat gtc att tca cat gag aag gat tcc gcg att cag 355
 Tyr Thr Arg Ala Asn Val Ile Ser His Glu Lys Asp Ser Ala Ile Gln
 70 75 80 85

gat gag ggc ctt cat tcc att gtc gca gtt ccc gtg atc gtg cac cgc 403
Asp Glu Gly Leu His Ser Ile Val Ala Val Pro Val Ile Val His Arg

[illegible]

90	95	100	
gaa att cgt ggc gtt ttg tat gtt	ggc gtt cac tct gcg gtg cgt ctc		451
Glu Ile Arg Gly Val Leu Tyr Val	Gly Val His Ser Ala Val Arg Leu		
105	110	115	
ggc gac act gtt att gaa gaa gtc acc atg act gcg cgc acg ttg gaa			499
Gly Asp Thr Val Ile Glu Glu Val Thr Met Thr Ala Arg Thr Leu Glu			
120	125	130	
caa aac ctg gcg atc aac tcc gcg ctt cgc cgc aat ggc gtt cct gat			547
Gln Asn Leu Ala Ile Asn Ser Ala Leu Arg Arg Asn Gly Val Pro Asp			
135	140	145	
ggt cgc ggt tcc ctc aaa gct aac cgc gtg atg aat ggg gcg gag tgg			595
Gly Arg Gly Ser Leu Lys Ala Asn Arg Val Met Asn Gly Ala Glu Trp			
150	155	160	165
gag cag gtt cgt tcc act cat tcc aag ctg cgc atg ctg gca aat cgt			643
Glu Gln Val Arg Ser Thr His Ser Lys Leu Arg Met Leu Ala Asn Arg			
170	175	180	
gtg acc gat gag gat ctg cgc cgc gat ttg gaa gag ctt tgc gat cag			691
Val Thr Asp Glu Asp Leu Arg Arg Asp Leu Glu Glu Leu Cys Asp Gln			
185	190	195	
atg gtc acc cca gtc cgc atc aag cag acc acc aag ctg tcc gcg cgt			739
Met Val Thr Pro Val Arg Ile Lys Gln Thr Thr Lys Leu Ser Ala Arg			
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gaa tct gga tat gac ggc atc aag gtg ctg atc aag cag gga gcc aat Glu Ser Gly Tyr Asp Gly Ile Lys Val Leu Ile Lys Gln Gly Ala Asn 230 235 240 245			835
gcg att atc gct ggt gac tcc atg atg acc atc ggt gcg ttg ttg gct Ala Ile Ile Ala Gly Asp Ser Met Met Thr Ile Gly Ala Leu Leu Ala 250 255 260			883
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 Gly Gly Tyr Arg Gln Glu Ser Gly Tyr Asp Gly Ile Lys Val Leu Ile
 225 230 235 240
 Lys Gln Gly Ala Asn Ala Ile Ile Ala Gly Asp Ser Met Met Thr Ile
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 Ala Phe Glu Ile Leu Gln Lys Leu Ile Asn Gly Asp Thr Ala Gln Lys
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 Ser Val Val Ile Pro Thr Gln Leu Ser Ile Asn Gly Ser Thr Ala Val
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Gly Leu Ala Lys His Leu Asn Val Ser Val Phe Trp Val Arg Ala Leu
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Leu Ile Phe Ala Ala Leu Leu Ser Gly Ala Gly Leu Phe Ala Tyr Ala
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Glu Arg Ala Asp Ile Ala Ser Arg Leu His Asp Ser Val Leu Gln Thr
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Gln Asp Lys Thr Pro Gln Thr Thr Gly Thr Val Phe Thr Ala Leu Glu
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1. **Introduction**
 2. **Background**
 3. **Methods**
 4. **Results**
 5. **Conclusion**
 6. **References**
 7. **Appendix**
 8. **Figure 1**
 9. **Figure 2**
 10. **Figure 3**
 11. **Figure 4**
 12. **Figure 5**
 13. **Figure 6**
 14. **Figure 7**
 15. **Figure 8**
 16. **Figure 9**
 17. **Figure 10**
 18. **Figure 11**
 19. **Figure 12**
 20. **Figure 13**
 21. **Figure 14**
 22. **Figure 15**
 23. **Figure 16**
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 29. **Figure 22**
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 31. **Figure 24**
 32. **Figure 25**
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Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
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 Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg Glu Ala Val Val Glu
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gat ttc ccc ggc gta acc cgt gac cgc atc tcc atc tct gac tgg 547
 Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser Tyr Ile Ser Asp Trp
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ggt gga cac cgt ttc tgg gtt cag gac aca ggc gga tgg gat cct aac 595
 Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly Gly Trp Asp Pro Asn
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 200 205 210

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 230 235 240 245

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 265 270 275

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gga acc acc gtt gac ccc gtt gac tcc ctg att cag ctg gat caa aaa 1075
 Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile Gln Leu Asp Gln Lys
 310 315 320 325

ctg tgg aaa ttc gtg gat act gct ggt ctt cgc aaa aag gtc aag act 1123

00220-42000000

Leu Trp Lys Phe Val Asp Thr Ala Gly Leu Arg Lys Lys Val Lys Thr
 330 335 340
 gca tct ggc cac gag tac tac gca tca ctg cgt acc cac ggt gcc atc 1171
 Ala Ser Gly His Glu Tyr Tyr Ala Ser Leu Arg Thr His Gly Ala Ile
 345 350 355
 gat gca gct gag ctg tgt gtt ttg ctt atc gat tcc tcc gaa ccc atc 1219
 Asp Ala Ala Glu Leu Cys Val Leu Leu Ile Asp Ser Ser Glu Pro Ile
 360 365 370
 acc gag cag gat cag cgc gtg ctc gca atg atc acc gat gcc ggt aag 1267
 Thr Glu Gln Asp Gln Arg Val Leu Ala Met Ile Thr Asp Ala Gly Lys
 375 380 385
 gca ctg gtt att gcg ttc aac aag tgg gat ctc atg gat gaa gat cgc 1315
 Ala Leu Val Ile Ala Phe Asn Lys Trp Asp Leu Met Asp Glu Asp Arg
 390 395 400 405
 cgc atc gat ttg gat cgc gaa ctt gat ctc cag ttg gca cac gtg cct 1363
 Arg Ile Asp Leu Asp Arg Glu Leu Asp Leu Gln Leu Ala His Val Pro
 410 415 420
 tgg gca aag cgc atc aac atc tcc gcc aaa acc ggt cgt gca ctg cag 1411
 Trp Ala Lys Arg Ile Asn Ile Ser Ala Lys Thr Gly Arg Ala Leu Gln
 425 430 435
 cgc ctc gag cca gca atg ttg gaa gcg ctc gac aac tgg gat cgc cgt 1459
 Arg Leu Glu Pro Ala Met Leu Glu Ala Leu Asp Asn Trp Asp Arg Arg
 440 445 450
 atc tcc act ggt cag ctg aac acc tgg ctg cgt gaa gca att gct gcg 1507
 Ile Ser Thr Gly Gln Leu Asn Thr Trp Leu Arg Glu Ala Ile Ala Ala
 455 460 465
 aac cca cca cca atg cgt ggc gga cgt ttg cct cga gtg ctg ttt gcc 1555
 Asn Pro Pro Pro Met Arg Gly Gly Arg Leu Pro Arg Val Leu Phe Ala
 470 475 480 485
 acc cag gca tct act cag cca cca gtg atc gta ctg ttc acc acc ggc 1603
 Thr Gln Ala Ser Thr Gln Pro Pro Val Ile Val Leu Phe Thr Thr Gly
 490 495 500
 ttc ctc gaa gca ggt tac cga cga tac ctg gag cgc aag ttc cgt gaa 1651
 Phe Leu Glu Ala Gly Tyr Arg Arg Tyr Leu Glu Arg Lys Phe Arg Glu
 505 510 515
 cgt ttc ggc ttt gaa ggc act cca gtg cga atc gct gtg cgt gtt cgc 1699
 Arg Phe Gly Phe Glu Gly Thr Pro Val Arg Ile Ala Val Arg Val Arg
 520 525 530
 gag cgc cgc ggc aag ggc gga aac aag cag taaagcttga ttttcctaa 1749
 Glu Arg Arg Gly Lys Gly Gly Asn Lys Gln
 535 540
 aag 1752

<210> 316

<211> 543

<212> PRT

<400> 316

Val Thr Asp Lys His Thr Met Pro Gly Glu Glu Asp Asp Thr Val Phe
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Val Tyr His Thr His Lys Gly Glu Met Asp Val Glu Gly Ala Phe Ala
20 25 30

Asp Glu Glu Glu Leu Ala Pro His Gly Gly Trp Ala Ser Ala Asp Phe
35 40 45

Asp Pro Ala Glu Phe Gly Tyr Glu Asp Ser Asp Asp Asp Phe Asp Ala
50 55 60

Glu Asp Phe Asp Glu Thr Glu Phe Ser Asn Pro Asp Phe Gly Glu Asp
65 70 75 80

Tyr Ser Asp Glu Asp Trp Glu Glu Ile Glu Thr Ala Phe Gly Phe Asp
85 90 95

Pro Ser His Leu Glu Glu Ala Leu Cys Thr Val Ala Ile Val Gly Arg
100 105 110

Pro Asn Val Gly Lys Ser Thr Leu Val Asn Arg Phe Ile Gly Arg Arg
115 120 125

Glu Ala Val Val Glu Asp Phe Pro Gly Val Thr Arg Asp Arg Ile Ser
130 135 140

Tyr Ile Ser Asp Trp Gly Gly His Arg Phe Trp Val Gln Asp Thr Gly
145 150 155 160

Gly Trp Asp Pro Asn Val Lys Gly Ile His Ala Ser Ile Ala Gln Gln
165 170 175

Ala Glu Val Ala Met Ser Thr Ala Asp Val Ile Val Phe Val Val Asp
180 185 190

Thr Lys Val Gly Ile Thr Glu Thr Asp Ser Val Met Ala Ala Lys Leu
195 200 205

Leu Arg Ser Glu Val Pro Val Ile Leu Val Ala Asn Lys Phe Asp Ser
210 215 220

Asp Ser Gln Trp Ala Asp Met Ala Glu Phe Tyr Ser Leu Gly Leu Gly
225 230 235 240

Asp Pro Tyr Pro Val Ser Ala Gln His Gly Arg Gly Gly Ala Asp Val
245 250 255

Leu Asp Lys Val Leu Glu Leu Phe Pro Glu Glu Pro Arg Ser Lys Ser
260 265 270

Ile Val Glu Gly Pro Arg Arg Val Ala Leu Val Gly Lys Pro Asn Val
275 280 285

Gly Lys Ser Ser Leu Leu Asn Lys Phe Ala Gly Glu Thr Arg Ser Val
290 295 300

Val Asp Asn Val Ala Gly Thr Thr Val Asp Pro Val Asp Ser Leu Ile

305						310						315					320
Gln	Leu	Asp	Gln	Lys	Leu	Trp	Lys	Phe	Val	Asp	Thr	Ala	Gly	Leu	Arg		
				325					330					335			
Lys	Lys	Val	Lys	Thr	Ala	Ser	Gly	His	Glu	Tyr	Tyr	Ala	Ser	Leu	Arg		
			340					345					350				
Thr	His	Gly	Ala	Ile	Asp	Ala	Ala	Glu	Leu	Cys	Val	Leu	Leu	Ile	Asp		
		355				360						365					
Ser	Ser	Glu	Pro	Ile	Thr	Glu	Gln	Asp	Gln	Arg	Val	Leu	Ala	Met	Ile		
		370				375					380						
Thr	Asp	Ala	Gly	Lys	Ala	Leu	Val	Ile	Ala	Phe	Asn	Lys	Trp	Asp	Leu		
				390						395					400		
Met	Asp	Glu	Asp	Arg	Arg	Ile	Asp	Leu	Asp	Arg	Glu	Leu	Asp	Leu	Gln		
			405						410					415			
Leu	Ala	His	Val	Pro	Trp	Ala	Lys	Arg	Ile	Asn	Ile	Ser	Ala	Lys	Thr		
			420					425					430				
Gly	Arg	Ala	Leu	Gln	Arg	Leu	Glu	Pro	Ala	Met	Leu	Glu	Ala	Leu	Asp		
		435					440					445					
Asn	Trp	Asp	Arg	Arg	Ile	Ser	Thr	Gly	Gln	Leu	Asn	Thr	Trp	Leu	Arg		
		450			455						460						
Glu	Ala	Ile	Ala	Ala	Asn	Pro	Pro	Pro	Met	Arg	Gly	Gly	Arg	Leu	Pro		
				470						475					480		
Arg	Val	Leu	Phe	Ala	Thr	Gln	Ala	Ser	Thr	Gln	Pro	Pro	Val	Ile	Val		
			485						490					495			
Leu	Phe	Thr	Thr	Gly	Phe	Leu	Glu	Ala	Gly	Tyr	Arg	Arg	Tyr	Leu	Glu		
			500					505					510				
Arg	Lys	Phe	Arg	Glu	Arg	Phe	Gly	Phe	Glu	Gly	Thr	Pro	Val	Arg	Ile		
		515					520					525					
Ala	Val	Arg	Val	Arg	Glu	Arg	Arg	Gly	Lys	Gly	Gly	Asn	Lys	Gln			
		530				535					540						

<210> 317

<211> 386

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (1) . . (363)

<223> RXS00738

<400> 317

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Cys Gln Glu Glu Thr Asp Gly Phe Phe Asp Phe Gly Arg Asp Met Arg

1

□

10

19

ccc ggt gag cgc cgg tcg tat ggc act ttg ctt aac gac gcc acg acg 96

Phe Gly Gln Glu Lys Glu Ser Glu Ala
115 120

cgc ctg cag atc ggg gaa atg ttt caa gac att ccc ctt gca gtg gca 739
Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile Pro Leu Ala Val Ala
200 205 210

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<210> 320
<211> 220
<212> PRT
<213> Corynebacterium glutamicum
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Leu Phe Arg Ala Glu Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu
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Ala Glu Val Ile Gly Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys
35 40 45

Lys Leu Asn Pro Glu Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile
50 55 60

Glu Leu Thr Pro Ala Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg
65 70 75 80

Arg Arg Ile Ile Glu Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala
85 90 95

His Glu Leu His Gly Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro
100 105 110

Leu Val Leu Glu Lys Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp
115 120 125

Pro His Gly Asp Pro Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn
130 135 140

Asp Gly Leu Met Leu Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val
145 150 155 160

Thr Arg Val Arg Asp Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly
165 170 175

Val Gly Ile Thr Val Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser
180 185 190

Asp Ile Ala Thr Leu Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile
195 200 205

Pro Leu Ala Val Ala Asn Ala Val Arg Val Ser Arg
210 215 220

<210> 321
 <211> 570
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(547)
 <223> RXS01123

<400> 321
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 gtggcgggttg gtggaaacac gtggctgggc gaatgtgagc atg cga acc ctg gcc 115
 Met Arg Thr Leu Ala
 1 5
 ggc gag cta aat atc aag gcg ccg tgc ctg tac aag cat gta aaa acg 163
 Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr Lys His Val Lys Thr
 10 15 20
 cgc gag gat atc gcc gca cac atc gcc acg aag gca ttt att cag ctg 211
 Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys Ala Phe Ile Gln Leu
 25 30 35
 ggg caa agc ctg cat gaa cat tgt gaa agt gtg gag gat ttg ctt gcg 259
 Gly Gln Ser Leu His Glu His Cys Glu Ser Val Glu Asp Leu Leu Ala
 40 45 50
 gaa tac cgc tcc atg gct cgg gaa aat cca aat att tac cgg ctt ctc 307
 Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn Ile Tyr Arg Leu Leu
 55 60 65
 acc agt tca gag ttc ccc cgc gag cta ctt cca gaa ggc cta gaa act 355
 Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro Glu Gly Leu Glu Thr
 70 75 80 85
 tgg gca gga acg cca ttc tac ctg gtc acc ggc cac gat ccg atc aag 403
 Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly His Asp Pro Ile Lys
 90 95 100
 ggt caa gca ctg tgg gca ttc gcg cac ggc atg gcc atc ctg gaa atc 451
 Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met Ala Ile Leu Glu Ile
 105 110 115
 gac gcc cga ttc gcc ggc ccc aac aat gga tcc ccc gcg gat ggc gtg 499
 Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser Pro Ala Asp Gly Val
 120 125 130
 tgg gag atc ggc gcg cgg gca ttt gac sca caa gta ttc gac caa ggc 547
 Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln Val Phe Asp Gln Gly
 135 140 145
 tgagcaaaaa ggcgctaagc tgt 570

<210> 322
 <211> 149
 <212> PRT
 <213> Corynebacterium glutamicum

Met Arg Thr Leu Ala Glu Leu Asn Ile Lys Ala Pro Ser Leu Tyr
1 5 10 15

Lys His Val Lys Thr Arg Glu Asp Ile Ala Ala His Ile Ala Thr Lys
20 25 30

Ala Phe Ile Gln Leu Gly Gln Ser Leu His Glu His Cys Glu Ser Val
35 40 45

Glu Asp Leu Leu Ala Glu Tyr Arg Ser Met Ala Arg Glu Asn Pro Asn
50 55 60

Ile Tyr Arg Leu Leu Thr Ser Ser Glu Phe Pro Arg Glu Leu Leu Pro
65 70 75 80

Glu Gly Leu Glu Thr Trp Ala Gly Thr Pro Phe Tyr Leu Val Thr Gly
85 90 95

His Asp Pro Ile Lys Gly Gln Ala Leu Trp Ala Phe Ala His Gly Met
100 105 110

Ala Ile Leu Glu Ile Asp Ala Arg Phe Ala Gly Pro Asn Asn Gly Ser
115 120 125

Pro Ala Asp Gly Val Trp Glu Ile Gly Ala Arg Ala Phe Asp Thr Gln
130 135 140

Val Phe Asp Gln Gly
145

<211> 732

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (709)

<223> RXS01189

<400> 323
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taatgcacct gcaaatacac ctgcagaaaa ggaagcttaa atg att tcc att tcc 115
Met Ile Ser Ile Ser
1 5

atc gcc gac gac gaa gcc ctg atc gca agc tcc ctg gca acc ttg ctc 163
Ile Ala Asp Asp Glu Ala Leu Ile Ala Ser Ser Leu Ala Thr Leu Leu
10 15 20

agc ttg gaa ccc gat tta gac gtc cga cct acc gca gga tcc ggt gaa 211
Ser Leu Glu Pro Asp Leu Asp Val Arg Pro Thr Ala Gly Ser Gly Glu
25 30 35

gaa ctc att gaa acg tgg gcg gat cca agc aac cga acc gat gta tgc 259
Glu Leu Ile Glu Thr Trp Ala Asp Pro Ser Asn Arg Thr Asp Val Cys
40 45 50

[illegible]

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400> 324
Met Ile Ser Ile Ser Ile Ala Asp Asp Glu Ala Leu Ile Ala Ser Ser
  1             5             10             15
Leu Ala Thr Leu Leu Ser Leu Glu Pro Asp Leu Asp Val Arg Pro Thr
          20             25             30
Ala Gly Ser Gly Glu Glu Leu Ile Glu Thr Trp Ala Asp Pro Ser Asn
          35             40             45
Arg Thr Asp Val Cys Val Leu Asp Leu Gln Leu Gly Gly Ile Asp Gly
          50             55             60
Ile Asp Thr Ala Thr Arg Leu Met Glu Thr Thr Pro Asp Leu Ala Val

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Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys
 70 75 80 85
 gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctg gat 403
 Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp
 90 95 100
 gcg gga act act gtt act gct ttg gcc gat ctg att tct gag cat cct 451
 Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro
 105 110 115
 agc tcc aag cag tgg tgg atc gtg acc aac tgc ctg ccc atc gca ctt 499
 Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu
 120 125 130
 aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc 547
 Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser
 135 140 145
 gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act 595
 Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr
 150 155 160
 ctg gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg 643
 Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu
 170 175 180
 acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg 691
 Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met
 185 190 195
 aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac 739
 Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp
 200 205 210
 tcc acc aag atg ggc acc gac tac ctg gtg agc ttt ggc gca atc agc 787
 Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser
 215 220 225
 gat atc gat gtg gtg gtc acc gat gcg ggt gca cca gca agt ttc gtt 835
 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
 230 235 240 245
 gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877
 Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val Ile Ala Glu
 250 255
 tgattottact agtcaactgca agt 900

 <210> 326
 <211> 259
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 326
 Met Tyr Ala Glu Glu Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val
 1 5 10 15
 Glu Gly Arg Val Asn Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr
 20 25 30

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
 35 40 45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
 50 55 60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
 65 70 75 80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly
 85 90 95

Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu
 100 105 110

Ile Ser Glu His Pro Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys
 115 120 125

Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln
 130 135 140

Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp
 145 150 155 160

Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile
 165 170 175

Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser
 180 185 190

Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val
 195 200 205

Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser
 210 215 220

Phe Gly Ala Ile Ser Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala
 225 230 235 240

Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val
 245 250 255

Ile Ala Glu

<210> 327
 <211> 753
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(730)
 <223> RXS01607

<400> 327
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 ttctcgcccg ttttccctat ccacaaaagg accaagataa gtg atc cgt att ctg 115

Val Ile Arg Ile Leu
1 5

ttg gct gat gat cat ccc gtt gtt cgc gca ggc ctt gcc tcc ttg ctg 163
Leu Ala Asp Asp His Pro Val Val Arg Ala Gly Leu Ala Ser Leu Leu
10 15 20

gtg agt gaa gat gat ttt gag ata gtg gac atg gtg ggc acc cca gat 211
Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met Val Gly Thr Pro Asp
25 30 35

gat gcc gtt gcg cgc gcc gcg gaa ggc ggg gtg gat gtg gtg ttg atg 259
Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val Asp Val Val Leu Met
40 45 50

gat ctg cgt ttt ggt gat caa cca ggc atc gag gtc gcc gcc ggg gta 307
Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu Val Ala Gly Gly Val
55 60 65

gag gca acg cgt cgc atc cgt gcg ctg gac aac ccg cca cag gta ctg 355
Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn Pro Pro Gln Val Leu
70 75 80 85

gtg gtg acc aac tac tcc aca gac ggc gat gtg gtg ggc gca gta tct 403
Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val Val Gly Ala Val Ser
90 95 100

gct ggt gcc gtg ggg tat ttg ctc aaa gat agc tcc cca gaa gat ctc 451
Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser Ser Pro Glu Asp Leu
105 110 115

att gcc ggt gtt cgc gat gcc gcg cgg gga gaa tca gtg ctt tca aag 499
Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu Ser Val Leu Ser Lys
120 125 130

cag gtc gcc agc aag atc atg ggg cgg atg aac aac ccc atg act gct 547
Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn Asn Pro Met Thr Ala
135 140 145

ctc agt gcc aga gaa att gaa gtg ctg tcc ttg gtg gcg caa ggg caa 595
Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu Val Ala Gln Gly Gln
150 155 160 165

agc aat aga gaa atc ggc aag aaa ctt ttc ctc act gag gcc acg gtg 643
Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu Thr Glu Ala Thr Val
170 175 180

aaa agt cac atg ggg cat gtg ttc aac aag ctg gat gtc acc tct aga 691
Lys Ser His Met Gly His His Val Phe Asn Lys Leu Asp Val Thr Ser Arg
185 190 195

aca gct gcg gta gct gaa gcc aga cag cgc gga att atc tagacgcaca 740
Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly Ile Ile
200 205 210

cgtgttggtta acc 753

<210> 328

<211> 210

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 328

<400> 328
Val Ile Arg Ile Leu Leu Ala Asp Asp His Pro Val Val Arg Ala Gly
1 5 10 15

Leu Ala Ser Leu Leu Val Ser Glu Asp Asp Phe Glu Ile Val Asp Met
20 25 30

Val Gly Thr Pro Asp Asp Ala Val Ala Arg Ala Ala Glu Gly Gly Val
35 40 45

Asp Val Val Leu Met Asp Leu Arg Phe Gly Asp Gln Pro Gly Ile Glu
50 55 60

Val Ala Gly Gly Val Glu Ala Thr Arg Arg Ile Arg Ala Leu Asp Asn
65 70 75 80

Pro Pro Gln Val Leu Val Val Thr Asn Tyr Ser Thr Asp Gly Asp Val
85 90 95

Val Gly Ala Val Ser Ala Gly Ala Val Gly Tyr Leu Leu Lys Asp Ser
100 105 110

Ser Pro Glu Asp Leu Ile Ala Gly Val Arg Asp Ala Ala Arg Gly Glu
115 120 125

Ser Val Leu Ser Lys Gln Val Ala Ser Lys Ile Met Gly Arg Met Asn
130 135 140

Asn Pro Met Thr Ala Leu Ser Ala Arg Glu Ile Glu Val Leu Ser Leu
145 150 155 160

Val Ala Gln Gly Gln Ser Asn Arg Glu Ile Gly Lys Lys Leu Phe Leu
165 170 175

Thr Glu Ala Thr Val Lys Ser His Met Gly His Val Phe Asn Lys Leu
180 185 190

Asp Val Thr Ser Arg Thr Ala Ala Val Ala Glu Ala Arg Gln Arg Gly
195 200 205

Ile Ile
210

<210> 329

<211> 1017

<212> DNA

<213> *Corynebacterium glutamicum*

 $\langle 220 \rangle$

<221> CDS

<222> (101) .. (994)

<223> RXS01674

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<400> 329
cagcgctcgaat tccagaaggt ttgtagacat gcttcaaggt tgcgctaatt gaaaagaacg 60

cggtagacgg tactttcata tccaccata taatgttgat atg gat aat ggg tgg 115
Met Asp Asn Gly Trp

1 5

cgc aac ctg caa act ctc gca ctc ttt gtg gcg att gtg gaa gag ggg 163
Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala Ile Val Glu Glu Gly
10 15 20

agc ctc ggt gcc ggt gct cga aaa gtc gga atg gcc caa cct aat gcc 211
Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met Ala Gln Pro Asn Ala
25 30 35

agt cgg gct atc gca gag ctt gag gca gac atg aaa gcc gaa ttg ttg 259
Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met Lys Ala Glu Leu Leu
40 45 50

gta cgt cat cct cga gga tca cat cca aca gct gct gga ctt gcg ctt 307
Val Arg His Pro Arg Gly Ser His Pro Thr Ala Ala Gly Leu Ala Leu
55 60 65

gtt gag cat tcg cgc gat ctg ctt caa tct gta caa gaa ttt act gaa 355
Val Glu His Ser Arg Asp Leu Leu Gln Ser Val Gln Glu Phe Thr Glu
70 75 80 85

tgg gtg aca gag gga cga act gag cag cgc ctg aaa ttg cat gtt ggg 403
Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu Lys Leu His Val Gly
90 95 100

gcc agt atg acc att gcc gag gct cta ctt cca gct tgg gtt gcg gac 451
Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro Ala Trp Val Ala Asp
105 110 115

atg cgc acg cgt ttt cct gcc tgc cgt gtc gac gtc tct gtg atg aat 499
Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp Val Ser Val Met Asn
120 125 130

tct tct caa gta att gaa gcc gtc cag aaa ggg cac ttg caa cta ggt 547
Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly His Leu Gln Leu Gly
135 140 145

ttt att gaa aca cgc cat gtt ccc gta cgg ctt cat gct cgt gtg gtg 595
Phe Ile Glu Thr Pro His Val Pro Val Arg Leu His Ala Arg Val Val
150 155 160 165

caa gag gac aag ctg att gtg gtg att tct cct aat cat gag tgg gct 643
Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro Asn His Glu Trp Ala
170 175 180

aat cgc acg ggt agg atc agt ctt cgg gag ttg tcg gaa act cgc ctg 691
Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu Ser Glu Thr Pro Leu
185 190 195

ata gtg agg gaa gtc ggc tca ggt acc cga gaa gca tta caa gaa tta 739
Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu Ala Leu Gln Glu Leu
200 205 210

ctt gcg gat tat gac atg gct gag cgc att caa gtg tta aac agc aat 787
Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln Val Leu Asn Ser Asn
215 220 225

gct gcg gta cgt gtt gtt gtt gaa gca ggg gca ggt cct gca gta ctt 835
Ala Ala Val Arg Val Val Val Glu Ala Gly Ala Gly Pro Ala Val Leu
230 235 240 245

ggt gaa tta gcc ttg cgt gat cat ctt gcg ctc ggc agg ctg ttg agt 883
 Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu Gly Arg Leu Leu Ser
 250 255 260
 gtg cca ttt gaa ggc agt gga gtt act cgt cct ctt aca gct gtg tgg 931
 Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro Leu Thr Ala Val Trp
 265 270 275
 agt gga ccc cgc aga ttg ccg att cta gcg gga gaa tta gtg tcc atc 979
 Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile
 280 285 290
 gca tcg aac cac atc tgattttgag ccctggctaa cgg 1017
 Ala Ser Asn His Ile
 295

<210> 330
 <211> 298
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 330
 Met Asp Asn Gly Trp Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala
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 Ile Val Glu Glu Gly Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met
 20 25 30
 Ala Gln Pro Asn Ala Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met
 35 40 45
 Lys Ala Glu Leu Leu Val Arg His Pro Arg Gly Ser His Pro Thr Ala
 50 55 60
 Ala Gly Leu Ala Leu Val Glu His Ser Arg Asp Leu Leu Gln Ser Val
 65 70 75 80
 Gln Glu Phe Thr Glu Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu
 85 90 95
 Lys Leu His Val Gly Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro
 100 105 110
 Ala Trp Val Ala Asp Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp
 115 120 125
 Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly
 130 135 140
 His Leu Gln Leu Gly Phe Ile Glu Thr Pro His Val Pro Val Arg Leu
 145 150 155 160
 His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro
 165 170 175
 Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu
 180 185 190
 Ser Glu Thr Pro Leu Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu

ctg gac ttc atg cat tcc ttg ggc act tgg atg gtc ccc gaa ctt atc 451
 Leu Asp Phe Met His Ser Leu Gly Thr Trp Met Val Pro Glu Leu Ile
 105 110 115

cga aca ttc cgc gcc gaa cac ccc aac gta gaa ttc caa ctc cac caa 499
 Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu Phe Gln Leu His Gln
 120 125 130

gcg gca gca atg ctc ctg gta gat cgt gtt ttg gct gat gaa act gac 547
 Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu Ala Asp Glu Thr Asp
 135 140 145

ctc gca tta gtt ggc ccc aaa cct gcc gag gtt ggt acc tct tta ggg 595
 Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val Gly Thr Ser Leu Gly
 150 155 160 165

tgg gcg cca ctg ctt cgt caa cga ctt gcc cta gct gtt ccc gca gat 643
 Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu Ala Val Pro Ala Asp
 170 175 180

cac cgg ctt gcc tcc ttt tct ggc caa gga gaa ttg ccg ttg att act 691
 His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu Leu Pro Leu Ile Thr
 185 190 195

gcg gcg gaa gaa cct ttc gtg gcg atg cga gca ggt ttc gcc acc cga 739
 Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala Gly Phe Gly Thr Arg
 200 205 210

ctc ctc atg gat gca tta gcc gaa gaa gcc ggt ttt gtt ccc aat gtg 787
 Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly Phe Val Pro Asn Val
 215 220 225

gtt ttc gaa tcc atg gaa ctc acc acc gtc gca ggg ctt gtc agc gca 835
 Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala Ala Gly Leu Val Ser Ala
 230 235 240 245

ggt ctc gcc gtt ggt gtg gtt ccg atg gat gat ccc tac ctt tcc aca 883
 Gly Leu Gly Val Gly Val Val Pro Met Asp Asp Pro Tyr Leu Ser Thr
 250 255 260

gtg gga atc gtg caa cgc cca ctt agt cca ccc gct tat agg gaa 928
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 265 270 275

<210> 332

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe
 1 5 10 15

Ile Ser Val Ala Gln Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu
 20 25 30

Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
 35 40 45

ctatgagtcc agacgttttt aaaggagcg aattaccata gtg tct aca gat cca 115
Val Ser Thr Asp Pro

	1	5	
gaa gag ttc gac caa gct gaa acc ctc gat caa ctc gcg tat gag atc Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln Leu Ala Tyr Glu Ile	10 15 20		163
atc ctg ctc acc cgg tat ggt gtc caa aac aca ccg acc aac aag cgc Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr Pro Thr Asn Lys Arg	 25 30 35		211
gaa gcc atc atg gat cgc agc gcc ctc atc ttg ctc acc cgc ctt gac Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu Leu Thr Arg Leu Asp	 40 45 50		259
gct caa gga cct atg aca gtt aat gag cta gct gaa agc ttt gga ctt Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala Glu Ser Phe Gly Leu	 55 60 65		307
aac gtt tct acc gtg cac cgc caa ctc aaa gca gcc att gcc aat ggc Asn Val Ser Thr Val His Arg Gln Leu Lys Ala Ala Ile Ala Asn Gly	 70 75 80 85		355
tta att gaa gtc gtc gat gat caa gca tgc ccc gct aaa ctt cat cgt Leu Ile Glu Val Val Asp Asp Gln Ala Cys Pro Ala Lys Leu His Arg	 90 95 100		403
cca act gag ttg ggt aaa gaa aaa ctg cag cag gag ctt ctt gcc cgc Pro Thr Glu Leu Gly Lys Glu Lys Leu Gln Gln Glu Leu Leu Ala Arg	 105 110 115		451
cag cag gat ctc acc cgc att ctt cat gat tgg gat gag gaa gac att Gln Gln Asp Leu Thr Arg Ile Leu His Asp Trp Asp Glu Glu Asp Ile	 120 125 130		499
aaa acg cat gcc aag cta ttg cgg aag cac aat gaa agc ttg gaa gaa Lys Thr His Ala Lys Leu Leu Arg Lys His Asn Glu Ser Leu Glu Glu	 135 140 145		547
tac ctc gat atg aag tgg ccc cgc ccc taagtgccca taaacgcacc Tyr Leu Asp Met Lys Trp Pro Arg Pro	 150 155		594
tct			597
<210> 334			
<211> 158			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 334			
Val Ser Thr Asp Pro Glu Glu Phe Asp Gln Ala Glu Thr Leu Asp Gln	1 5 10 15		
Leu Ala Tyr Glu Ile Ile Leu Leu Thr Arg Tyr Gly Val Gln Asn Thr	20 25 30		
Pro Thr Asn Lys Arg Glu Ala Ile Met Asp Arg Ser Ala Leu Ile Leu	35 40 45		
Leu Thr Arg Leu Asp Ala Gln Gly Pro Met Thr Val Asn Glu Leu Ala			

50				55				60							
Glu	Ser	Phe	Gly	Leu	Asn	Val	Ser	Thr	Val	His	Arg	Gln	Leu	Lys	Ala
65					70					75					80
Ala	Ile	Ala	Asn	Gly	Leu	Ile	Glu	Val	Val	Asp	Asp	Gln	Ala	Cys	Pro
				85					90					95	
Ala	Lys	Leu	His	Arg	Pro	Thr	Glu	Leu	Gly	Lys	Glu	Lys	Leu	Gln	Gln
			100					105					110		
Glu	Leu	Leu	Ala	Arg	Gln	Gln	Asp	Leu	Thr	Arg	Ile	Leu	His	Asp	Trp
		115					120					125			
Asp	Glu	Glu	Asp	Ile	Lys	Thr	His	Ala	Lys	Leu	Leu	Arg	Lys	His	Asn
	130					135						140			
Glu	Ser	Leu	Glu	Glu	Tyr	Leu	Asp	Met	Lys	Trp	Pro	Arg	Pro		
145				150					155						

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<210> 335
<211> 969
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(946)
<223> RXS02288
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 Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys
 105 110 115

ttg ccg cag cgg tca cca tcg gcg ttg att acg cat tct ttg aag aca 499
 Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr
 120 125 130

atg gcg gat cat cgt gtg cgc gcc ggg atg agc gat atc cgt ttg att 547
 Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile
 135 140 145

gcg tgt gcg gga ttg tat ttc gcg gag act gat tct ttc ttg ggc aag 595
 Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys
 150 155 160 165

gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt 643
 Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val
 170 175 180

tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat 691
 Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His
 185 190 195

cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt 739
 Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly
 200 205 210

agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt 787
 Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly
 215 220 225

gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat 835
 Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp
 230 235 240 245

cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg 883
 Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala
 250 255 260

cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca 931
 Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro
 265 270 275

acg gaa gag gat ttt taagatggct ttggttcttg gaa 969
 Thr Glu Glu Asp Phe
 280

<210> 336
 <211> 282
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 336
 Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
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 20 25 30

Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
 35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
 50 55 60

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
 65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
 85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
 100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
 115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
 130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
 145 150 155 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
 165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
 180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
 195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
 210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
 225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
 245 250 255

Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
 260 265 270

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
 275 280

<210> 337

<211> 567

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(544)

<223> RXS02573

<400> 337

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gaagtgaagt actttccgaa agattcacag ggagcatgca atg acg aac aaa acc	115
Met Thr Asn Lys Thr	5
atg ctg gtt gct ttt gat ggc tca cgg gaa tcc cgg cgc gct ttg gaa	163
Met Leu Val Ala Phe Asp Gly Ser Pro Glu Ser Arg Arg Ala Leu Glu	20
tat gcg cgc aaa ttg ttg cag cgg cgc acc gtg gaa att tta act cgc	211
Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val Glu Ile Leu Thr Ala	35
tgg gag cca ttg cat cgg caa gct gcg cgc tcg gtt tcg ttg atc acc	259
Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser Val Ser Leu Ile Thr	50
ttg ggg gtg gaa ccc gaa gac ccc gcc cat tcc gct gca cta aaa acc	307
Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser Ala Ala Leu Lys Thr	65
tgc cag gaa ggc gta gag cta gcc caa tct cta ggt ctg gaa cgc cga	355
Cys Gln Glu Gly Val Glu Leu Ala Gln Ser Leu Gly Leu Glu Ala Arg	85
gcc cac atg gtg gaa tcc gca acg gcc gtg tgg agc gcc atc gtt gat	403
Ala His Met Val Glu Ser Ala Thr Ala Val Trp Ser Ala Ile Val Asp	100
gct gct gac gag ctg cgc ccc gac gtg att gtc acc ggc acc cgc ggg	451
Ala Ala Asp Glu Leu Arg Pro Asp Val Ile Val Thr Gly Thr Arg Gly	115
atc tcc gga tgg aaa tcc ctg tgg caa tcc tcc acc tca gac agc gtg	499
Ile Ser Gly Trp Lys Ser Leu Trp Gln Ser Ser Thr Ser Asp Ser Val	130
ctc cac cac gcc gac gta cca gtt ttt gtc gtt cca ccc ctg gac	544
Leu His His Ala Asp Val Pro Val Phe Val Val Pro Pro Leu Asp	145
taaaaccgag acgagaacca aga	567
<210> 338	
<211> 148	
<212> PRT	
<213> Corynebacterium glutamicum	
<400> 338	
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Arg Arg Ala Leu Glu Tyr Ala Ala Lys Leu Leu Gln Pro Arg Thr Val	30
Glu Ile Leu Thr Ala Trp Glu Pro Leu His Arg Gln Ala Ala Arg Ser	45
Val Ser Leu Ile Thr Leu Gly Val Glu Pro Glu Asp Pro Ala His Ser	

50					55					60					
Ala	Ala	Leu	Lys	Thr	Cys	Gln	Glu	Gly	Val	Glu	Leu	Ala	Gln	Ser	Leu
65					70					75					80
Gly	Leu	Glu	Ala	Arg	Ala	His	Met	Val	Glu	Ser	Ala	Thr	Ala	Val	Trp
				85					90					95	
Ser	Ala	Ile	Val	Asp	Ala	Ala	Asp	Glu	Leu	Arg	Pro	Asp	Val	Ile	Val
			100					105					110		
Thr	Gly	Thr	Arg	Gly	Ile	Ser	Gly	Trp	Lys	Ser	Leu	Trp	Gln	Ser	Ser
			115				120					125			
Thr	Ser	Asp	Ser	Val	Leu	His	His	Ala	Asp	Val	Pro	Val	Phe	Val	Val
	130					135					140				
Pro	Pro	Leu	Asp												
145															

<210> 339
<211> 866
<212> DNA
<213> *Corynebacterium glutamicum*

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<220>  
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<222> (1)..(843)  
<223> RXS02627
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400> 339																	
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Ala Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp																	
1 5 10 15																	
gga gat gct gag gct gcg ctg gaa ttc ggt gtg cag cct gtg ggt gca	96																
Gly Asp Ala Glu Ala Ala Leu Glu Phe Gly Val Gln Pro Val Gly Ala																	
20 25 30																	
tca gat tgg ctc gca ttc ggt ggt gaa ggc gtg gga ccg tgg att gag	144																
Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu																	
35 40 45																	
gat tct gcc tac gat gaa cgc cca gaa ata atc gga acc atg gaa ccg	192																
Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro																	
50 55 60																	
gag tat gaa aag att gca cgc ctt gaa ccg gat ctg att ttg gac gtg	240																
Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val																	
65 70 75 80																	
cgc agc tct ggc gac cag gaa cgc tat gac aag ttg tct tca atc gca	288																
Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala																	
85 90 95																	
ctg acc atc ggc gtt cca gaa ggt ggc gat agc tac ctc acc cca cgc	336																
Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg																	
100 105 110																	
gct gaq cag gta acc atg atc gcc act gct ctg ggg cag gct gaa cgt	384																

Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
 115 120 125

ggt gaa gaa gtg aac gct gaa tac gag cag ctc act gct gat att cgt 432
 Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg
 130 135 140

gca gct cac ccg ggc tgg cct gag aag acc gcg gct gct gta tct gca 480
 Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Val Ser Ala
 145 150 155 160

acg gca acc agc tgg ggt gca tac atc aag ggc tcc aac cgt gta gat 528
 Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
 165 170 175

act ttg ctg gac ctg ggc ttc cag gaa aac cct gag ctg gct aaa cag 576
 Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln
 180 185 190

caa cct ggc gat acg ggt ttc tcc atc aaa ttc agt gaa gag act ttc 624
 Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Glu Thr Phe
 195 200 205

ggc gtt gtg gat tcc gac ctg gtt gtc ggc ttt gcc atc ggt atg act 672
 Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr
 210 215 220

cct gag gaa atg gca gag cag gtt cca tgg cag atg ttg acc gcc act 720
 Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr
 225 230 235 240

cgt gac ggc cgt tcc ttt gtg atg ccc cgt gag att tcc aat gcg ttt 768
 Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe
 245 250 255

tct ttg ggt tcc ccg cag tcc act cgg ttc gcg tta gac gcc ttg gtg 816
 Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val
 260 265 270

cca ctt ctg gag gat cat gca ggg gag tagtggtccg gtggtgcggg 863
 Pro Leu Leu Glu Glu His Ala Gly Glu
 275 280

cag 866

<210> 340
 <211> 281
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 340
 Asp Val Thr Val Glu Ser Gln Pro Glu Arg Val Val Ala Leu Gly Trp
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 20 25 30

Ser Asp Trp Leu Ala Phe Gly Gly Glu Gly Val Gly Pro Trp Ile Glu
 35 40 45

Asp Ser Ala Tyr Asp Glu Ala Pro Glu Ile Ile Gly Thr Met Glu Pro
50 55 60

Glu Tyr Glu Lys Ile Ala Ala Leu Glu Pro Asp Leu Ile Leu Asp Val
65 70 75 80

Arg Ser Ser Gly Asp Gln Glu Arg Tyr Asp Lys Leu Ser Ser Ile Ala
85 90 95

Leu Thr Ile Gly Val Pro Glu Gly Gly Asp Ser Tyr Leu Thr Pro Arg
100 105 110

Ala Glu Gln Val Thr Met Ile Ala Thr Ala Leu Gly Gln Ala Glu Arg
115 120 125

Gly Glu Glu Val Asn Ala Glu Tyr Glu Gln Leu Thr Ala Asp Ile Arg
130 135 140

Ala Ala His Pro Gly Trp Pro Glu Lys Thr Ala Ala Val Ser Ala
145 150 155 160

Thr Ala Thr Ser Trp Gly Ala Tyr Ile Lys Gly Ser Asn Arg Val Asp
165 170 175

Thr Leu Leu Asp Leu Gly Phe Gln Glu Asn Pro Glu Leu Ala Lys Gln
180 185 190

Gln Pro Gly Asp Thr Gly Phe Ser Ile Lys Phe Ser Glu Thr Phe
195 200 205

Gly Val Val Asp Ser Asp Leu Val Val Gly Phe Ala Ile Gly Met Thr
210 215 220

Pro Glu Glu Met Ala Glu Gln Val Pro Trp Gln Met Leu Thr Ala Thr
225 230 235 240

Arg Asp Gly Arg Ser Phe Val Met Pro Arg Glu Ile Ser Asn Ala Phe
245 250 255

Ser Leu Gly Ser Pro Gln Ser Thr Arg Phe Ala Leu Asp Ala Leu Val
260 265 270

Pro Leu Leu Glu Glu His Ala Gly Glu
275 280

<210> 341

<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> RXS02691

<400> 341

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cacaaaaacc acacccctgg ttatgaccag atcggctaaa atg aac acc atg cct 115
Met Asn Thr Met Pro

1 5

gac caa ccg ctc aac cag gac gga ttc cct acc gca tcc aaa ggg gtg 163
 Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr Ala Ser Lys Gly Val
 10 15 20

gaa ccc gac aac ctc ccc gac cgc gtt ctc gtg gac ggc ctt aaa cca 211
 Glu Pro Asp Asn Leu Pro Asp Arg Val Leu Val Asp Gly Leu Lys Pro
 25 30 35

aag cat cag cag ctt cgt gaa att ttg gag gaa atc tgc acc acc cag 259
 Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu Ile Cys Thr Thr Gln
 40 45 50

ctt cag cct ggg gac atg ctg cct ggt gag cgc atc ctg gaa gaa aag 307
 Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg Ile Leu Glu Glu Lys
 55 60 65

tat ggc gtc agc cga att acg gtt cgt cgg cgc att ggt gat ctg gtc 355
 Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala Ile Gly Asp Leu Val
 70 75 80 85

gcg tcc ggc agg ttg aag cga gct cgc ggc aaa ggt acc ttc gtg gcc 403
 Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys Gly Thr Phe Val Ala
 90 95 100

cac tcg ccg ttg att tcc cgc ctg cat ttg gcc tcg ttt tcc gca gag 451
 His Ser Pro Leu Ile Ser Arg Leu His Leu Ala Ser Phe Ser Ala Glu
 105 110 115

atg gcc gcc cag aag cta tcg gct acc agc agg att ttg agt tct tcc 499
 Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg Ile Leu Ser Ser Ser
 120 125 130

cgc ggt ccc gcc cca gat gat att gct gat ttc ttt ggt acc gat cgc 547
 Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe Phe Gly Thr Asp Arg
 135 140 145

gcg gcc cag cac atc acg ttg cgc cgc ctg cgc ttt gga aat ggt cga 595
 Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg Phe Gly Asn Gly Arg
 150 155 160 165

ccc tat gcc att gac aac ggt tgg tac aac tcc gaa ttc gca cct gac 643
 Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser Glu Phe Ala Pro Asp
 170 175 180

ctg ctg gaa aat gat gtg tac aac tcc gtg tac tcc atc ctg gac cgc 691
 Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr Ser Ile Leu Asp Arg
 185 190 195

gtc tat ggc gtc ccc gtc acc cag gcc gag caa acg gtc acc gcc gta 739
 Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln Thr Val Thr Ala Val
 200 205 210

gca gcc gac gaa gac acc gca cgg ctt ctg gac gtc acc ccc ggc gcc 787
 Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp Val Thr Pro Gly Ala
 215 220 225

cca ctc ctt cgt atc ctt cga cag tca ctt tct ggc gat aag ccc gtg 835
 Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser Gly Asp Lys Pro Val
 230 235 240 245

000000 7 20200000

gaa tgg tgc gtt tcc ttg tac cga acc gac cga tat tct tta aaa aca 883
 Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg Tyr Ser Leu Lys Thr
 250 255 260

ttg gtt aca cgc tcc gaa gat ctc tgacgtgaac ccattttggg ggc 930
 Leu Val Thr Arg Ser Glu Asp Leu
 265

<210> 342

<211> 269

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 342

Met Asn Thr Met Pro Asp Gln Pro Leu Asn Gln Asp Gly Phe Pro Thr
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 20 25 30

Asp Gly Leu Lys Pro Lys His Gln Gln Leu Arg Glu Ile Leu Glu Glu
 35 40 45

Ile Cys Thr Thr Gln Leu Gln Pro Gly Asp Met Leu Pro Gly Glu Arg
 50 55 60

Ile Leu Glu Glu Lys Tyr Gly Val Ser Arg Ile Thr Val Arg Arg Ala
 65 70 75 80

Ile Gly Asp Leu Val Ala Ser Gly Arg Leu Lys Arg Ala Arg Gly Lys
 85 90 95

Gly Thr Phe Val Ala His Ser Pro Leu Ile Ser Arg Leu His Leu Ala
 100 105 110

Ser Phe Ser Ala Glu Met Ala Ala Gln Lys Leu Ser Ala Thr Ser Arg
 115 120 125

Ile Leu Ser Ser Ser Arg Gly Pro Ala Pro Asp Asp Ile Ala Asp Phe
 130 135 140

Phe Gly Thr Asp Arg Ala Ala Gln His Ile Thr Leu Arg Arg Leu Arg
 145 150 155 160

Phe Gly Asn Gly Arg Pro Tyr Ala Ile Asp Asn Gly Trp Tyr Asn Ser
 165 170 175

Glu Phe Ala Pro Asp Leu Leu Glu Asn Asp Val Tyr Asn Ser Val Tyr
 180 185 190

Ser Ile Leu Asp Arg Val Tyr Gly Val Pro Val Thr Gln Ala Glu Gln
 195 200 205

Thr Val Thr Ala Val Ala Ala Asp Glu Asp Thr Ala Arg Leu Leu Asp
 210 215 220

Val Thr Pro Gly Ala Pro Leu Leu Arg Ile Leu Arg Gln Ser Leu Ser
 225 230 235 240

002250-12222222

Gly Asp Lys Pro Val Glu Trp Cys Val Ser Leu Tyr Arg Thr Asp Arg
245 250 255

Tyr Ser Leu Lys Thr Leu Val Thr Arg Ser Glu Asp Leu
260 265

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<210> 343
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(1138)
<223> RXS02730
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<213> Corynebacterium glutamicum

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Ser	Leu	Arg	His	Met	Asp	Pro	Trp	Gly	Leu	Val	Pro	Glu	Arg	Asp	Arg
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Ile	Tyr	Leu	Val	Gly	Phe	Asp	Leu	Asp	Arg	Gln	Glu	Ala	Arg	Thr	Phe
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1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Index**
 10. **Table of Contents**
 11. **Figure 1**
 12. **Figure 2**
 13. **Figure 3**
 14. **Figure 4**
 15. **Figure 5**
 16. **Figure 6**
 17. **Figure 7**
 18. **Figure 8**
 19. **Figure 9**
 20. **Figure 10**
 21. **Figure 11**
 22. **Figure 12**
 23. **Figure 13**
 24. **Figure 14**
 25. **Figure 15**
 26. **Figure 16**
 27. **Figure 17**
 28. **Figure 18**
 29. **Figure 19**
 30. **Figure 20**
 31. **Figure 21**
 32. **Figure 22**
 33. **Figure 23**
 34. **Figure 24**
 35. **Figure 25**
 36. **Figure 26**
 37. **Figure 27**
 38. **Figure 28**
 39. **Figure 29**
 40. **Figure 30**
 41. **Figure 31**
 42. **Figure 32**
 43. **Figure 33**
 44. **Figure 34**
 45. **Figure 35**
 46. **Figure 36**
 47. **Figure 37**
 48. **Figure 38**
 49. **Figure 39**
 50. **Figure 40**
 51. **Figure 41**
 52. **Figure 42**
 53. **Figure 43**
 54. **Figure 44**
 55. **Figure 45**
 56. **Figure 46**
 57. **Figure 47**
 58. **Figure 48**
 59. **Figure 49**
 60. **Figure 50**
 61. **Figure 51**
 62. **Figure 52**
 63. **Figure 53**
 64. **Figure 54**
 65. **Figure 55**
 66. **Figure 56**
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 68. **Figure 58**
 69. **Figure 59**
 70. **Figure 60**
 71. **Figure 61**
 72. **Figure 62**
 73. **Figure 63**
 74. **Figure 64**
 75. **Figure 65**
 76. **Figure 66**
 77. **Figure 67**
 78. **Figure 68**
 79. **Figure 69**
 80. **Figure 70**
 81. **Figure 71**
 82. **Figure 72**
 83. **Figure 73**
 84. **Figure 74**
 85. **Figure 75**
 86. **Figure 76**
 87. **Figure 77**
 88. **Figure 78**
 89. **Figure 79**
 90. **Figure 80**
 91. **Figure 81**
 92. **Figure 82**
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 94. **Figure 84**
 95. **Figure 85**
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 112. **Figure 102**
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 114. **Figure 104**
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 117. **Figure 107**
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 151. **Figure 141**
 152. **Figure 142**
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 154. **Figure 144**
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 157. **Figure 147**
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 Gly Pro Thr Val Ser Gln Thr Val Ala Arg Met Glu Arg Asp Gly Leu
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gaa gcc aca caa cgc gga atc cgc gaa gaa cta cga ttc cgg gta gtt 739
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Gly Pro Ala Glu Leu Ser Thr Ala Arg Asp Arg Lys Ala Gly Phe Ile
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195 200 205

Asn Arg Arg Ile Gly Leu Val Tyr Arg Ser Ser Ser Ser Arg Ala Glu
210 215 220

Glu Phe Glu Gln Phe Ala Leu Ile Leu Gln Arg Ala Phe Gln Glu Ala
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APPENDIX A: DNA SEQUENCES

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>RXA00221-downstream
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>RXA00253-upstream
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>RXA00253
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>RXA00253-downstream
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>RXA00291
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>RXA00400
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>RXA01375
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>RXA01375-downstream
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>RXA01418-upstream

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>RXA01418
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>RXA01450-upstream
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>RXA01450
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>RXA01500-upstream
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>RXA01500
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>RXA01537
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>RXA01573
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>RXA01655
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>RXA01687
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>RXA01687-downstream
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>RXA01759-upstream
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>RXA01759
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>RXA01763
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>RXA01826
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>RXA01827-upstream
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>RXA01827
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>RXA01830-upstream
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>RXA01830
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>RXA01836-upstream
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>RXA02127

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>RXS00481

Appendix A, page 57

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>RXS01607-downstream

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>RXS01674-upstream

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>RXS01674

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>RXS01674-downstream
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>RXS01872-upstream
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>RXS01872
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>RXS02117-upstream
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>RXS02117
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>RXS02117-downstream
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>RXS02288-upstream
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>RXS02288
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>RXS02573-upstream
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>RXS02573
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>RXS02573-downstream
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>RXS02627
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>RXS02627-downstream
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>RXS02691-upstream
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>RXS02691
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>RXS02730-upstream
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>RXS02730
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>RXS02818
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>RXS02911-upstream
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>RXS02911
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>RXS02911-downstream
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>RXS03066-upstream
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>RXS03066

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>RXS03200

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>RXS03208-upstream

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>RXS03208

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>RXS03219-upstream

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>RXS03219

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>RXS03219-downstream
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006290.4282960

APPENDIX B: AMINO ACID SEQUENCES

> RXA00004 (1-471, translated) 157 residues
 VLTQLIESSI FDNVASRESS EFLGHAIDL LAGLVYEKAT PYAPDEALRV AVYGYIRENL
 GSSQLTVAAV AGAHRIAVRT LHLRFEGEAY GVAELIRHLR LEAVYEDLDR FRLQNLITLA
 IGMRGISSQ AHLRLFRAX YGVPPAEFRR GYINSAA

> RXA00006 (1-435, translated) 145 residues
 MVDFTDIAAR LVTETFEAII YATRDGIIRL WNGGSEKLFQ YTAGEALGKS LDIIPKHKR
 KAHWDGWRV MESGETRYGS EPLNVPGIRA DSGKMSLEFS ITILKDDSGK IEGVAAFLDR
 VTANWDKKA LRIRIKELER QIEGH

> RXA00029 (1-537, translated) 179 residues
 LAQATAQLIA DDEAVIFDNG TTCQVAQEL AGRPITALCL SLHSAVALGS RAGTNVFIPI
 GPVENDSLAR SGPAVITALR DFSADVILG SCSTSLHGL ATTTYDDAEN KRAAIHAATR
 RILVVSARKL NHVSTFRFAD VADLHQLVTT SDAPREILAE IRDLGVQVIT VPAPDEQRS

> RXA00126 (1-663, translated) 221 residues
 VTPAENNNIL SPETKVSITG RNVEVPDHEA ERVNTKLAKI ERLDPTLTFF HVELQHEPNF
 RRAEDSDRIQ ITATGKGHIA RAEAKEDSFY AALETALAKM ERLSRKVYAR RSISRSGRHA
 PLGTGVEGQA LVAESQEARQ ADELGKYVDV PYADKVDVDM PGQVVRTEKH PATPMSVDDA
 LSEMLVGVDH FYLFVNEETN QPSVYVRRAH FDYGLISLSD A

> RXA00129 (1-1497, translated) 499 residues
 VLGSIFTASA VVMILLGLGM LTVFTQRLVD QKIDIASSEI DRARVIVEEQ ITASGASTSV
 VLGNSNSARA LSSLGTSGGT ETNAAYDPVV LVNDDDLVVS PEGYQIPERL RYFVSENVQS
 YQFSSIDQGG QSSYQALIIG TPTESDIPNL QVYLVFSMES DESSALMRG LLSAALLIVV
 VLLVGIAWLA TQVQTAPVRS ASRIAERFAQ GKLRERMVVE GEDEMARLAV SFNAMESLS
 AQITKLEEEG NLQROFTSDV SHELRTPLT VMMAADLIAD SEDELSPGAR RASQLMNRRL
 DRFESLLSD LELSRHDAGV AELSTALHDV RIVPVSALAQ VQHLATELDV ELLVNLPEEA
 INIQDSDRII ERIIRNLLAN AIDHSGKLPV ELKVADNVDA VAIVVIDHGV GLKPGQDELV
 RNRFRWADPS RVRRSGGTGL GLAISREDAM LHGGNLDAAQ TICVGSIFRL VLPKEPHNGY
 REAPIPLIAP ETPWEGEQQ

> RXA00130 (1-678, translated) 226 residues
 MSQKILVDD DPAISEMLTI VLSAEGFDTV AVTDGALAVE TASREQPDLI LLDLMLPGMN
 GDICRLIRIQ ESSVPIIMLT AKTDTVDVVL GLESGADDYV NKPFKAKELV ARIRARLRAT
 VDPESEIIEV GDLSIDVPAH TVKRNGAES LTPLEFDLLL ELARKEQGVF TREELLGKVV
 GYRHASDTRL VNVHVQLRA KIERDPENPO IVLTVRGVGY KTGND

> RXA00182 (1-3102, translated) 1034 residues
 MTSHELLGLW IKDRGLQLWI EQVEGHRIVL PEAVEKGTFF PVVEQILDGK TFRARMNVHL
 RTPKGRHVLEL PPTPTAAFTPE EAVTVFSQSL FLKAEPTAAT RAQRDSIAPD LWLIVVMYQG
 LARFVQAGRV TLRTVMMDNA WWPQWQLSAS LSEKGLWAEV NHAAPGILRI NGRDLAGSM
 SNELPHWIAN AILRDYRDET MPYARHEFVE ALLFNHSLRK GSTMLTHALN QWKNTITSAS
 LQLVILVEEP PAESDYEDPM DSVWPFVRLMV RTGVDAPOAI QKGSIDSQGM EQLRISQYETA
 KTTSMMLDQA REDAMLGHMV DIAQNGDWDI FLTTEEVINF ISHDVAKLRK AGIPVMLPKG
 WSTYETRADQV EARTPNDAAD SSTKAIIGLD QLVYNNWRIS VGDQLSDDEE MRELIDSKTG
 LIRLRAGDWM AQDQALRRIT SYMEELSKSS EKRAEMTEK VAMQAKLAEV NGEEGQQLLA
 AKAEATLRKEF NEKFSGDGQG EVTLAELREI ALKAAENEPV EFTGSCQFNS LGGTETPAP
 VRVDIPDTVL ADLREYQRRG VDOWLWMSAN NLGAVLADM GLGKTLQLLS LLAVERAENP
 ELERGPTFLV CPTSVVGNWA AEAARFVPSL KVLMMHGQSR LNDADLISQS KGMDLIITSY
 GVITRDFKLM GQVGFERVVL DEQAQIKNS TRVSKAVRSR PSRRHVALTG TPVENRLSEM
 RSILDFCFNG VLGSASFRRN HPAKAIEREQ DDTMTERLRQ LTAPFILLRL KTDPNILDDL
 PERKEQIIRV DMTTEQASLY KALVEDVCQK LDERQGMRSR GLVIATITRI KQCNHPAHE
 LBGDSGVTLK GKHRSGKVEA LMEIDTAVK EEERMLIFTQ YAAFGRIILAP YLSDRLGTNI
 PFLHGVTVKR GRDRMVAEFQ SEDGPPAMIL SLKAGGTGLN LTAASIVVMH DRWNPAVEN
 QATDRAFRIG QRKNVDVYKM ITVGTMEESI QDILDGKTHL ASATVGELEG WITELNPEEL
 AMLMSYREKE GADD

03602874-062300

> RXA00221 (1-219, translated) 73 residues

MNAEEIGMAL LNRKELGLR QGELADLAGV SERFIRDVEK GKTTVRLDKV IDVLRVLGLE
LSVGIHDPLK VNQ

> RXA00253 (1-738, translated) 246 residues

MPSETMKPAV ASTLAATSTG RRPGRPTQRI LSVESIVERT LNIAGREGFA AVTMNRLRAD
MGVTPRALYN HVLNRQEIID RVWVRIIDDI KVPDLDPDNW RQSIHTLWSS LRDQFRETFR
VLLVALDEGI STOGTSPLRI AGAEESLKLFL TDIGLSLKEA TIIREMMMAV VFSFTLTSY
TFDNRPEGEK PDVFAVPKPK WLDENPDVEA PLTRKAVEES VSTSDELFYG MVEARIAIYE
KLLAAK

> RXA00284 (1-1065, translated) 355 residues

MARKLKDCLK RSFDKIVESG DFDAFKEVET ERALDAKNRH GNTALHMRGV PEEFKIWMLD
QGLOVDIRNE DGDTPPLHVHS HDWNLSPPDL LKRGADVCV NNEGESVAYS AAFPPENLKK
LIDAGADPYS RANDGTTPLM RVIRSADTGG TIELAEITKL LSGTEHFDVAY FRETQERITA
MGERFEDVRE VYNEESVDQA SADMIWLDR FDIPEELRAN TPILHDGVSP IELPGDITWQE
QFIEGYDLVL PAMGAKKSLO GEAIRIAGRV SNEFHNGGV NWDDKFKRMA KSLNHICEQG
VPLGEPELEE LAAAVKSVRK GEPTEEEDIT LPLRATKWVA QNPQPLPLGE VDYKR

> RXA00287 (1-474, translated) 158 residues

MHHLRYESPI GELLVLASDQ GLTYVAFSDE NYAACTVGST PGTNVLEQA VAELEYFAG
KRKEFTPLD WPSQNLLSFR GKQVPELLSI PYGESKTYKQ IAAELNNVGA VAEVGSACAT
NPLPIFAPCH RVLRTDGAIG GYRGGLEAKQ WLELERP

> RXA00291 (1-1074, translated) 358 residues

AALALISVLG ILIGGVVAMG MRRRWERTVL GLQPEELVTL VQMQTAVIDG IDEGVLLALSP
NGTIGVHNEG AQSMIGAGPM SGRTLKELGL DLGLDGVVLH GQHPETVAHN GRILYLDLPH
VRRGDQDLGV VVTIRDRDI IELSERLDSV RTMTHALRAQ RHEFANRIHT ATGLIDAGRV
HDAEFLGCI SRNMGQSHPL IGSZHLNEAF LSSFLSTASI SASEKGVSLR INSDTLILGT
VKDPEDEVATI LGNLIINNAID AAVAGEAPRW IELTLMDDAD TLVISVADSG PGIPGEGVDVF
ATATQIGDSE DNERTHGHGI GLKLCLARAL SHGGDVWVID RGTEDGAVFG VKPLPGVME

> RXA00292 (1-654, translated) 218 residues

MDQTLKVLVI DDDERVAGIH ASIVDASPGF SVVCTARTLA EAKTLIATFS PDLVLVDVYL
PPGDGIDLVG TSNIDAFVLIS AADDIKTVRR AMRAGALGYL LKPFPPQKVL ERLDYRVYR
HVLSTGQLS QDKIDQATAI LNGTQAPVTV SRSATGLLL DALEGGQELSA TEASEAAGVS
RATAGRIILAA MASQGVQVR LRYQSGRPE HLYSKPLL

> RXA00307 (1-462, translated) 154 residues

VKDLDVDTTEM YLRTIYELEE EGIVPLRARI AERLEQSGPT VSQTVARMER DGLVHVSPDR
SLEMTPEGRS LAIAVMRKRH LAERLLTDII GLDILKVHDE ACRWEHVMSD EVERRLVEVL
DVBHRSFPGN PIPGLGEIGL DQADEPDSGV RAID

> RXA00319 (1-426, translated) 142 residues

MSEVIKAKA EEAGLEDNVI FSSCGMGNWH VQGPADKRAL AELKSAGYNG DTHRAAQLGP
EHMRADLFA LDSGHAGELA ATGVPNDKIR LMRSFDPESN PTDDVADPPY GTSQDFVLTR
ENIEDAMPGL LEWVRDHIRT DS

> RXA00348 (1-456, translated) 152 residues

TRERLENAQY QVQRDRVRGA MEVFIEAGID PGTVPIMECW INNQRHNFV AKELLETHPD
LTAVLCTVDA LAFGVLEYLK SVGKSAAPAD SLTGFDGTHM ALARDLTTVI QPNKLKGPKA
GETLLKMDIK EYVEPEVELE TSFHPGSTVA PI

> RXA00350 (1-327, translated) 109 residues

LPAKITDTRF TPESLHAAVEE ETAAGARRIV ATYSKDFDGD VTLMCMLGVE PQGLRYTKVA
SEHEEAQPKK ATRKTRKAPA KKAANKTKTK KTKTKTKTK TAKKTKTKS

> RXA00363 (1-684, translated) 228 residues

RSILDQVMDF VRESTLDKTM VTGEWYSVYQ VSDQLGISRS PVRDALLRLE EAGLIRFTRN
RGQIVETPK SDVAEIFALR LGIEPAAAYR AAQLRTEFQL HEADDITAM AQAEADNDDEE
AFFTHDRQFH RQIMTMGHSQ RGADLVEKLR AHTRILGAST AGNKRTLGD ILEEHEPILDA

IKRQSAEMAR ATMREHIQVT GKLLLEQAVE KSGEGAAQKI WDQYTAGV

> RXA00400 (1-879, translated) 293 residues

LFTLEQLRCF VAVANHLHFG KAAAELSMTQ FPLSRQIQKL EKIVGATLLD RDNRKVELTT
 AGFAFLKQAR LIINSTEKAA ERARLASSGM WGQLNIGYTA AAGFSILGPT LNQLHEKMPG
 VSVDLFEMVS TEQIAALESG LLDLIGIGRLS SPVEGLQTRR LQADSLVLAA PKGHPLLDQN
 RPLLRKHLTG VPFLQHSPTK AKYLYDIVVR NFTINDAQVQ HTLSQITTMV SLVASGLGVA
 LVPEASAKLN YSGVEYRHFY DLPVGLAELQ AYSTSNDNP AVRKFINKID DTF

> RXA00464 (1-258, translated) 86 residues

VWFGENLVE EWDIAQORIA EADLMIIVGT SGIVHPAAAL PQLAQQRGVP IVEISPRTTE
 LSRIADFTWM STAAQALPAL MRGLSA

> RXA00494 (1-297, translated) 99 residues

MTLPHQLPGP NADFDWQLH GTCRGSTSDV FYHPDGERGR ARQRRLEAK AICACPVLE
 SCRKHALAVA EPGVVGGLS ESERLVIILN NERKQPPAV

> RXA00516 (1-720, translated) 240 residues

MVQKDAQSP ATRKADQVYT QIRREIEDGT LNPQORMSEV WLVEHTGASR TPVRDALRRL
 AADELILPE RQAPMVSPIS LRHIKDLFEF RRIVEVALE EISVGASKSP RIFGEFTSLA
 ADFRELENSA DDADFTADFR RLTSKFDLV AANTHNQFLG RSILSLKPH TRLRIIAHSD
 HARLRQSVQE HIEMCEAVAS GDLRSAGAAC RQHLIHVEKS ILTALINADS TGSQGDIRS

> RXA00551 (1-348, translated) 116 residues

MLAGMPNLNA EELAVRVPA LTKLYLVYFR RSVNSDLSGP QLTILSRLEE NGFSRISRIA
 ELEDIRMPFA SNALHQLQL NLVERIRDTK DRRGVQVQLT DHGREELERV NNERNA

> RXA00583 (1-738, translated) 246 residues

YVERRLIREL DGAKQPGHVA IMCDGNRRWA REAGFTDVSH GHRVGAKKIG EMVRWCDDVD
 VNLVTYVLLS MENLGRSSEE LQLLEDIAD VADELARPET NCRVRLVGHL DLLPDPVACR
 LRKAEZATVN NTGIAVNMVA GYGGRQEIIV AVOKLLTIGK DEGLSVDELI ESVKVDAIST
 HLYTSGQDPD DLVIRTSGEQ RLSGFMLWQS AYSEIWFDT YWPAFRIDF LRAIRDYSQR
 SRRFGK

> RXA00592 (1-459, translated) 153 residues

MASNSERLAE LGISLPSVAA PVAAYVPAIQ TGNQVMTSGQ LPFVDGQLPA TKVGAEVSA
 EDAEKLARAA ALNALAIDA LVGIDKVTIV LKIVGFVASA DDFSGQPAVV NGASNLMGVE
 FGEAGAHARS AVGVAEPLN SPVEVEVIVE IAQ

> RXA00593 (1-348, translated) 116 residues

MTSVIPEQRN NPFYRDSATI ASSDHTERGE WVTQAKCRNG DPDALFVRGA AQRRAAAICR
 HCFVAMQCCA DALDNKVEFG VWGGLTERQR RALLRKKPHI TNWAEYLAQG GEIAGV

> RXA00603 (1-453, translated) 151 residues

MKLDISIDRAI IAEALSANARI SNLALADKVH LTPGPCLRV QRLEAEGILL GYSADIHPAV
 MNRGFEVTDV VTLSNFDRST VDNFESSVAQ HDEVLELHRL FGSPDYFVRI GVADLEAYEQ
 FLSSHIQVTP GIAKISSRFA MKVVKPARPQ V

> RXA00609 (1-666, translated) 222 residues

MSKILLAEED AGIADFIVRG LIREGFECEV TESGAEEAFAR AHSGDFDLMV LDGLPLHMDG
 TDVLEQLRNL QVTLPRIIVLT ARTNIEDRLR TLEGGAADDY PKPFQFAELL ARIKLRLAKH
 TPQETPTDAR VLANGDLELD LRTQRLVLDG SHHDLSSREV DLLETLMRPH GQILSRVQLL
 RLWVMDMDWP GSNVVDVYIR ALRKKIGAGR VETIRGSGYR LR

> RXA00638 (1-384, translated) 128 residues

MEIEIKMDNQS DQGIQVVLVD DEPNIVELLT VSLKQFGFV MTANDGNEAL KIAREFRPDA
 YILDVMPGM DGFEILLTKLR GEGLDSPVLY LTAKDVAEHR IHGLTIGADD YVTKPFSLEE
 VITRLRVI

> RXA00645 (1-2331, translated) 777 residues

LGAHSANSIR GVIDRLDAST VVIVADVHWA DVESMQKLEI YSMRMVSGRF ALIMIGLDEE
 NLVHFDEYVS LPSIADSTYV LPFMSIEEIR QALTDVVRG ISTTTADIQ RITGGIYGRV
 KEVLHSESPD HWRMNPNNIP IPQSWHANLL RRITNEEVWH VLLAVAVLVS GGPIDLVLKI
 GNDPTGMCLD DAVRSGLLRV LPSDGOQPQV LVLPIDRAVL QSRTPTNIIA QLHKKAAEY
 SNKYLLESID SLIAAADLPQ ARSRASLTDL GETGIQQDSM LGYLAHEGR RLEARNLLHR
 ASEELLAQHP IDPIHGPRMA QRKVLNLVD WNPEELLVWA DRAVAMTEED AGEKVEAQAI
 SLTGQSILDG CLPEDKPIPG ETTLHAQRH MAMGWLVMVH DDPVTARQL ERRTSINGSE
 RISLWQDGWL ARSLLLLGEW ESAARTVEIG LARAEQFGIR FLEPLLWSG ATIATARGNS
 DLARNYMSRL STDQDSFIVQ SMPSAMCRMV VERRHNEIPG AIVAGEQLEK IAAKHVNPAP
 GFWEWDVHA THLIRIGETE RAQELVNSTL EELRGSDIMS AHAKIAPDA MLMIHHGDVVK
 KGKFKRFDAL DMIDPLTLPY YRARICFEYG QALRRQQRH RADEQFARAA SLQDMGADA
 MVTLANRERR VGGLQQRSEQ AGGLTPQEYE IARLVSSGHA NREVAQELFL SPKTVEY

> RXA00651 (1-1332, translated) 444 residues

MQSSLDRVSE TGRNELDVET LVKKGQFPA MSYRNSIHL TASLLVVGLG ASARLTIPMF
 ALSCLVLLFVW GFLYFYGSTK RVDLSHGMLL GWLFVLTIVW IFMVPIPVPS IYLLFPLFL
 YLQVMDYVRG IIAILGATAI ATASQYVGL TFGGVMPGVV SAIVTVAIDY APTLTWRVNN
 EKQELIDQLI ETRSQLAVTE RNAGIAAERQ RTAHEIHDTV AQGLSSIOML LHVSEGEILV
 AEMEEKPEKA IVKMKRLARQ TASNLSER AMIALQPA A LSKTSLEALP HRVTEPLLGI
 NFVIVSDGVQ RQLPKMTEAT LLRIAQGAIG NVAKHSEAKN CHVTLTLYEDT EVRLDVIDDG
 VGFEPESEVH TPAGLGHIGL TALQQRAMEL HGEVIVESAY QGQTAVSAL PVEPPEGVG
 APVLADSDSS ATGEVELSSP TDDE

> RXA00655 (1-639, translated) 213 residues

VAASAGSKKS TSAGANRRRN RPSRQRLLD SATNLTFTTEG IRVIGIDIRL READVAKASI
 YSLFGSKDAL VIAYLENLDO LWREAWRERT VGMKDPEDKI IAFPDQCEIE EPEKDFRGSH
 FQNAASEYPR PETDSEKIV AAVLEHREWC HKTLTDLTE KNGYPGTTQA NQLLVFLDGG
 LAGSRIVHNI SPLETARDLA RQLLSAPPAD YSI

> RXA00813 (1-1131, translated) 377 residues

MTIDILVVEN VQRIATKET PPTSABIASL IREQAGVISN EDIVMVLRLR RSDSVGVGGL
 ESLLALPGVT DVLVNAHDSV WIDRGQVEK VMDLGSSEA VRLATRLAL TCGRRLDDAQ
 PFADGRITRD DGSVLRIHAV LAPLAESGTC ISVRVLQAR LSLDDLQSC TYPEDIAPLA
 RNIINQRSSP LVVGGTGTGK TLLSAMLTE VPADQRIIC EDTAELHFGH PSTINLVSRQ
 ANVEGAGAVS MADLLKQSLR MRPDRIVGE IIRGAEVVOLL AAMNTGHDGS AGTIHANSIS
 EVPARMEALA ATGGLDRMAL HSQLAADV DI VLVMKHTPFPG RRLAQLGLVR GNPVTTQVWV
 LDHGMHEGS EEAWFMP

> RXA00822 (1-681, translated) 227 residues

VEGVQEILSR AGIFQGVDP AVNNLIQDME TVRFPFGATI FDEGEPPGRL YIITSKVKVL
 ARHAPGREN LTIIMGPSDM FGELSIFFDG PRSSAVCVT EVHAATMNSD MLRNWADHP
 AIAEQLLRVL ARRLRRTNAS LADLIFTDVP GRVAKTLQL ANRFCTQEG ALRVNHDLTQ
 EETIAQVLGAS RETVKNALAT FAHRGWIRLE KGSVLIVDTE HLARRR

> RXA00839 (1-369, translated) 123 residues

MPVTHPEFR NVAIVAHVDH GKTTLVNAML EQSGVFSHDG EVADRVMDSG DLEKEKGITI
 LAKNTAIRK GAGKGDNDLI INVITDPGHA DFGGEVERAL SMVDGVVLV DASEGPLPQT
 RFV

> RXA00845 (1-903, translated) 301 residues

SSFGRIGILV RVHAGTLRKG QQVAWIHYDE EGNQHTKTAK IAEELLATVG ARVPATEVVA
 GDIAAISGIE DIMIGDTLAD PENPVALPRI TVDEPALSM TIGVNTSPMAG RGGGDKLTAR
 VVKARLENEE IGVNLSKVNP TERPDTEVQ GRGEMALSIL VETMRREGFE LTVGKPOVVT
 QTIDGKLHEP YEIIIVDVP EYQGNVTQL ATRKGLMQSM STTEGSDWIR MEFRIPARGI
 IGFRTQFMTE TRGTGIANSY SDGMDWAGE IKGRAHGSIV ADRSGQITAY ALTQLADRG
 S

> RXA00849 (1-321, translated) 107 residues

MVTYTTLLDK PISESAPKA PEPLLREALG AALRSFRADK GVTLRELAEA SRVSPGYLSE
 LERGRKEVSS ELLASVCHAL GASVADVLE AGSMAQLQAA QEDLARV

> RXA00885 (1-1026, translated) 342 residues

MVSATEKRRY EVLRAIVADY IASQEPVGSK SLLEHKLNV SSATIRNDMS VLESDGFIVQ
EHASSGRVPT ERGYRLFVDS IHDIKPLSLA ERRAILGFLE GGVLDLDVLR RSVQLLSQLT
HQAAVVLQPT LKTARVKHCE VVPLSPMRL LVLITD7GRV DQRNVELEEF LAEEVENVLR
DLLNGALGEK TLTAASDALE ELAQQAPTDI RDAMRRCCDV LVNLTVDQPS DRLLAGTSN
LTRLGRETSR SLPMLLEALE EQVVMLKLLS NVTDLQDQVR HIGGENEDIE LRSATVITTG
YGSQGSALGG LGVVGPTYMD YSGTISKVSA VAKYVGVRLA GE

> RXA00894 (1-1128, translated) 376 residues

MGTEFKRSPR PTLGVEWEIA LVDPETRDLA PRAAEILEIV AKNHPEVHLE REFLQNTVEL
VTGVCDTVEP AVAELSHDLD ALKEAASDLG LRLWTSGSHF FSDFRENPVS EKGSYDEIIA
RTQYWGNGML IWGIHVHVGI SHEDRVWPTII NALLTNYPHL LALSASSPAW DGLDTGYASN
RTMLYQQLPT AGLPYQFQSW DEWCSYMAQD KSGSVINHTG SMHFDIRPAS KWTGIEVRVA
DSTSNLRRLS AIVALTHCLV VHYDRMIDAG EELPSLQQWH VSEKNWRAAR YGLDAEIIIS
RDTDEAMVQD ELRRLVAQLM PLANELGCAR ELELVLEILE RGGGYERQRR VFKETGSWKA
AVDLACDELN DLKALD

> RXA00947 (1-336, translated) 112 residues

MARKLEHPSL AEMNLNAIMF ALSDPIRRQI LSQLSGCHND QACVAFELPV SKSTSTHHRF
VLREAGLITQ RYEGTAILSA LRSEDMEARF PGLLTSMVRA EVEERNAADL EV

> RXA01001 (1-318, translated) 106 residues

VTVSWHQATD APPSIRITTL AFSLQPNQRK VAEVMLVDAP SIVELTAQGL ADRVGVGRAT
VIRTAQSLGY DGFPQLRVAL AQELALAQGA SRSMVEGALS SSSLGH

> RXA01065 (1-582, translated) 194 residues

ILEAVRKVSP KTLPIGLIITK ADSVSRDLVA AQLMAVHELL GGNSEVVPVS STSGENVETL
IKVMTDLLPE GPKFYPPDDHI TDDETNTRIA EAIRAALSG LKNELPHSVA VEVDEILPDP
ERNQGLAVHA IIVYERVQGK DIIVGHKGQR LGRIHTSRQ DIIKILQGNV FLDLRIKVLK
NQWSDPKALN RLGF

> RXA01110 (1-573, translated) 191 residues

MLAIVQLSKE SIIGAASVIL SEFGLSDMTM RRVAQLNVA PGALYWHFKN KQELIDATSR
YLLAPVLGRN DEQRASISAQ ETCAEMRSLM MQTKDGAEEVI SAALSNQQLR QAELSLSIDS
LKEPNEVGAF TLLHFVVGA VLTEQTQLQM EFTAGAGDDT QENPADANFE ERFNQGIEII
LVGLDALGHI R

> RXA01118 (1-765, translated) 255 residues

MVEQSPDFVQ SFARGLSVIR SFSADNPSQT LSEVASQTGL SRATARRFLH TLTDLGAVN
NDSRFQLTPR VLELGASYSL ALSPLAIAQP RLEVLRSQVG ESSSMSVLGD TDIIYVCRVP
VRRIRVNIT ICTRFPAYAT SMGRIMLANL PEEELDEMLA AAPPEQLTRT SLTSTIASIRE
EIIATRERG W SLVDQLEPG LRSLAAPITN AQGEVVASIN VSTQASHSV EDIRKLVLPO
LLETAQAIST DLSAL

> RXA01125 (1-213, translated) 71 residues

MAIIVDIDVM LARRKMGVGE LAEKIGITPA NLSVLKNGRA KAIRFSTLEA ICRELGCQGP
DILRYDASLH N

> RXA01211 (1-795, translated) 265 residues

MNKDFWTAGW TARWFSRGVS LLASPVTAPL NSWRRLPNLA KYTLTRYVSL QAIPVLLSA
YFLGIVANAG TILNPSFWLL GFSVILLIIV VLVVEYQPSL NSHPRRSVQP FFTGLVLNV
LGVVVSVVLQ IPGLMMSDNT RATALIFTLT CVFLLSIAY IPWMNYRWLVNT IAMSALVWNT
STTDYLSAL WVVIPLPMAG TVRLSVMTVD VMKEVERSR E LEASLRVTEE RLRFAQELHD
TLGQHLAAMS VKSELALALA KRGDD

> RXA01241 (1-480, translated) 160 residues

VDVRHLPETE SRSSKAATQA KSKAPQAGVH DPFLAGQTSF VPVVGKIAAG SPITAEQNIE
EYVPLPAEIV GGGDLFMLQV VGESMRDAGI LTGDWVVVRS QPVAEQGEFV AAMIDGEATV
KEPHKDSGGI WLLPHNDTFA PIPAENAEIM GKVVSVMRKL

00602874-062300

> RXA01248 (1-429, translated) 143 residues

MAQRTEPTTAT PPGRVLVVDD EQPLAQMVAS YLIRAGFDTR QAHTGTQAVD EARRFSPDVV
VLDLGLPELD GLEVCRRI RTSDCYILMLT ARGSEDDKIS GLTLGADDYI TKPFSIRELV
TRVHAVLRRP RTSTTPPQVT TPL

> RXA01272 (1-603, translated) 201 residues

MSNSFTILT CTGNICRSPL AKOLLELELP GADIIRVDSA GVQAMVDSM PEQSLEIARK
QGIENPEEHR AKQITEELVN QSDLILAMDR GHRKSIVQLS PRATRKVFTV VDLARLIEAT
TDADLQELN LAGDSVIDRL HATVEAARLS RSELNPLDNL ADEDIVDPYG KQSVSYEASA
SQLIPAIRLI ASYLNKALES A

> RXA01368 (1-129, translated) 43 residues

KRICQCPCVR DECLEFALEH DERFGIWGGL SERERRRLKR EIS

> RXA01375 (1-1455, translated) 485 residues

VTEKYRPVRD IKPAPAAQMS TKQAGHPVFR SVVAFVSVLV LVVSGGLGYLA VGKVDGVASG
NLNLGGGRGI QDGNAAADGAT DILLVGSDSR SDAQNTLT EELAML RAGD EENDNTDTIM
VIRVPNDGSS ATAVAI PRDT YIHDDYGNM KINGVYGAYK DARRAELEMEQ GFTNESELET
RAKDAGREGL IDAVSDITGI TVDHYAEVGL LGFVLLTDAV GGVEVCLNNA VDEPLSGANF
PAGROTLLGS DALSYVRQRH DLPRGDLDRI VRQQSYMASL VNQVLSGGTL TNPAKLSAIA
DAVTRSVVID EGWEIMSFAT QLQNLAGGNV TFATIPVTSI DGTGDYGESV VTIDVQVHA
FFQEALGEAE PAPEGSDSQ SDAQPLDSE VEVHVLNASY VEGLANGIAA QLQELGYSIA
ETGNAAEGLY YESQILAAEE DSAKALAISE ALGGLPSWPT LPSTTPSSS YPPAITLALP
RKQTP

> RXA01418 (1-246, translated) 82 residues

MLGDRTLRRL LIALHYHGP EATVSEIADI VGVTLPTASA ALQLLADNGV VESFKEGRVT
RYKLVDATTH TLLHHLGGTH RH

> RXA01450 (1-564, translated) 188 residues

VPVTLTLGIV GLPNVGKSTL FNALTRNDVL AANYFFATIE PNVGLVELPD ARLERLSEIF
GSRILPATV SFYDIAGIVK GASEGEGMGN AFLANIREAD AICQVVRFA DENVIHWGDE
VNPATDISVI NTEILILADLQ TVEKALPRLE KDARKDKGLG EVVDETKKAL AILSDDRTLF
LCSKSNRH

> RXA01451 (1-567, translated) 189 residues

MTAPCFSAAK AGDIDLALL DLHMTAKPF LYVFNSEKLV LTDDAKKDEL RALVAPADCV
FLDAQTETEL LELEDEAAE LLEAVGQTEP GLHSLARAGF ETLGLQTYLT AGPKESRAMT
IHKGDTAPEL AGVIHSDFER GFIAEIVSF EDLDAAGSMA EAKAQGKVRG EGKDYVMVDG
DVVEFFENV

> RXA01500 (1-444, translated) 148 residues

MATHPDIPTE LLESPSYQLE RLRRRTDRHV EALAKHETT MREFWTLTCL VHSDAASQSV
LCELLAIDAS DMVRLVDSLE RGVWAKRERD PKDRRRQIVA STKKGKNAQA DLHKVVLAE
DAALDESTSK QLKLRLKLA AISTEED

> RXA01537 (1-651, translated) 217 residues

MTQIAASLD LAARITAKID QGVLTGTRL PEVALAEELG VSRNTLREAF RVLMDGDLVD
HIPNRGVFVH TTFKSDVEDI YAYRTFIEVA AIRSARKNPQ LLEQSLGVMR EAYERGAAN
AVGWDQTVGS ANSAFLAIV DLAGVARLSA DARKVLALAR IGFMATYNVE TFHSIYVEKN
HQILKYLAAG EFEEAEQYLQ KYFEDSRDDL SAHLPEF

> RXA01573 (1-2082, translated) 694 residues

MKRLSRAALA VVATTAVSFS ALAVPAFADE ASNVELNILG VTDFHGHIEQ KAVKDDKGVI
TGYSEMGAAG VACYVDAERA DNPNTFRITV GDNIGGSPFV SSILKDEPTL QALSAIGVDA
SALGNHEFDQ GYSDLVNRVS LDGSGSAKFP YLGANVEGGT PAPAKEIEIE MDGVKIAIYVG
AVTEETATLV SPAGIEGITF TGDIDAINAE ADRVIEAGEA DVVIALIHAE AAPTDLFSNN
VDVVFSGHGH FDYVAEGEAR GDKQPLVVIIQ GHEYKGVISD VEISYDREAG KITNIEAKNV
SATDVNENCE TPNTAVDAIV AAAVEAAEEA GNEUVATID GFYRGADEEG TTGSNRGVES
SLSNLIAEAG LWAVNDATIL NADIGIMNAG GVRADLEAGE VTFADAYATQ NFSNTYGVRE

VSGAQFKEAL EQQWKETGDR PRLALGLSSN VQYSYDETRE YGDRITHITF NGPEMDMKET
YRVGSSPELL AGGDSFTATA EGGPIATGM VDIDLNNYI AAHPDAPIRA NQSSVGIALS
GPAVAEDGTL VPGEEITVDL SLSYSTGPEA KPTTVEVTVG TEKKTADVDN TIVPQDSTG
KATVTLTVPE GATSVKIATD NGTTFELPVT VNAGEGNDDD DDKEQSSSGS SDAGSLVAVL
GVLGALGLV AFLLNSAQGA PFLAQLQAMF AQFM

> RXA01655 (1-1359, translated) 453 residues
MLADLPIALN PHEPTSIPTQ LTEQIRRLVA RGILTPGDPL PSSRSLSTQL GVSRSVSVTA
YDQLAGEGYL STARGSGTTI NPDLHLKLPV ELEKKETSRS VPPPLNLSP GVPDATTADL
SAWRAAWREA CAKPPTHSPE QGLLRRLRIE ADHLRQMRGL MVEPEQIIIVT AGAREGLSL
LRTMDAPARI GVESPGYPSL RRIPOVLGHE TIDVPTDESG LVPRALPHDL NALLVTPSHQ
YPYGGSLPAD RRTALVAVAA ANDALLIEDD FDSRLRYVGM PLPLRALAPL RRTILLGTFS
SVITPQVACG YLIAPTPQAR VLATLRGILG QPVGAITQHA LASYLASGAL RRTQRRLRL
YRHRRSIVQD TLGDLPNTQL RPIINGGLHAV LLCCKPQDLV VTTLASRGLN VTALSHYWG
TGADNGIVFG FGSHEDETLR WVLAETSDAV SLG

> RXA01687 (1-1071, translated) 357 residues
VFMLAQRTLP IHITAPHLPV ARVFHQIRAT DADRTSLQRD LELSQAIGTR HVSAIDAGL
VEETRVDSGA RSGRPRTKLG IDGRHLTAWG VHIGLRSTDF AVCDDLGRVY RYERVDHVES
HSTPSETLNF VAHRQTLISA GLPEPRNVGV ALSAHLISANG TVTSEDYGWS EVEIGHALFF
PATIGSGVAA MAGSEIINAP LTQSQSTSLY FYAREMVSHA WIFNGAVTHPR NSGRTPTAFV
NTWNTLKDAFR RGLTPPTTFSD LVQLSHTNPL ARQILNERAH KLADAVATVR VDVDPPEAVF
AGEAFTLDPE TLRIVVTQLR ANTGSQRLRI RADAYILRTA AIQVALHPIR QDPLAFV

> RXA01759 (1-762, translated) 254 residues
MTKRLSLLEGL RYAQAVAEETH SPSAAAREYG VTQPALSNGI AKLEDRLGEG LFDRSTQGV
PTSGFGLHLP LIQRALTEID AITAEAHRLI NSEARSIRVG ISPLINPQLV ARTYAVREL
PTADHLVLE ANMKELHEGL LAGELNVILI PAVKPLPHFE HRIIDSEPVV IVESTQDSTD
PIELRETOHE PFILVPDTCG LTTFTNQLFE TNDLALNAYS GEAASYQVLE QWATLGLGSA
MLPLSKLSSP TAPH

> RXA01763 (1-465, translated) 155 residues
MTTSNPTAEI IGGPERFLEA ELSQQIQFLT ARARAKGSAK GNEALVDLGL KVRQYSTLSL
AASGLKPTQR ELGAFDLDDP SQIVALVDLF EKRGVAREV DPRDRRSKII IATEKGLEIH
DEATKRLLLA EGESLKNLTS DEQEQLRELL LKIAF

> RXA01826 (1-1938, translated) 646 residues
VTFVIADRYE LDAVIGSGGM SEVFAATDTL IGREVAVKML RIDLAKDPNF RERFRREAQN
SGRLSHSHIV AVFDTGEVDK DGTSVVPYVM ERVQGRNLRE VVTEDGVFTP VEAANILIPY
CEALQASHDA GIHRDVKFA NIMITNTGGV KVMDFGIARA VNDRSTAMTQ TSAVIGTAQY
LSPEQARGKP ADARSDIYAT GCVMYELVTG KPFFEGESPF AVAYQHQQVD PTPPSDFIAD
LTPTSANVND AVULITAMAKH PADRYQTASE MAADLGRSLR NAVSHAAAHV VETEETPEEP
ETREFSTRST QVAPAAAGVAA ASTGSGSSSR KRGSRGLTAL AVILSLGVVG VAGAFITYDYF
ANSSSTATSA IPNVEGLPQQ EALTELQAAG FVVNIVEEAS ADVAEGLVIR ANPSVGSEIR
QGATVITITVS TGREMINIPD VSGMTLEDAE RALEVDGLIL NQNVREETSD DVESGLVIDQ
NPEAGQEVVV GSSVSLTMSS GTESIRVPNL TGMNWSQAEQ NLSIMGFNPT ASYLDSSPE
GEVLVSQQG TELPKGSSIT VEVSNGMLIQ APDLARMSTE QAISALRAAG WTAPDQSLIV
GDPHTAALV DQNKIGFQSP TPATLFRKDA QVQVRLFEED LAALVQ

> RXA01827 (1-1407, translated) 469 residues
MSQEDITGKD RLQELIGADY RLQWIIGHGG MSTVVLADDV VNDREVAIVK LRPEFSNDQE
FLNRFERNEAQ AENIDSEHV VATYDYREV DPAGHTFCFI VMEFVRGESL ADLLEREGL
PEDLALDVME QAAHGLSVIH RMDMVHRDIK PGNMLITANG IVKITDFGIA KAAAAPVLT
TGMVVGTAGY VSPQAQQKE VTAASDIYSL GVVGYYEMAG RRPFTGDSV SVIAHAINQY
PQPMQTSISA QRELIGIAL RKDPGRRRPD GNEMALAVSA VRLGKRPPQ RTSAMAAQE
APSPSESTAM LGRVARPATI TQEAAPKRG GIGIGLFIAA LLAVIIGAVI YAGTTGILFN
DTPPETTTTPE TITETYPPTV EETTSQWVPP TPPTSTTFTE PETTSRPTT SEESTSEPT
TEAPTSSRTP PQIPTSPRT SASVPVETNA PADLDLDAVN GLLDVGGAQ

> RXA01830 (1-1353, translated) 451 residues
MLKLKYAVAS DRGLVRGNNE DSAYAGPHLL ALADGMGGHA AGEIASQMTI NHLRALDVDP

GDNDMLALVG MVAGEANAIAI AEGIAEDPAR DGMGTILTAF MFNGRDLAMC HVGDSRGVYL
 RDDKLVQVTV DDTFFVQSLVA EGKLPDEPVS THPQRSILIK AYTGHPEVPT LEQFPALPFG
 RLLLCSDGLS DPVTHSTIEE TVRVGTPQDA STKLVELALR SGGPDNVTVI VADVVEVTEA
 EAAAEASVPV TAGAINGEQP EDPREDTAAG RAAAITRRAQ VIDPAPKISD AGTEDIPTIE
 EPPEKSSSKL AVLILVALVIL IGVVAAGWGW YSRIDSTFFY AVNDEEAIIV EHGVDYRIFG
 KDLHSGQFVA CLNEAGTILSL KESCENGTSF KLDLDPASVR GSVAGLPSGS YDEVQAQMQR
 LAAQALPVCV NLEVALTTGDR NEPGVNCREV S

> RXA01836 (1-705, translated) 235 residues
 MGQOEIIEDS TEGGIKVLDR TVLILNVIAE QPRSLAELAA ATDLPRATAH RLASALEVHG
 MLARSRDNWR TIGARLASLG ARGADTLIDT AVPINADLME RTGESVQLYR LTGTTRTCVA
 SQEPSSGLKN VVPVGRMPL NAGSAARVFA AYLPIPSASV FSREELDQVR ASGLAESVGE
 RELGLASLSS PVFDSNGSMI AALSISGVAE RLKPHPAAMW GTELIDAAER LGALL

> RXA01840 (1-654, translated) 218 residues
 ISEEDGASEP ATFAERSQRL IQQECVAAVF GGWTSASRKA MLPVFEGNNS LLFYVPQYEG
 MESSPNIFYT GATTNQIIF ALDYLRNGL NRLFVGSODY VFPRTANSII KDYAEANGME
 IVGEDYAPLG STDFTTIANR MRDSNADAVF NTLNGDSNVA FFRQYNSLGF NADTLFVMSV
 SIAEEVGGI GTANIEGQLV AWDYQITIDT PENETFFVE

> RXA01860 (1-885, translated) 295 residues
 VNPFILADQL LYDAKHAGRN RVAVRRAENT IVRSKAPFS VEELSEILES HSIRLELQPI
 LELETGRVGA AEGLLRINLD GTDVPTGQFV QSVEQAGLAP KLDIAVMREG INHIERLRAV
 CPTFLSALNL SGYLSSSAKI REELRAEFRA RDLPRGSIRF EITETAFIED IDAAKEFVQM
 LKDFGFHIVI DDFGAGHEPY QYLKFFDFS LKIAGEFIEG MVTNRVDRSI VESIAQLAKD
 EEMETVAEFV SSKELLEAVR EIGVTYAQGF HIGKSKPIDE FIATYLETNQ TATWG

> RXA01861 (1-1965, translated) 655 residues
 VVARDLQKLE KRLICGYVF LVPAYILHFF AETSIRGVIL AGIAHAIAGP GVALVMFME
 NAQLPELLRK RHAFAPFSHI RLPQGVFRLL VAGIVMAIS KLIVILAYAL ADLPYSFTLY
 LTMALRDLTG IIVVAGPGIA LSTPLVLNIH RSAWREFAVV IATVGVADLPT
 VYLAMLPYLV SATRLPVLVA VLHAVFTSAI VVILVFLGT GSFATIDESI LVQATTIQLF
 VLMCILLSLV VSTTVQQTSA LVEELEVVAK QVEGVGLAKL GEVLGEDPDL ARRIFEISAS
 DGHYSMPKIQ NIDGEPMEDE ESFSSMALRG QGVEGVGLAKL GEVLGEDPDL ARRIFEISAS
 PMYLGETEP GHALVIWHDS TNEYTYMQQL TLAYEESRLI FEKAPQGIAM LDPGGEIVMA
 NRSFGDLVGT TPVRLGRNL EDFGVVEGTM EYVTPVLSDP EAVVHLDRSL ETLRGQKQNV
 AMSFSSMGNV GGRIGTLLVN VVDVTERQEL IELVEHLADH DSLTGLVNRR RLESIDELI
 LKNERDSTDS ALLLLDLDFY KEVNDSLGHE AGDQLLIEFA EILKDSVRDS DIVRIGGDE
 FVIVLPDTR DGAEATGIRI IELVNQHFKG RGKVLRSVSS KVSAGRSFLM LVPKV

> RXA01898 (1-693, translated) 231 residues
 MSVKAHESVM DWVTEELRSG RLKIGDHLPS ERALSETLGV SRSSSLREALR VLEALGTIST
 ATGSGPRSGT IITAAPGQAL SLSVTLLQVT NQVGHHDIEY TRQLLEGWAA LHSAERGDW
 DVAAELLEKM DDPSPLEDF LRFDAEFHVV ISKGAENPLI STLMEALRLS VADHTVARAR
 ALPDWRATSA RLQKEHRAIL AALRAGESTV AATLIKEHIE GYEEETAAME A

> RXA01935 (1-1164, translated) 388 residues
 MIGVGLPMPN QAHSFASFAF PSTPAACKMH HIRLQGQLIR NELVEATGLS QPTVTRAVTA
 LMQAGLVREER PDLTLSSGPG RPNIPLELAP SPWIHAGVAI GTKSSYVALF DTKGRTLRDA
 MLEASADLD PDTFIEHLIA GVNRLTGLD LPLVGIGVAT SGKVTNAGV TASNLGWDGV
 DIAGRLNYQF SVFATVASAI FAIAASELQA SPLPHFEQPT PITLTFYADD SVGAAYSNDL
 GVHWIGPLAT TRGSGDLTG MAAEDALSTQ GFLSRVSDQG IFANSLGELV TIAKDNETAR
 EFLNDRATLL AHTAAEAET VKPSTIVLSG SAFSEDPQGR SVFASQLKKE YODADIELRI
 PTHRENVRAA ARAVALDRLL NEPLTIVP

> RXA02127 (1-654, translated) 218 residues
 MSETVLVIGA TGSIGRHVVS EALNQCYQVK AFVRSKSRAR VLPAAEAIIV GDLLDPSSIE
 KAVKGVEGII FTHGTSTRKS DVRDVDYTG AVNTLKAVKGK DVKIVLMTAV SVTRPGVAYA
 EWKRHGQQLV RASGHGYTIV RFGWFDYNNND DERQIVMLQG DTNQGSGGPAD GVIARDQIAR
 VLVSSLNDAK ARNKTFFELSA TYGFAQGKPD RNCSTSG

> RXA02210 (1-564, translated) 188 residues
 VSVAAQDKPT NSRQBIIEGA RRCFAEHGYE GATVRRLEEA TGKSRGAIFH HFGDKNLFL
 ALAREDAARM AEVVSGLV EVMRGMLSD ERYDWMVRL EISKQLRTDP VFRAKWIDHQ
 SVLDEAVRVR LSRNVKGGQM RTDVPVIEVLH TFLETVLQDG ISRLATGAST EGLSEVLDLV
 EGTVRKRD

> RXA02232 (1-1527, translated) 509 residues
 MDEKKNLSHD ELLAQAFRGH KNTVRPGSDE TSGFDLSGFT RAEEPSTGDL DLEARDAQRR
 RDTEIHADA EADGVEYERK LRLERVILVG VWTGTTAEI DASLAELAL ADTAGAEVIE
 TLYQKRDKPD PGTYIGSGKV RELKEIIEAT SADTVVCDGE LSPSQLVALE RELDIKVIDR
 TMLILDPAQ HAKSREGKAQ VALAQMEYLI SRVRGWGNL SRQAGGRAGS NGGVGLRGGP
 ETKIEADRRR LRSDMARLR ELSGLDTSRS IKRAQRAASL VPQIAIAGYT NAGKSSLINA
 MTGAGVLVEN ALFATLDPTT RKAELADGRH VVETDTVGCV RHLPTSLEVA FKSTLEEVVE
 ADLMLHVVDG SDPFLKQID AVNTVISDIV RSTGAVPPPE IIVVNKIDQA DPLTLAELRH
 AVDDVVVFVA LTGEGIKLE ARIELFLNSR DAHLLLKIPF TRGDIVSRHL QHGTVLSSEY
 AEDGTLMDVR IPTQLAQELQ SYVVEPTSA

> RXA02270 (1-621, translated) 207 residues
 MDQARNRTH YAMVELEQHG FLSSGVVTQNV DGLHAEAGTK NLVALHGDLA HVMCLNCGFG
 EDRLHFDERL EAAANGPYAS IRLEPGAVNP DGDVFLDEEQ VRRFTMIGCL RCGSLMLKPD
 VVVYGFVPA ARKKDLKKLL DASSLLIAG SSLAVMSGYR IVIEAQRGK QVSVINGGPG
 RADSRVDILW RTRVAFAPDD ILDALDL

> RXA02306 (1-291, translated) 97 residues
 MQPEEVHIDK ETIKLGQFIK LANLVESGGA AKDAIANGDV TVNGEVDTRR GKTLRDGDVV
 CIGEVCAQVS TGAADDDYF DEATANDDDF PEKWRNM

> RXA02376 (1-1503, translated) 501 residues
 MNRFDIRVVL HLAAGDGGNG CVSVRHFKFK PLGGPDGGNG GHGGDIILEV TAQVHTLLDF
 HFHBPVKAER GARGAGDHRN GARGKDLVLE VPPGTVVINE KGETLADLT VGMKFIAAAG
 GNGGLGNAAL GANKAKAPGF ALIGEPGEAH DLILELKSMA DVGVLGFPFA GKSSLSIVMS
 AAKPKIGDYP FTLQPNLGV VNVGHETFTM ADVPLGIPGA SEGKGLGLDF LRHIRTSTVL
 VHVVDATMD PGRDIPISOLE ALEAELAAQY SALDEDTCLG DLSQRPLRV LNKADVPEAE
 ELAEFLKEDI EKQFGWPFVI ISAVARKGLD PLKYKLEIV QDARKRKEPE KAESVILKPK
 AVDHRTKGQF QIKPDPVQGG GFIIITGEKE RWILQTFDEN DEAVGYLADR LAKLGIEDGL
 RKAGAHVGAN VTIGGISFEW EPMTTAGDDP VLTGRGTDVR LEQTSRISAA ERKRASQVRR
 GLIDELDYGE DQASERERWE G

> RXA02392 (1-1260, translated) 420 residues
 MAEKFAETTF TDPARIRNFC IIAHIDHGKS TLADRILQLS NVVDARDMRD QYLDNMIDIER
 ERGITIKAQN VRLPWIPRSG EYEGQOIVMQ MIDTPGHVDF TYEVNSRALEA CEGAILLVDA
 AQQIEAQTLA NLYLAMENDL EIIPVLNKID LPAADPDKYA LEIANVIGCE PEDVLRVSGK
 TGMGVPELLD KVVELIAPFT SEFEEDAPAR AMIFDSVYDT YRGVVTYIRM MDGKLTPRQK
 IKMMSTGATH ELLEIGIVSP TPKKCVGLGP GEVGYLITGV KDVRQSKVDG TWTWAIHGA
 QPLRGYQEPF PMVYSGLFPI SQADFFDLRD ALEKQLLNDL SLTYEPETSV ALGFGFRGCF
 LGLLHMEIFR DRLEREFGLD LISTAPSVNY RVIDEAGKEF RVHNPSDWPG GKLSVVEYPT

> RXA02450 (1-555, translated) 185 residues
 MNLDLKAEE TRQRFIDVAH ELFLEHGYGS TSMNQIAQAA GGSRLNLYLH FRNPKPLMMA
 KMRLEPAVR TPVLKVFIDL EHTLESILRW LDSMTEVWKA NAKVFGAMEQ AMVEDAAVAD
 EWLMMQRLS QSVPELVENE ERRVQFLASL MGMDRNFYFL YVRGQDVDEE LLKLAVARQW
 LAVFQ

> RXA02493 (1-1239, translated) 413 residues
 VSTLLAFVLG VVLMGLALPA YTIKIDRMRR HKSAVTILSEN QVTTVGQVLH LAIQCSPTGI
 TVVDRTDGVI LSNGRAHELK IVHERSVGDN VWRVAQEAFQ DQETHSLDVH PDNRPRRPGS
 RITAVQAVVK PLTLIDDRFV IYASDESEN VMESARRDF VANVSHELTQ PVGGMALLAE
 ALMESSDDPE QVEYFGSRLH REAHRMADMI NELISLSKLO GAERLPDMEP VQADDIISEA
 IERTQLAAND ANIEIIRGDR TGVVWEADRS LLVTALANLI SNAINYSPKS VEVVSQSIR
 NDVMVIRVVD RGIGIAPEDQ GRVFERFFRV DKARSRTGGT TGLGLAIVKH VMANHGGSIS
 LWSRFGTGST FTLELVVYH ESKEPAGSKQ GPSLDSPIRT TASKASGRKK EKS

> RXA02494 (1-696, translated) 232 residues
 MTRILIVDEE ESLADPLAFL LRKEGFDTHI AGDGPTALVE FSRNEIDIVL LDLMLPGMSG
 TDVCKELRSV STVPVIMVTA RDSEIDKVVG LELGADDYVT KPYSSRELIA RIRAVLRRRG
 VTEEAELP LDDQILEGGR VRMDVDSHTV TVGGEFVSMF LKEFDLLEYL LRNAGRVLTR
 GQLIDRIWGA DYVGDTKTLD VHVKRLRSKI EEPSPRPLY VTVRGLGYKF EL

> RXA02631 (1-1365, translated) 455 residues
 MSLRWRLALL SATLVAFVAVG VITVAAYWSV SSVYVNSIDR DLEKQADAML GRASEAGFYA
 TAETEIALLG EYASDTRIAL IPPGWEYVIG ESIISLPDSDF LKSKEAGKQI LVTSAERILM
 KRDSGCTVVV FAKDMVDVTDRL QLTVLGVILL IIGSGVGLAS ILLGFLIAKE GLKPLSKLQR
 AVEIEIRIDE LRAIPVVGND EFAKLTRSFN DMLKALRESR TRQSQLVADA GHELTKPLTS
 MRTNIELLLM ATNSGGSGIP KEELDGLQWR VLAQMTXMSD LIGDLVDLAR EETAETSSIV
 DLNQVLEIAL DRMESRRMTV RIDVSETVDW KLLGDDFSLT RALVNVLDNA IKWSPENGIV
 RVSMQSIDKA TVRIVDDSG PGIAEKERGL VLERFYRAVS SRSPGSGGL LAIVNQVVMR
 HGGQLVVGES DDGGLTRITD LPGEPIRSGF ENVDD

> RXA02632 (1-696, translated) 232 residues
 AVRDLSLRRSL SFNGYNVVL A EDGIALEMI DKEQPALVIL DVMMPGMDGL
 EVCRHLRSEG DDRPILILTA RDNVSDRVGG LDAGADDYLA KPFALIELLA RVRSILVRRSA
 VESNQSSIE QALLSCGDLT LDFESRDVYR NGRALISLRT EFALLQLLLK NQRKVLTRAQ
 ILEEVWGCFD PTSGNALEVY IGYLRRKTEL EGEDRLIHTV RGVGYVLRET AP

> RXA02667 (1-594, translated) 198 residues
 MEFKVGDTVV YPHGAAIIS ALEQREMNGE TVDYVLVLQIN HSDLVVRVPA KNAELVGVRD
 VVGEGLQKQV FSVLREIDVE EAGNWSRRYK ANQERLASGD VNKVAEVVRD LWRDQDQRL
 SAGEKRLMSK ARQVLVGLA LAETVDDEKA DAFLSQVDET IARHRADLLG DEEEKKDAFD
 DFDSDVDLD DLSFDEED

> RXA02668 (1-723, translated) 241 residues
 MTNPSPALNE TSGSRVLIVE DERPLARMIS LYLKAGGFD TTIHDGAAAP DKVAHLRPDV
 VILDGLGPGI DGLEVCRRIR AFTDCYIIML TARGSERDRI TGLEIGADDY ITKFNIRNEL
 VIRIQSVMR PRKIDETIQN GLTLTYGHIE LDTLAHEVTV KGVGVTLTTR KVELLQALMH
 KPGEAVSRD LVSQVWDTTW VGDERIVDVH IGNLRKKLEA PAPGSHFIDT IRGVGYRMAF
 K

> RXA02669 (1-1116, translated) 372 residues
 MTALIPARHS LTFRLTLAQL AVVLISLLAA LIVAALVGP A IFNSHLDLSG PIDPRQTDHF
 IQEAYRDANY IALAAALPTA VLSSIGVSFW LSHRLGQPLW RLSRAATAMS SGDYQVRVPI
 SDVDKEVAAL SLAFNSMADQ LEHTEELRRN MSLDLSHEMN TPLSVLLVYV DGLQDGMVEW
 DADTHAVFAE QLGLRSLRLTS DLDDVSRAQE HRFDLVYSTV AIGGLIHNA GAAAGSYQEK
 GVALEVTGSD STELIRVDSQ RFAQVMANLF SNALRHTFAG GKVHVRVLQV GVGTVIEVIV
 DNGEGIAPEH VKYVFEYFR AKRSDSDQS GSGIGLTISR ALIEAQGGTL TAESAGLKGK
 AKFTIRLPLL SK

> RXA02698 (1-369, translated) 123 residues
 VSSNNESSFA LPONEPLTL PETAERLGVV VTKVMDLVNE HKLIVVRRDG IRYIPEAFLS
 TKKENTRNFI PGVIALLDG GFSDEEILAF LFTEDTLFG RPIDALHGQL AREVMRRAQA
 MAF

> RXA02699 (1-2148, translated) 716 residues
 MSTVYRCLDL RLGRSMALKV MEEDFVDDPI FRORSRRER SMAQLNHPNL VNVYDFSATD
 GLVYLVMLLI TGGTLRELLA ERGPMFPHAA VGMVRGVLGT LAAAHRAGMV HRDIKPNVL
 INSDHQVKLS DFLGLVRAAHA GQSQDNQIVG TVAYLSPEQV EGGEIGPASD VYSAGIVLFE
 LLTGTPFSG EDDLDHAYAR LTVVVPASS LIDGVPSLID ELVATATSN PEDRFDDSGE
 FLSALEDVAT ELSLPAFRVP VPVNSAANRA NAQVPDAQPT DMFTTHIPT PEPDHTAIP
 VASANETLTL PAQNMAQNMMA QNLPQPEFD FAPEPPPDAT LNIQDQELAR ADEPEINTVS
 NRSKLKTSLV SIEFVAVIAA VAVGGWVFGS GRYEIPQVL GMDEVQAVAV VEEAGFVAVA
 EPQYDNEVPT GSIIGTEPSF GERLPRGEDV SVLVSQGRPV VPDLSEDRSL STVREELEQR
 TVFVVDGEGE YSDVDPEGQV VSFTPSSGTQ LDVGETVQIH LSRGPAPEVI PDVSGMGVDQ
 ATRVLERAGL SVRETEEGFD AETPNGDVYG TSPKVSDEVK RGTSVVLQVS NAISSVPDVG

MTKDEATAAL AEEGLVVAST SIIPGEAASS ADAVVTVPEPE SGRSVDPAHP QVSLGLAGEI
QVPSVVGKRV SDARSILEEA GLTLTTDADD NDRIYSQTFR ARSEVSVGGE VTVRAF

> RXA02724 (1-867, translated) 289 residues
MLIGEVSKLS GVSARMLRHY EKLGLVEPKQ STAGYREYSE GDVRRIFWHE GLRSLGLSLK
QVGDALEDPD FDPQAVISSEM IAETSARISM ERELLARLKA VRHAQASDWE SALDAVQILR
RLRSGDPQAR QAVAVDVSOG KEAVALETLV ESALGESHLN AEGALSWAVV QRGEEAVALA
ARGLSRMDAA VRLRAVRIVA SAPSAAVADR EWLRFPMIRD DALVRAETAL ALGKSGDESA
VEQLVSMVLT GLRDVEAAEL LAGFGEVPQL DVFKKFARTL DDEETMSPT

> RXA02747 (1-2076, translated) 692 residues
MNNPAQLROD TEKEVLALLG SLVLPACTAL AATGSLARSE LTPYSDLDLI LIHPGATPD
GVEDLWYPIW DAKKRLDYSV RTFDECVAMI SADSTAALAM LDLRFVAGDE DLCAKTRRRI
VEKWRQELNK NFDADVVDTAI ARWRRSGPVV AMTRPDCLKH RGGLRDFELI KALALGHLCN
LPQLDAQHQL LLDARTLLHV HARRSRDVL DPEFAVDVAMD LGFVDRVHLG REIADAARAI
DDGLTTALAT ARGILPRRTG FAFRNASRRP LDLDVVDANG TIELSKDKPDL NDPALPLRVA
AAAATTGLEV AESTWVRLNE CPPLPEPWPA NAAGDFFRIL SSPKNSRRVV KNMDRHGLVS
RFVPEWDRIK GLMPREPSHI STIDEHSLNT VAGCALETVT VARPDLLVLG ALYHDIGKGF
PRPHEQVQAE MVARAASRMG LNLDRASVQ TLVAHTTAVA KIAARLDPESS EGAVDKLLDA
VRYDLVTLLN LEVLTEADAK ATGPGVWTAR LEHALRIVCK RARDRLTDIR VPAPMIAPRS
EIGLVERDGV FTQVWHGEDL HRLGVIVAK GWTITAAARML ANQWQSAEFD VRANGPDQFD
PQHFLQAYQS GVFEVPIFA LGITATFWHG NTLVRETEL R TGAIFALLRT LPDALWINAV
TRGATLIIQA ALKPGFDRAT VERSVVRSLA GS

> RXA02760 (1-954, translated) 318 residues
MSDENINEFE QDEDLNFGAS FSDEFADDDF DAEADVEADA AAEASALEAE QDEEETLDA
PEEAEEAEPAA AAESEAPVEE DEEADSLAQAA AALGDTDEQ DADAERYKAR RKFTRELKQ
PGVWYIQQY SGYENKVKAN LDMRAQTLEV EDDIEFVVVP IEQVTEIRDG KRKLVRKLL
PGYVLVRMDM NDRVSVVRRD TPGVTSFVGN EGNATFPVKHR DVAKFLMFQE QAVVTGEAAA
AAAEQEQVVA METDTKKPQV AVDFTVGEAV TILTGAFAV SATISSIDPE LQKLEVLVSI
FGRETPVDLS FDQVEKVS

> RXA02763 (1-984, translated) 328 residues
VKLTDAAREA GVGYGTASRA ISGRGSDVAA TRDKVLAAAE KLGVRTNAMA RALRENKTRT
VGLIVPGIIN KFYTESATVL QDELDKSGYQ LVVSTTGND A EKERAIESM LNRQVDAVHV
APVNPQAKFE KGKFVVVELNR RSDLNRPVT SDDATGLKEL ALHILDQGYR DIGIIVGPAE
LSTARDKAG FINALETEAT QRGIREELFR RVVHSRYSPT GGYEAFAEFR NDLPQIVVPL
STQTLTGVLK ATQENGKIS DDLSLACYGV AEWLAVWPGG ITVFAPDLPA MGAAATQVIL
TLLDAAPLPE NHLISPGQLI VRGTTPKV

> RXA02787 (1-1377, translated) 459 residues
MAQDSLFEPT ETPGSGAGNTS SVSNSKAAASK YFHPGGHAPL AARMRPRETLD EVVGQOHLG
EGRPLRLRIE GSGDASVILI GPPCTGKTTI ASLISAAAGD RFVAMSALSS GVKEVRVIE
RARMDLQGGQ RTVLFIDEVH RFSKTQQDAL LSAVENRTVL LVAATTENFS FSVVSPLLSR
LILLQLESLS DEDIKTVLNK ALEDERGLAG RITATDEAVD QVLVLAGGDA RRGITYIEAA
AEAVEDGGVL DIDTVMANVN RAVVRYDRDG DQHYDVVSVAW IKSIRGSDVD AALHYLARI
DAGEDPRFIA RRLVHSSSED IGMADPSAMQ VAIAAAQAVQ LIGMPEARVN LAQATIHIAL
AFKSNVAVIMA MDAALTDVQQ GHIGTVPAHL RDGHYEGAKK LGNAVGYSSP HDDPRGVVRQ
EYXLENLRDR VYIEPTTHGG EKRIAIEYIGR LRRIIRGKT

> RXA02830 (1-495, translated) 165 residues
LEPDSIGVSLF ERAGRGALAT GAGDQLLSQA RRLIALNDEV YARLNAGAYE GEVTLGVPPQD
VIFYVPIRVL QQFARDFFRV QIHLSNFTL MLKEQFRRGE IDVMLTTEDE LGEGETLQAQ
RELIVWVGAGP GSANTRRPLP LAFERACIFR SFLQRRLDAN SIYWQ

> RXA02831 (1-408, translated) 136 residues
MTHRITPELS AELRGVAHSL ADAARPVTLQ YFRATAVAADN KGALRGMAYD PVTIADRASE
QAMROILARL RPDDAILGEE FGPKAGTTGL TWLVIDPDT RAYIAGAPTW GVLIADSDQD
GPLFGIVDQP YGGERF

> RXA02880 (1-414, translated) 138 residues

VETQAFQRQN TGLIAMVAAD ASNPFLEIF RGAQHAASSTQ GYTVALVDAR ESAIKSREVL
DKIVPHADGL LLAASRMDSG EHKVAREIP TVLMSREVQG IPSVMVDNYD GAPKAVVHLV
DQGCRSITYI AGPNKSWA

>RXN00031 TRANSLATE of: rxn00031.seq check: 1852 from: 1 to: 402
VAAQGWLAGNIGIEDHVLCSDATRTQLTWERVQLGGATAGKSSFHNDIYENQVSEFKHLI
TGLPDVGTALLIGHWPGVEELAHYFGIRDEHPGWDQMEKFPTSIAIVLEFNTFWSKLE
RNSARLTDFVIRPG

>RXN00035 TRANSLATE of: rxn00035.seq check: 7800 from: 1 to: 357
VPLYQIASLIEDSIDVGLTSLIDQRVPSTNELAAFRINPATARNGLTLVEAGILYKKR
GIGMFVSAQAPALIRERRRDAFAATYVAPLIDESIHLGFTRARIHALDQVAESRGLYK

>RXN00049 TRANSLATE of: rxn00049.seq check: 4399 from: 1 to: 687
MPTPSQHKDASTAQTNDQVPTGRRRAQKREQTRARLIITSARTLMAERGVDNVGIAEITEGA
NIGTGTFYNYFPDREQLLQVAEDAFAESVGIALDQVLTKLDDPAEVFAGSLRHVRHSLE
DRWGGGFIQMGAAHPVLMRI LGPRARRDLHLGLETRFTIEDLDLATTCTFGSLIAAIQ
MALSAQDSDNDKDQIFAAAMLRMVGVQAAEAAREIASRPLFEISPVKQC

>RXN00291 TRANSLATE of: rxn00291.seq check: 8375 from: 1 to: 1572
VATVAIVVAICTGIFAVLMMDQMKTEAEHTALSIGRWVASNPQIREEVALDTQTGANPSA
EELADGDIQAQAANERTGALFVVITDGLGIRLSHPDEERLGEQVSTSEAAARGEETM
AETGTGLGASARAKVPFIAPDSSVPVGEVSVGFERDSVYSRLPMFLAALALISVGLGILG
VGVAMGMRRRWERTVLGLQPEELVTLVQNQTAVIDGIDEGVALSLPNGTIGVHNEQAQSM
IGAGPMSGRTLKELGLDLGLDGVVLHGQHPETVAHNGRILYLDFHPVRRGDQDLGVYVITI
RDRTDIIEISERLDSVRTMTHALRAQRHEFANRIHTATGLIDAGRVDAAEFGLDISRNG
QQSHPLIGSAHLNEAFLSSFLSTASISASEKGVSLRINSDTLILGTVKDPEDVATILGNL
INNAIDAAVAGEAPRWIELTMLDDADTLVTSVADSGPGIPEGVDVFATATQIGDSEDNER
THGHGIGLKLCLARALSRHGGDVWVIDRGTEGAVFGVKLPQVME

>RXN00363 TRANSLATE of: rxn00363.seq check: 1381 from: 1 to: 720
MSDMPTKRVPARSLTDQVMDVFRESTDLMVTGWEYSVYQVSDQLGISRSPVRDALLR
LEEAGLIRFTRNRGFQIVETKPSDVAEIFALRLGIEPAAAYRAAQLRTEEQHHEADIIA
LMAQAEADNDEAAFTHDRQFHRQIMTMGHSQRGADLVEKLRATRI LGASTAGNKRKTLG
DILEEHEPILDAIKRQSAEMARATMREHIQVTGKLLLEQAVEKSGEGAAQKIWDQYTAGV

>RXN00464 TRANSLATE of: rxn00464.seq check: 3000 from: 1 to: 774
MSERQLEKSIHAEVLAREARNIEVFTGAGMSADSGLETYRDDKTGLWSNVDPQAMASID
AWRKDEPBMWAWYRWAGVAARAEPNAGHQAIYSWEGSDTVEHVHITQNI ONLHERAGS
SDVTHLHGLSLFEYRCSDCATFWEDDKNYPQEPARLAPPQCEKCGGLIRPGVWVFGENLP
VEEWIDIAEQRIAEADLMIIVTSGIVHPAAALPQLAQQRGVPIVEISPRTRELSRIADFT
WMSTAAQALPALMRGLSA

>RXN00467 TRANSLATE of: rxn00467.seq check: 7535 from: 1 to: 669
MHISDLPRSDQYLKTIWDITELLDDQPAALGDIAEKMNQKPTASEAIKKAARGLVNH
EKYAGVTLTEQKTLAI DMVRRHRLETF LHDVLGYTWDVEHADADLLEHAASDQLIERI
DAHLGRPKDPHGDPIPTAEGVIEESPRTTLEAVQPEFVTISRVKDIDPELLRYLAQYN
VSPGCRITVASGFLAGMVHVVEGTDTSFPLAETQLPLITVQD

>RXN00486 TRANSLATE of: rxn00486.seq check: 5776 from: 1 to: 909
VLNLNRHLHIEFHLRGITITVAEBSMNYSRSAISQOMALLEKEIGVKLFKSGRNLIFYTE
QGEVLASETHAIMAAVHDHARAALVDSLSEVSGTLKVTFSQSLLETLAPKAIARLTEKYPH
LQVEISQLEVTAAEELRARRVDVALGEEYPEVPELVEASIHREVLFEDEPMLLVTPASGP
YSGTLPELRDIPAIADPPDLPAGEVWVHRLCRRAGFEPRVTFTETSDPMLQAHLVRSGLAV
TFSPFTLLTPMLESVHIQPLPGNPTRLTYTAVREGRQGHPAIKAFRRALAHVAKESYLEAR
LVE

>RXN00551 TRANSLATE of: rxn00551.seq check: 7796 from: 1 to: 471
MLAGPMNLNAEELAVRVRPALTKLYLVYFRSSVNSDLSGFQLTILSRLEENGSPSRISRIA
ELEDIRMETPSNALHQELQLNLVERIROTDRRGVQVQLTDHGREELERYNNERNNAEMAR
LLEMLTPQLERTEDLVDIITELAEVYGSWKETDSGS

>RXN01160 TRANSLATE of: rxn01160.seq check: 9223 from: 1 to: 975
 KSSNKISDLARQLNLFPYTRYKGRVTMEAADLGGQSSQIMEDLNRLWMCGLPGLLEPGD
 LVLELDHSPFKEVKIHNAQGMKPLRLTPTAGVLLLTLESLESLPGIAKQCAVVSAAKRLR
 AIMGEYSSTVFDSTGEDLOAEVLEIIRDAMDLDHQQVSFEYHSHRSNDTSLRQVSPAHIFT
 HEGETIYIKAWEEAVNQWRTFRDLRIRSVLLDSKAVHPARGVSVSTDDPFEFAKSSDIAT
 LLRLREDAMWLGNYMAMEVDETVPEIRDSGFSWHTVHFLLSRDWFVRFAIGHAEHLKVT
 SPEDLRKCIQKAKFSGLSAYDHHVE

>RXN01211 TRANSLATE of: rxn01211.seq check: 9180 from: 1 to: 1257
 MNKDEFTAGTWARWFSRGVSLASPVTPAPLNSWRRLPNIAKYTLYTRVSLQAIPTVVLSSA
 YFLGIVANAGTLNFSFVWLLGFSVILLIVTVLVVEYQPSLNHPRRSVPQFFFTGLVLNV
 LGVVVSVVVLQIFGLNMSDNTATALIFTTCTCVFLSIAYIPWMNYRWVWLLAMSVAVLWMT
 STTDDYLSALWVVIPLMAGTVRLSVWTVDVNKEVERSRLEASLRVTEERLRFAPQLHD
 TLGQHLAAMSVKSELALALAKRGDORLENELRELQKLTRTSMSEMRDVVSCYRTVNLATE
 IEAKSLLADAHILHSVIGTTSQVSPAHRELCAWLVRATTNILRHSDATDATLTLSSTE
 VRMDNNGVKNKIDIGRLSGLSALRSRAESAGMTLIVSRDDQGFVSRMLINAPANTPAEKEA

>RXN01315 TRANSLATE of: rxn01315.seq check: 4618 from: 1 to: 651
 VDIEEQPSLRLEIKRQMTLEAIEDNATRLILERGFDNVNITIEDICAEAGISKRTFFNVVESH
 ESVAIGHTAKPTDEEREAFATRHENIIDTVFDLVINLFGNHDNSKSGVAGDIMRRKE
 IRVKHPELAVQHFARFHQAREGLEHLIVEYFEKWFGSQHDEPADREAIAIVGLLISVML
 QGSREWHMPQGTQADFAQCCRKAIKNTFLLRGGFSE

>RXN01349 TRANSLATE of: rxn01349.seq check: 9951 from: 1 to: 777
 MATSRDAENIDQAGSEFIESDSGHTATPEEVVATALTFFAEDGFSETKLEKIAKASGMS
 KRMIHYHFGDKKGLYIKAVSYALLRLRPEAEAMQLDSAVPVDGVRKIVEALYTCITKHFE
 AVRLLLMENLHSQDSVDSTAAYSDESNNVLLNLDKLLMGQDAGAFRPGISAEDVLVLSS
 LAIFYRVSNKVTLLKNLYSLDLESEANIEGMRKRVVDTVLAFLTSNIQNSGNSSYLVGGKT
 AEPETDDSVYSFDTDFEN

>RXN01368 TRANSLATE of: rxn01368.seq check: 7182 from: 1 to: 312
 MEDSAGDVSAKLKAGQTRTALEMTLDDLFGAVEQEWQEQALCAQTDPEAFFPEKGGSTRE
 AKRICQGCQVPRDECELEFALEHDERFQIWWGLSERERRRLKREIS

>RXN01445 TRANSLATE of: rxn01445.seq check: 6964 from: 1 to: 993
 MIPLINRVFFAALPLALVATVWLNAWADHLLLTGFIYVLAWEYATSRGRFALALILGVE
 WILIAYGVALERPLEAKDSPSLITEILLIILVAAGTGAGRWKILSERKQRAITQOEIIKKI
 RTDIAHYLHDSMARSLAIMIVQSKLTELEPDPKKIQEKLNSIAKIQCEAVADHLQVRLR
 VVEESAETKATAGAWAAVSIHDTVNSATQLLVVAGHVVSFDSRKKNYKLDHIAETAFALA
 FNEAVCAETAKHSSPPKANVTIRITEKAQSLQILVMNPIGDWHANGESAIPTGVIGVESLTR
 RIRNIKQVCVTSLQGYWKVVISLPLKCEDS

>RXN01773 TRANSLATE of: rxn01773.seq check: 9269 from: 1 to: 477
 MTVDLYQARIPFQDQGRVDFDHTMITHIQAGLHLGGCRAAGLLPIPAHIDHIVRLTADEY
 DTQSAQQLSNTVLDVLDTTTQDLKALWPVAEHIATTIPESENVLIHCQMGINRSAAALMT
 RVLMRLNDCTADEAIALLRDRRSPFVLNFEHFVEQLRAL

>RXN01845 TRANSLATE of: rxn01845.seq check: 6514 from: 1 to: 408
 MINSWAIETTCALYLPVEALAEVVDAYPQLALAMRMQQDQLVRSREREQAQTTSTVSEQ
 RVAAALQHLDAKLGQIRQDGSLLQVRLRRDDVAGTTVESASRAMARMKKTGVIDSGREW
 IAITNHQALADLVAGL

>RXN02097 TRANSLATE of: rxn02097.seq check: 7698 from: 1 to: 3372
 MPAGIADMTDSLLGWASQTELDLNRQLAGVEYFQIQLRHDELERIHFYQFTFLSRQVGA
 GASGLDLPFEMTCLTVTTLVSRASRISDPADFFGEYIGGLGLSAEHAADVLEGLTEKFAQ
 AGLLVPEGTASPLELLSIHAGISNHEVAAVLTVENGTTIEYPMFDVAVRLTLPFWAQTLI
 GGVQELIEFATTHRTSWSDRQRESSLPAMIDEIVVAELRERPVGTADRENSVGVVALREL
 RLRLDLDAERKVCRLRLPEQRVSDDEINWRVSELTTRIFSTRRAWGDTSGYSEALDITVE
 RQIRETTVTDTSNQITWVVPVVDNDPVLVFSARGENLTKVSLHHQEYIYVLAPEAKLE
 MDTVGQEPVPIEQFLVEGWSWVCSRVDARGLSLKVNEKVRICDPRRRVAFHHPAELPV
 HVRISISGLPVHAQSLIAEFPTTSLSQDETWMLISAFAGVGAAGEETAEPEFLEVPADGG

LFAIFDPEIYDAPWVGEYLVRRLGRPNESFRPEFAIVEDMTTEFEVASGASFRIPITTTGL
SEASLRVRSSEKGHFTAEPLRVTEATDPNASFVVTDEGDQMPFRVFPQIAIELEPLTE
PPTWRVTRTCGRDLDGAGELRIRTVGDVDPKVSVRNHHGSPRLTKVMVTPDNRTWI
ASMKEIAASTFVMPGRSIEFEWTDKRVDRRVSTIAVIDKTENFTGITIEDGKLVEFEELA
AGRLAAWVWPQTAPVWSAVELAVTGPPELPEVLVAGNLIQLHTADPFTTSVTPLSP
GKAAVTVEQEGYSAQTEEYAQLSAFFGGEVEEPPISDAVVPALWDVSHWITEGNTHEHL
PVVHAALRSSPAAALKGLSASLVPAQALPGKVISSGLAASPFTTESPAVEVHRTAWIGTL
QLLGALPSAFKEAELGNRTPLLPLGQLEEVAGKNILSTLATGRDSTLDTACTDQSTVA
IAGMNETQKALLDMFFSNADIVPGPLMEDNTRLMVAFETFKKRDALREVLQTEGLIKTA
VELLRAMRGTRQQLYSSAIRFDKLDGVTNDNEENMWALTPEVSLVFALSSRLHAHELIG
KTRTLDRAAGWGRIADLVDPDLVTDGLISAEAMVLGARNPLGVD

>RXN02266 TRANSLATE of: rxn02266.seq check: 6363 from: 1 to: 513
MTQDEHPROADSHFNMLLPDGNENAHQLSVALNQVAHLLAYDADSSIHFRDGLSLASYRI
LFSLWTDGPMPLQVTDKTMKKSIAISNLLKPLLAESLIVQVTAENDRRSKVLSSEKGT
TYIQKTATRQNALESEWFGTLTDIEQDLLESLLRKLKLLDSNRASKVRNRNRSN

>RXN02270 TRANSLATE of: rxn02270.seq check: 1360 from: 1 to: 621
MDQARPNRTHYAMVELEQHGLFSGVVTQNVGLHAEAGTKNLVALHGDLAHVMLCNGCGF
EDRHLFDEKLEAANPGYVASIRLEPGAVNPDGVDLDEEQVRRFTMIGLCRCGSLMLKPD
VYVYFGEVPAARKKDLKLLDASSLLIAGSSLAVMGYSYRVIVIEAQRQKGQVSVINGGPG
RADSRVDILWRTRVAPAFDDILDALDL

>RXN02362 TRANSLATE of: rxn02362.seq check: 8315 from: 1 to: 3699
VTISRRLKQERSFADDLQDLKTLNDQLRFTNAKQARISGIGNDGKKITRPTFLALDFQ
LTVEEYETIAILVEAVGNGQSKPAIKDLFIEYPLVLAALSGTAMLDQAEGGFPAWFK
RTQVSVPEVHYDAIRKELVNSIRKNGLTFSLADLNRRYVGLIQLHSGLSAKMDLALVK
FTDHTRAENCGWDSGEDFASVAKSVFSSGDNLLTTESLKQLVTHIPARSVDIFARVYELT
NWYRDLKDLNEVEAFVGTGHLPELSEKILLECLSGEAEQIAEKTAAAPASLENLEPPHLY
LDQPQSFELSIVFPAISKTAALQIPAPEWTVIYDGNISIKVRPEQDWSYGGFAEYRLPLOK
LSSLRVITPTPEKSLILIEGFHGNPIMPFKNNQGPYANQEMLSGNVATVPAAPAIIRAR
MRASKTFNYQDLPLSGWNKWKVIRSIFLKRAESTITVSHSGFRKELPVRRKVDVQWITEDL
TIENLQGLDHEPVEFHTSPRIEFPPTSGSNWVIQYSQILPDGSLIEMEDYPVEPENEGYELD
LFEESDDFPWVGQFLVTLTKDEKVEYTRKFNLAELGLDLSLTFSSGGGPNRRFRYPSINQGT
GTETAFDRFSSNSEKHIFRFPDEIIGLDAFTSQAFNIASGDFPEDYNLDVFTPPQLHYQ
VPVTHSQTKWESTKTTLDNFDFADGNLQIRFPNEVYDPNLKIIKMWAYKKFESSEPKYLS
KIGSSKWSIFMDRIKELMDDDAQFLIAEWAFAESKDQHREKIISEAKRTKISNAAKLS
ARFPQOASSHIATIEKKPLLAALAEIKLSTVELELGRHTSKRLEGWASALNPLDPPKVD
FQGTSGSLPDTHFVVGPLIVEVREKEFLSQWQPKVPSVKAVVANDPSFELDPQFDPFLTH
RWMFAPRSGKVLLPQELRTVWDARENMRHLAQENLHVKS IQDFDDATSTYLTSDPRFVA
LDELKKSIPSNHSFESFIRSKLAELSFEVDVDTAGDIHRVPWIGLIQEMNDRLILQIQY
ETEERAIERRNSQSYIREIGGSELWNILKGNSEGLSLAKQCAPQATEINVRINSGLEAMR
NGLGADQFSAEFISADSRLRAQLEWLENRRRLNDLQLPTLDFDAEKYEYILIDLHGDRI
KVTARELSTLASEHRRGNAENWLYAPYVSFIYSLLNRMIAHEVIRPIAQINYSRHDWANA
ARLIPRLTGFLVSAEAKVLSAINNNNNIIPAI

>RXA02365 (1-540, translated) 180 residues
MELCQTKRQG MGGMDYLED RVELRYTMPL GEIIFDDFM LKSRTKGYAS LNYEEAGEQT
ADLVKVDILL QGEPVDAFSA IVHRDNAQWY GNKMTVKLKE LIIPROQFVQ VQAAIGSKVI
ARENTRALRK DVLAKYCGD ISKRKRLLEK QKAGKRMKN IGSVEVPQEA FVAALSTDEA

>RXN02450 TRANSLATE of: rxn02450.seq check: 5093 from: 1 to: 555
MNLKDLKAAETQRQFIDVAHELFLHEGYGSTSMNQIAAGGSRANLYLHFNKPDLMMA
KMRELEPAVRTPVLKVPDLPEHTLESILRWLDSMTVEVWAKAKVFGAMEQAMVEDAAVAD
EWLSSMQRLSQSVPELVENEERRVGLFASLIMGMDRNFYFLYVRQGDVDEELKLAVARQW
LAVFQ

>RXN02493 TRANSLATE of: rxn02493.seq check: 2568 from: 1 to: 1239
VSTLLAFVLGVLMGALPAYTKIKDRMRHKSAVTLSENQVTVVQGVHLALAIQGSPTGI
TVVDRTGDVLLSNGRAHELGIHVHRSVDGNGVWRVAQAFQDQETHSLDVHPDRNPRRPGS
RITAVQAVVKPLTLIDDRFVVIYASDESENVMESARRDFVANVSHELTKPVGGMALAE

ALMESSDDPEQVEYFGSRLHREAHMADMINELISLSKLQGAERLPDMEPVQADDIISEA
 IRTQTLAANDANIEIIRGDRTGVWVEADRSLVTALANLISNAINSPKSVPVSVSQSIR
 NDVVMIIRVTRDGIAGIAPEDQGRVFERFRVDKARSQTGGTGLGLAIVKHVMHANGGSIS
 LWSRPGTGSTFTLELFPVYHSPESKEPAGSKQGPSLDSPIRTTASKASGRREKS

>RXN02506 TRANSLATE of: rxn02506.seq check: 9674 from: 1 to: 882
 MHLNLQLEFFIAVAQHGGQINRAAEELISQPALSRQISALEKSVGAPLFEHRSGVSLTKA
 GEILHHEEARLTLRMRQSVVDEIQSGEHLITSINIGVPPGPIIDWLRCQLIDLGPETRISL
 IESPTDDQGLKLLKQRELDIALCRQSEAFATTLVHEQDEGLIVVRKNSLEHQKVAGKDNAT
 LFDLEGLRVLAHSRGEVRIQEELKNAMLAAGVNATWIFRKFGQYSSLIADLVQADVALT
 TEESARTNFPSPQWVPIEGEDASGNDLVVRTWITWNPQPTPAVKALIQKIEDGN

>RXN02553 TRANSLATE of: rxn02553.seq check: 2092 from: 1 to: 564
 MAVKRNELEPELTSNPNPLSAEVVHLYPEETRLATEILERTNNWLAKEGIPPLPPAEVVA
 ISLHLVNAGFRTEDLAETYVMTGVFEQLFEVIDSSFGITLDRQSVNAARFITHMYRFVVR
 VHHDGGLNDGMSVLRSLEISHPDSVACAERLSQILSLRLGAELSSDEQTYLALHVARLA
 EDGTTAD

>RXN02620 TRANSLATE of: rxn02620.seq check: 2192 from: 1 to: 666
 MAGAVGRPRRSAPRRAGKNPREIILDASAELETRQGFATTSTHQIADAVGIRQASLYYHF
 PSKTEIFLTLKSTVEPSTVLAEDLSTLDAGPEMLRAIVAASEVRLLLSTKWNVGRLYQL
 PIVGSEFAEYHSQREALTNVFRDLATEIVGDDPRAELPFHITMSVIMERNNDGKTPSPSL
 SADSLEPETAIMLADASLAVLGAPLFADRVEKLTLELIKQADAK

>RXN02758 TRANSLATE of: rxn02758.seq check: 5860 from: 1 to: 1299
 VTLEIQNESQETIAELEAGQQVALREGYLPVAVITVSGKDRPGVTAAFFRVLSANQVQVLQV
 EQSMFRGFLNLAAAFVGIAPERVETVTTGLTDTLKVHGQSVVVELQETVQSSRPRSSHVVV
 VLGDPVDALDISRIGQTLADYDANIDTIRGISDYPTGLELKVTPVDVSPGGGEAMRKAL
 AALTSELNVDIAIERSGLLRSKRLVCFDCDSTLITGEVIMLAHAAGKEAEVAAVTERA
 MRGELDFEESLRERVKALAGLDASVIDEVAATIELTPGARTTIRTLNRMGVQTAVVSGGF
 IQVLEGLAELELDYVRANTLIVDGLKLTGNVTGKIVDRAAKAEFLREFAADSLGKMYQT
 VAVGDGANDIDMLSAAGLGVAFNAKPAKLEIADTSVNHFFLDEVLHIMGISRDEIDLADQ
 EDGTFHRVPLTNA

>RXN02910 TRANSLATE of: rxn02910.seq check: 4179 from: 1 to: 705
 VEIRWLEGFIAVAEELHFSNAAIRLGMPQSPSLQLIRLSELGKQLFDRSTRSLVETAA
 GRAPLPHARGIVASAAREAVNAAGEIIVGVVIRIGFSGVLNYSTLPLLTSEVHKRLNPV
 ELELVGQKLTREAVSLLRLGALDITLMGLPIEDPEIETRLISLEEFCVVLPKDHLRAGEG
 VVDVLDAKDGCVTTPEFAGSVFNRNSTFQLCAEAGFVPRISQQVNDPYMALLAR

>RXN02946 TRANSLATE of: rxn02946.seq check: 8998 from: 1 to: 459
 MTTEAPIWPAELFEDLDRNGPIPLYFQVAQRLEDGIRSGVLPPGARLENEISVAKHLNVS
 RPTVRRAIQEVVDKGLLVRRRRGVGTQVVQSHVTRPVELTSFFNDLKNANLDPKTRVLEHR
 SLQQVPSQKNSFFQVTKSSSSAASAPPETSP

>RXN02954 TRANSLATE of: rxn02954.seq check: 5707 from: 1 to: 738
 MSAAALPHTAADPVHTTPAKPLLDHVLDSLGRSISGEMAGSTFKLDQIGKEFGISRTVA
 REAMKALEEGLVAVASSRIGITVLSHEHVAWFDKAIIRWLEDERQREQLQSLTELRIAL
 IEPTAARISVALHASSAETAIIGDLAARMRNLGEAGRASQEFLDADVKEFHILQYCHNE
 MFRAMAPPKIAVLVGRITLGLQPDRAPEEVLDNHDLAHLASVRNADLAEKASRSILNEV
 RDALTS

>RXN02990 TRANSLATE of: rxn02990.seq check: 3521 from: 1 to: 597
 MDIQAEKIEKLKALDNFERAHARGESDFFDHEKEEKKANVRRRALLLNQRRARSVNELS
 TRLKALEFEEDIINEVIGDLTRSKLLDDEVFAETWVRQRAARRGKSSRALDRELQEKQVD
 KQTRAAALEIQDQADERDARAVAVKARSETKIPQDRADYDALKARRVVGALARRGFFAG
 MMSDLAREALDARIEDLN

>RXN03023 TRANSLATE of: rxn03023.seq check: 7800 from: 1 to: 357
 VPLYKQIASLIEDSIVDGTLSIDQRPVSTNELAAFHRINPATARNGLTLLVEAGILYKRR

GIGMFVSAQAPALIRERRDAAFAATYVAPLIDESHLGFTRARIHALLDQVAESRGLYK

>RXN03071 TRANSLATE of: rxn03071.seq check: 1804 from: 1 to: 339
MLAPWQLHKDDIDIVARNEQITEAFERDVVYAEFLDASGQIPSSQEFFRVSLTGQYLPDS
EVLLRLRPVDSGPAFQSLTFPELENGQIVLVNRGYESSGTVPEIEPAPSHQ

>RXN03072 TRANSLATE of: rxn03072.seq check: 9857 from: 1 to: 435
MEDSGYTVQVGINTEQISDVTGLDLGTDYVQVAEGEPGVLPMPQMDRGNHLSYGGFQW
IAFGIMAPLGLGYFIWAEMRERRRDKAEREQMAELNTLPEVVTETPEVVETAETPTTAAAS
KRRSRYGQDHRNHYEKISKRDQERF

>RXN03090 TRANSLATE of: rxn03090.seq check: 1334 from: 1 to: 1221
MAKSTPLIASLRWRIVLWMTAVVFLTLASVVIITRSVLLSEVTNTANSVEQIEEFRFR
AAEGIDPTTAQPFESGHRLEMEVYLSRQIPDENEAVIGIFPGELIQVDVYQSLSGAHPLE
HSDPLISEIRQTTLNSGVFSDLERGTTWHGKVNQFTASGEADGEFVVAFFADNLKQDQNG
QIQILILITGGLIASILIAMIAGQIIAPIRKLSVSAKISNSDLTWRVPEVGRDEIAQ
LARTFNAMLDRIEIAYNDQRFVDDAGHELRTPIITVVRGQLELLATTPEEQARSIELAT
TELDNRMSRMVNDLLTLAVADSGTFIHAHPTDVTDLTIDEDKARTISORILLVDARPRAS
SASTSSGSPRQCLELFGNALRYSDDVVELSGSGFQGVWPPHFSHLGS

>RXN03100 TRANSLATE of: rxn03100.seq check: 173 from: 1 to: 318
LYQDQKVTSDPMEAAYSLSYLWKEMVEKADSDVAIAQAADGTTFDAPEGTVVVGDDNH
HISKTRPRIGRIRPGDLIDTIEWTDSFVDPDPYLYSSYDWAKTAAATS

>RXN03127 TRANSLATE of: rxn03127.seq check: 8598 from: 1 to: 720
MESSKKTSSRSRSTQEAVRDIKKYIRDNRLRTGDLPLSEAFCEELGCSRSIAIREAIRAL
VTLDIVEVHRGYGTFFVSRMSLEPLINGMVFRVTLNDNTSVENLFYVVDREILDSLGE
LIEVFDDDBRELLDLVDKMRHNDQGESFVVVEDQKFRALLARTKNPLIRELNDAFWQI
QTEAQPMNLAMPADIDETIKAHSDIVEALSSGNIDDRVSAVLAHYAPFRMISNMLDAH

>RXN03136 TRANSLATE of: rxn03136.seq check: 9294 from: 1 to: 2415
LGAHSANSIRGVIDRLDASTVIVADVHWADVESMOKLIEYSMRMVSGRFALIMIGLDEE
NLVHFDEVVSLPSIADSTYVLPFPMSEIEIRQALTDVGRISTTTATDIQRITGGIYGRV
KEVLHSESVDHWRMPNPNIPIQSWHANLLRRITNEEVWVHLLAVAVLPSGGPDLVKLI
GNDPTGMLCDDAVRSGLLRVLPSDQGPQVDLVLPIDRAVLQSRSTPLNLAQLHKAEEYY
GKWQKDAQLEHEAFAAIDPNDPAVRALAQRGYALGRTHGWMESAHLAANRTAHQEE
SNKYLLESIDSLIAAADLPQARSRASTLDLGETGIIQDQSMGLYLAIEGRRLEARNLLHR
ASEELLAQHPIDPIHGPRMAQRKVLNLDVWNPEELLVWADRAVWATEEDAGEKVEAAQI
SLIGOSLIDGCLPEDKPIPGETTLHAQRRHMAMGWLMSVHDDPVTARQKLERRTSINGSE
RISLWQDGLARSLLLLGEWESAARTVEIGLARAEOFGIRFLEPLLLWSGATITARGNS
DLARNYMSRLSDQDQSFIVQSMPSAMCRMVHRHNEIPGAIVAGEQELIAAHKHVNAP
GEFWPQDVHATHLIRIGETERAQELVNSTLEELRGSDIMSAAKIAVPMDAKMLTHHGDDVK
KGKFRDDALDMDLPLTPFYRARCIFEGQALRRQGGRRRADEQFARAASLFQDMGADA
MYTLANRERVVGLQRSEQAGGLTPEYEIARLVSSGHANREVAQELFLSPKTVVEYHLT
RVYKKLGINRMELAEALKYSHDA

>RXN03143 TRANSLATE of: rxn03143.seq check: 755 from: 1 to: 1131
VKTSGATIAIRIERVLIWGLHLLIAVLLVLCWRASHGWVWVLAFGYGVVVAGVVPNSPF
KNHPMAWFLVLSLLWASLIWDGPEPAYLVFPMFFLAVLITPLKSAIIITAILTAIVVTL
AMHLEGSVGVVTPILGALVAVWVGTCFQOLLAQALKELVDARASAI RASKSAGEQAEAR
IAGEIHDTVAQGLSSITQMLLHAAEKRVDDPQALSHIRLARQTTADNLAETROI AALQPT
PLIGADLPVALARLSSTTFMCQNITFEVDGSPRVLPDAMEAEIVRIAQTLLGNVVRHAQA
DSAKMTLIYQDDQILLDVIDNGQGFDAEVIRKKSIGLPTAQRRAEGLGTTIIESTIGS
GTGISAREFPYPQKDQK

>RXN03155 TRANSLATE of: rxn03155.seq check: 4295 from: 1 to: 1668
GYPPPTASKDAAGGLPQILRELLDTPIDHWSNDRPTTLPEHVVTIDIKNPVLEVA
SHFFDGPCTIGDLDAADFVEDGTLIHENGTLFRFSPEERTLVRASTPFSMARSPREWST
EGGVDKLIAAGNLPARLHVHEELPRADEQRAFLALYGGQSFEEAASAPFYALATNMPAL
RGDPTDFMADALDTGHYREVPRPDAPEESQIHDFISGWLALVYDDPLTARRLLSRRGFS
DLVGLQSAFLARAHVYVLEGEFQESAVVERGLATGDRTGASLEVPVHWTGAQVAAMTGR

TELANHYLQRLTVDPDDAFILQKLSASMGLITASMTSDTRAATLAGDRMASVVYTTNQ
PGFWANEDMYAISLIRTGRIIDAAAAMDGIPOSTIPSLRARNLVPOANIEIQRGSTARGV
KMLSEAVDLISSVNMPPAYEARILFEYGLVLRMRGRSSQAEMFTHAEVEVTAMGAVTLAA
RCHGERRVAGVGPRRSAQGLTPQEEQITLVDVGDGCSNQEVARELSLAKTVEYHLTRVYK
KLCVSSRGELRELLKV

>RXN03181 TRANSLATE of: rxn03181.seq check: 5678 from: 1 to: 414
VETQAFQRONTGLIAMVAADASNPFLEIFRGAQHAASTQGYTVLVDARESAIKSREVL
DKIVPHADGLLLAASRMDSGEIHKVAREIPTVLMSREVQGISVSMVDNYDGAPKAVVHLV
DQCCRSITYIAGPNKWSWA

>RXS00070 TRANSLATE of: RXS00070.seq check: 7466 from: 1 to: 432
VGINRISQGSAPKLGVSRTRQRKAVIDVLEEIDNFASAKEIHHELSTREHNVGLTIVYRTLQSLADIGA
VDVLTVTGGETLYRQCHDEGHHHLVCTNCGRTVEIDGGPVETWAQEIATKNGFALSHEABIFGLCAD
CKEKV

>RXS00133 TRANSLATE of: RXS00133.seq check: 4189 from: 1 to: 813
MLFVRRLLSLKTATGIPVMTFATVLQDNRLQITQWVGLRTPALQNLVIEPGVGVGVRVATRRPVGVS
YTRANVISHKDSAIQDEGLHSIVAVPVIVHREIRGVLYVGVHSVAVRLGDTVIEEVTMTARTLEQNLA
NSALNRNGVPPDGRGSLKARNVMNGAEWEQVRSTHSLKRLMANRVTDDELRRDLEELCDQMVTVPRIKQT
TKLSARELDVLACVALGHTNVAAEEMGIGAETVKSYLRSVMRKLGAHTRYEAVNARRI GALP

>RXS00144 TRANSLATE of: RXS00144.seq check: 1916 from: 1 to: 576
MSERNASVLELLNEDDVSRITARIAHQIEETALDSKADRVMLLGIPISSGVPLARRLAEKEEFESGV
VDTGAVDITLYRDDLNRNKPRAALQPTSIIPAGGIDNTVILVDDVLSFGRTIRAAALDALRDVGRPNYIQL
AVLVDRGRHQLPIRADYVGNLPTARAEVSVMLTEIDGRDAVTLTREDSEGS

>RXS00205 TRANSLATE of: RXS00205.seq check: 3895 from: 1 to: 1107
MASETSSPKKRATTLKIDIAQATQLSVSTVSRLANNASIPESTIRVVEAAQKLNRYRNAQARALRKSR
TDTTIGVITPNINENPVFSSLAASITQKAAAREAGVSTILSNSEENPELLGQTLAIMDDQRLDGIIVVPHIQS
EEQVTDLVNRGVPPVVLADRSFVNSISPVTSDPVPGMTEAVDULLAADVQLGAGPQDTSSTGQRLRNT
FERLCVDRGIVGASVYVGGYRQESGYDGIKVLIKQGANAIAGDSMTTIGALLALHEMNKLTGEDVQLI
GFDNNPIFRLQNPPLSIIDHQVEIGKRAFEILQKLINGDTAQSXVVIPTQLSINGSTAVSQKAAAKAA
KAAQKAAAKAANTQCHEVSLDGL

>RXS00470 TRANSLATE of: RXS00470.seq check: 9539 from: 1 to: 1269
MGESPEKVAFRVFPDGLVSQGHMIEDMSNTPAPYTPQPAQAVPLYPTFTRSRDGRVVGASGLAKH
LNVSVFVWRALLI FAALLSGAGLFAYALIWIPTRIEKKSGSEASTSKRWVSWCLVLLAIGGAASVMLS
TGFVAVGLTPIGVVGVGLLMVWLAYDRGVESGPNLLI IATGGVLMVAIVLVMNWNQDQGFVMAVLAV
VLTLVGVAALGVELWYRMWDQLGEERAEEKAAAERADIASRLHDSVLQTLALIQKRADDPAEVARLARG
QERELRQWLFDSDQDTPQTTGTVFTALERACGEVEDIYALRIVPVTVGTDEALTEKTQAAVMAVREALV
NVAKHAGVETADVYAEIMLGEELNIFVRDRGAGFDPNIPDGHGLAESQGRVERAGKVRIKSEIGEG
TEVAITMDV

>RXS00471 TRANSLATE of: RXS00471.seq check: 3433 from: 1 to: 690
MYDVELVDHDSVFRSGVKAELGNVAVTVVGEAGTVADAVAGIKAPVILLDVHMPDGGGLAVLQIND
SDVDTIFLALSVSDAAEDVIAIRGGARGYVTKTISGEELIEAINRVKSGDAFFSPRLAGFVLDAFAAP
DSAAAGAVDPAEKDAAEVSGKILDDPVVDALTRRELEVLRLLARGYTYKEIGELFISVKTVEATHASN
ILRKTQSNRHALTRAWHSRDL

>RXS00481 TRANSLATE of: RXS00481.seq check: 4415 from: 1 to: 585
MLNMQEPDKIHPAEPTLRNIYDVKTSDPKSELVDRSGMSEEDIAQIGRLMKSILASLRDVERSTIGEASAR
YMELSAPOMRALHYLIVAGNAGEVVTGMLGAHLKSPASVTKTLNRLEKGGHIVRNHVPDRRAFLAN
VTDATRGAMRTLKGKHAARRFDAAKRLTPQEREVVRIFLQDMAQELSINNAPWLNTE

>RXS00649 TRANSLATE of: RXS00649.seq check: 7418 from: 1 to: 456
MSTDPIAALEYESTIFARHNRQYTGQAGTNAGVLLDSSGYNLLTLQLRGFSTIGELSAITGLDASTLNR
QTKALLTKGFVERITPPDDGGIARKFHPTDLGNELNNEERTSSQEKYALLSDWPEDLRTFVKLEKLN
KAVETRVGKHWPRP

>RXS00650 TRANSLATE of: RXS00650.seq check: 1698 from: 1 to: 636

MIRVLLADDHEIVRLGLRAVLESAEDIEVVGVEVSTAEGAVQAAQEGGIDVILMDLRFPGVQGTQVSTG
ADATAAIKRNIIDNPPKVLVNYDTDTDLGAIEAGALGYLLKDAAPPSELLAAVRSAAEGDSLSMVA
NRLMTRVRTPKTSLTPRELEVLLVAGGSSNRDGRILFLSEATVSKHVLVHIYDKLGRVRSRTSAVAAA
EQGLL

>RXS00657 TRANSLATE of: RXS00657.seq check: 8495 from: 1 to: 903
MSTEDIVVAVDGSASQAVRWAAANTANKRGIPLRLASSYTMPQFLYAEQVMPQELFDDQLQAEALEK
INEARDIAHEVAPEIKIGHTIAEGSPIDMLLEMSPDATMIVMGSRLGGLSGVMGVSSGAVSHAKCP
VVVVREDSAVNEDSKYGPVVVGVDGSEVSQQATEYAFAEAEARGAELVAVHTMMMDMQVASLGLAAQ
QQWDEVERQQTDMILIERLAPLVEKYPVSVTKKIITRDRPVRLAALASNAQLLVVSGHGRGGFKMGLG
STSRALLQSAPCPMMVVRPEKIKK

>RXS00686 TRANSLATE of: RXS00686.seq check: 3127 from: 1 to: 804
MAGGNREPGRVTSKVIIVLGAFEHTMRPLGVTEIAELADLPSTTHRLVSELTEGGLSKKSDGRYQL
GLRIWELAQNTGRQLRDTARPPQIELYSLTSETAQLVVRDKDEALLIDRAGYTKPIPSARVGLRALPLN
STAVGKILLAFDEFWKQSYLLKPLINASTPKTIIVNPDVLAQLKQIHSGQFAITHDEQRIGGASIAVPV
WHTGKLGAAALGLVVPVTAQANLERYLPILQATSSQRIKATALIPDLTLLASHKNAERKGD

>RXS00719 TRANSLATE of: RXS00719.seq check: 7090 from: 1 to: 1629
VTDKHTMPGEEDDTVFVYHTHKGEMDVEGAFADEEELAPHGGWASADFPAEFYVRSDDSDDFDAEDFDE
TEFNSPDFGEGEDYSEDEWEEIETAFGFDPSHLEALCTVAIVGRPNVGKSTLVNRFGRREAVVEDFFGV
TRDRISYISDGGWGHRRFWQDTGGWDPNVKGIIHASIAQAEVAMSTADVIVFVVDTKVIGITETDSVMAAK
LLRESEVPVILVANKFSDSDQWADMAEFYSLGLGDPYPVPSAQHGRGGADVLOKVLVEFPPEPSKSIIVEG
PRRVAVLGPKNPVKSSLLNKFAGETRSVVDNVAAGTTVPDVSLLQLDQKLKFKFVDTAGLRKKVTKTASGH
EYYASLRTHGADAAELCVLLIDSSSEPIEQDQVRVLAMITDAGKALVIAFNKWLMDPDRRGLDLDRELD
LQLAHVPWAKRINISAKTGRALQRLPAMLEALDNWDRRISTGQLNTWLREIAIANPPMRGRGLPRVL
FATQASTQPPVIVLFTTGFLEAGYRRYLERKFRERFEGTPVRIAVRVRRRRGKGNQ

>RXS00738 TRANSLATE of: RXS00738.seq check: 6764 from: 1 to: 363
CQETDGGFDFGRDMRPGERRSYGTLNDATTQVSHILGNAFTRSLNAEYANLYGQALVGMVMSMTAQW
WLDERTPPKEEVAHIVNLCWNGLTGMEADPKLTPISSAEGAIFGQKESEA

RXS00774 TRANSLATE of: RXS00774.seq check: 6151 from: 1 to: 654
MDKATDALLRTSLASAESALGNAEKLLELRTGCESQAVELLEATPVARDLRQVSSIIYIVEEITRMGA
IAMHVANSVRRYPDPVIPEDMRGYFKEMARLAADMTDHIHQILIDPEPDLDALEMAKSDDAVDLHQH
MRILTLRPWPHDTKSAVDLTLLSRFYERYADHTVNVAAARTYLSLGLHPEEYMEKREQQRADAMEKRW
AELERQPTSE

>RXS01082 TRANSLATE of: RXS01082.seq check: 2555 from: 1 to: 660
LTQWGNNSNVEDYLTALFRAEWEDEEPTTGKLAEVIGVTASTVSA TLKLNPEGVNRYRPGYDIELTPA
GRDIAINIVRRRRIETLYLSEKLGGLGAHELHGEADLLEHAVSPVLVEKMFQAVGYPTLDPHGDPIPTES
GEMTINDGLMLLGLKAGASATVTRVRDGNPSVVRYLTGVGITVGTTVTVVELLSDIATLRLQIGEMFQD
IPLAVANAVRSR

>RXS01123 TRANSLATE of: RXS01123.seq check: 5460 from: 1 to: 447
MRTLAAELNIAKPSLYKHVKTREDIAAHIAIKAFIQLGQSLHEHCESVEDLLAEYRSMARENPIYRLL
TSSEFPRELLPEGLETWAGTFPYLVTHGDPIKQALWAFAHGMAILEIDARFAGPNNGSPADGVWEIGA
RAFDTPQVFDQ

>RXS01189 TRANSLATE of: RXS01189.seq check: 2136 from: 1 to: 609
MISISIADEALIASLATLLSLEPDLVDRPTAGSGEELIETWADPSNRDVCVLDLQGLGIDITAT
RLMETTPDLAVLIIVTSARPQLKRALAAGVLGFLPKTSTADEFATAIRTVHAGRRYIDPELAAMTISA
GESPLTNREEVLELAGQQLSAEEIAVAHAHAPGTTNRNYSQAMTKVGAQNRFEATPRARELGLWL

>RXS01242 TRANSLATE of: RXS01242.seq check: 954 from: 1 to: 777
MYAEERRRQIASLTAVEGRVNVTELAGRFVDVTAETIRRDLAVIDREGIVHRVHGGAVATQSFQTEL
DTRFRSASSAKYSIAKAAQFLPAEHGGLFLDAGTTVTAALADLISEHPSKQWSIVTNCLPIALNLANA
GLDDVQLGGSVRAITQAVGVDGTALRTLALMRADVFIGTNAITLDHGLSTADSQAAMKSAMITNAHK
VVVLCDSMTMGTDYLVSGAISDIDVVVTDAGAPASVEQLRDERDVVIAE

>RXS01607 TRANSLATE of: RXS01607.seq check: 90 from: 1 to: 630

VIRILLADDDHVVVRAGLASLLVSEDDFEIVDMVGTDDAVARAAEGGVVVLMDLRFQDQPGIEVAGGV
EATRIRALDNPPQVLVVTNYSTDGCVVGVASGAVGYLLKDDSPEDLIAGVTRDAARGESVLSKQVASK
IMGRMNNFMTALSAREIEVLSLVAQGGQSNREIGKKLFLTEATVKSMMGHVFNKLDVTSRTAAVAEARQR
GII

>RXS01674 TRANSLATE of: RXS01674.seq check: 1368 from: 1 to: 894
MDNGWPNLQTLALFVAIVEEGSLGAGARKVGMAGPNASRAIAELEADMKAELVVRHPRGSHPTAAGLAL
VEHSRDLQSVQEEFTETWTEGRTEQPLKLHVGAQSMTAEALLPAWVADMTRFPACRVVDVSVMMNSQVI
EAVQKHQLQGLFETETPHVEVRLHARVVQEDKLIIVISPNHEWANRTGRI SLRELSSETPLIVREVGVSGTR
EALQELLADYDMAEPIQVLNNSNAHVVVVEAGAGPAVLGELALRDHLALGRLLSVFEGSGVTRPLTAV
WSGPRRLPILAGELVSIASNIH

>RXS01872 TRANSLATE of: RXS01872.seq check: 8549 from: 1 to: 828
MGNDGGDLRIDDLRSFISVAQSGHLETETAQRGLGPQPTLSRRISRVEKHAGTPLFDRAGRKLVLNQRGH
AFLNHASAIVAEFNSAATEIKRLMDPEKGTIRLDFMHSGLTMMVPELIRTERAEHNPVEFOLHQAAMAL
LVDRLVLADETRDLALVGPKPAEVTSLGWAPLLRQRLALAVPADHRLASFSQGGELPLITAEAEFPVAMR
AGFGTRLMDALAEAGFPVNVFESMELTTVAGLVASAGLVGVVPMDDPYLSTVGIVQRPLSPPAYRE

>RXS02117 TRANSLATE of: RXS02117.seq check: 9965 from: 1 to: 474
VSTDPEEFQAEITDQLAYEIIILLTRYGVQNTPTNKREAIMDRSALILLTRLDQAQGPMTVNELEASFG
NVSTVHRQLKAAIANGLIEVVDDQACPAKLHRTTELKGKEKLQOELLARQQDLTRILHDWDEEDIKTHAK
LLRKHNESLEEYLDMKWPRP

>RXS02288 TRANSLATE of: RXS02288.seq check: 9420 from: 1 to: 846
MSQVIPASSQEKRRERISYVTRHGFAVEALAELEFVSAMTIHRDLEALAADNLVERIRGGARSVSPS
MSELAYEQRRHLHRTVKEALCTAAARLIPGAVVAIDDDSTLESLEVKLPORSPEALITHSLKTMADHR
VRAGMSDRLDLACAGLVFAETDSFLGKATSAQNLNLSADISFVSTTAVRATGVEPALHFPDMEAADTKR
ALIGIGSVRVLVVDSKFGSAGVFKVASIEEFDHIIIDQOCTREQRODLLRNSRAQIHVIDHNGDEILD
PTEEDF

>RXS02573 TRANSLATE of: RXS02573.seq check: 9274 from: 1 to: 444
MTNKTMLVAFDGPSPESRRALYAAKLLQPRTEVILTAWPELHRQAARSVSLITLGVPEPDPAHSAAKLT
CQEGVELAQSLGLEARAHMVESATAVASIAVDADELRPDVITVTRGTSGWKSLWSQSSSTSDSVLHHA
VPFVVPFPDL

>RXS02627 TRANSLATE of: RXS02627.seq check: 3594 from: 1 to: 843
DVTVESQPERVVALGWDGAEAALEFGVQPVGASDNLWAFGGEGVGPWIEDSAYDEAPEIIGTMEPEYEKI
AALEPDLILDVRSSGQDQERYDKLSSIALTIGVPEGGDSYLPRAEQVTMIATALGQAERGEEVNAEYEQ
LTADIRAAHPGWEKTAAYSATATSWGAYIKGSNRVDTLLDLGFQENPELAKQPGDGTGFSIKFSEET
FGVVDLVLVGFAIGMTPEEMAEQVPWQMLTATDRGRSFVMPREISNAFSLGSPQSTRFALDALVPLLE
EHAGE

>RXS02691 TRANSLATE of: RXS02691.seq check: 1824 from: 1 to: 807
MNTMPDQPLNQDGFTASKGVEPDNLPRVLVDGLKPKHQQLREILEICTTQLQEPGDMLEPGRILEEK
GVGSRTIVRAIGDLVASGRILKRARGKGTFAVHSPILSRHLASTSAEMAQKLSATSRILVSSRGPA
DDIADFFGTDRAAQHIITLRLRFPNGRPPYADNGWYNSEFAPDLLENDVNSVYGLDRVYGVPTQAE
QTVTAADAEDTARILDDTPGAPLLRILRQSLSGDKPEVWCVSLYRTDRSLKTLVTRSEDL

>RXS02730 TRANSLATE of: RXS02730.seq check: 6607 from: 1 to: 1038
MATEKFRPTKLDVARQGVSIATASRALADNPAAVASTRERIQQLASDLGYRANAQAARALRSRSNTIG
VIVPSQLINHYAAMVTIQSTASKAGLATIITNSNEDATMSGSLFELTSHGVGDIICVNEECANQLE
DLQKSGMPFVVLVDRELPGDSTIPTATSNPQPGAAAVELLAHNNALPIGYLSGPMDDTGREKLEDFKA
ACANSKIGELQVLFGGYEQSVGFEGATKLLDQAKTLFAGDSMMTIGVIEACHKAGLVIGKDVSVTGFD
THFLFALQPLFTVIDQNVQELAQRAVSILTELIAGTVPSVTKTITPAILIHRESIINSTLRKKDCLPN
E

>RXS02818 TRANSLATE of: RXS02818.seq check: 4037 from: 1 to: 606
YSRKFLTQVWIRDNVGDYKGLTDTAFRKKLQRLDAYLRRVGVPIEQFTVTSIAEGQQAYRLAQDSYK
LPEVEETPDEAAVLGMAGEMGHNLGAFARSGWTKLAAGGAQRDLSTSTALTNAGDGLSGSLATDLAI
IKARQLGKQISFEYRRAPKDAPSLRHMDPWGLVPERDRIYLVGFDLRQEAERTFRITRVRIKIL

>RXS03219 TRANSLATE of: RXS03219.seq check: 1 from 1 to: 978
VKLTDAARACVGGVGTASRAISGRGSVDAAATKRLGLVAAAEKLGYRTNMAARLENKRTVTGLIVPGII
NYFTESATVQGLDGLKSGYQLVTSVTDGAEKERRAISMLNRQVQAVVHVPVNPQAKFKPGFKVVELN
RRSDLNRPTVTSDDATGLKELALHLDQGYRDIQVGLPAELSTADRRKIGFIDNALETATQGRIGREEL
RFVRVHSRYSPTGGYEAFEFNRNDLPQIVPVELTGLVLKATQGRIGKISDDSLACYGVAEWLAVWG
PGIIVFAPDLPMAGAAATQVLTLDLAAPEPNHLSIPGLIVRGITPKV